

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:09:56 ; Search time 20.0758 Seconds
(without alignments)
394.147 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549

Sequence: 1 ELTQSPSSVASVGDRTVITR.....QANSPFYTGQGTKEIKR 106

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	518	94.4	233	US-08-812-586-45	Sequence 45, Appl
2	518	94.4	233	US-09-535-832A-42	Sequence 42, Appl
3	475	86.5	236	US-09-859-053-30	Sequence 30, Appl
4	466	84.9	109	US-07-934-373C-3	Sequence 3, Appl
5	466	84.9	109	US-08-437-642B-3	Sequence 3, Appl
6	466	84.9	109	US-08-146-206C-3	Sequence 3, Appl
7	466	84.9	109	US-09-705-686-3	Sequence 3, Appl
8	466	84.9	109	US-09-705-392A-3	Sequence 3, Appl
9	466	84.9	109	US-09-705-398-3	Sequence 3, Appl
10	466	84.9	109	PCT-US93-07832-3	Sequence 3, Appl
11	463	84.3	107	US-09-240-274-40	Sequence 40, Appl
12	460	83.8	107	US-08-276-852-104	Sequence 104, App
13	460	83.8	107	US-08-899-575-104	Sequence 104, App
14	460	83.8	107	US-08-899-575-104	Sequence 104, App
15	460	83.8	107	PCT-US95-08743-104	Sequence 104, App
16	460	83.8	108	US-08-974-889-3	Sequence 3, Appl
17	460	83.8	108	US-09-795-798-3	Sequence 3, Appl
18	459	83.6	128	US-08-253-372A-14	Sequence 14, Appl
19	459	83.6	128	US-08-468-671-14	Sequence 14, Appl
20	457	83.2	107	US-08-276-852-84	Sequence 84, Appl
21	457	83.2	107	US-08-899-575-84	Sequence 84, Appl
22	457	83.2	107	US-08-899-575-84	Sequence 84, Appl
23	457	83.2	107	US-09-240-274-175	Sequence 175, App
24	457	83.2	107	US-09-240-274-176	Sequence 176, App
25	457	83.2	107	PCT-US95-08743-84	Sequence 84, Appl
26	456	83.1	107	US-09-240-274-156	Sequence 156, App
27	456	83.1	109	US-09-157-370-3	Sequence 3, Appl

28	455	82.9	107	US-07-934-373C-18	Sequence 18, Appl
29	455	82.9	107	US-08-437-642B-18	Sequence 18, Appl
30	455	82.9	107	US-08-146-206C-18	Sequence 18, Appl
31	455	82.9	107	US-09-648-067A-14	Sequence 14, Appl
32	455	82.9	107	US-09-705-686-18	Sequence 18, Appl
33	455	82.9	107	US-09-705-392A-18	Sequence 18, Appl
34	455	82.9	107	US-09-705-398-18	Sequence 18, Appl
35	455	82.9	107	PCT-US93-07832-18	Sequence 18, Appl
36	454	82.7	109	US-09-025-7698-28	Sequence 28, Appl
37	454	82.7	109	US-09-025-7698-43	Sequence 43, Appl
38	454	82.7	109	US-09-480-070A-28	Sequence 28, Appl
39	454	82.7	109	US-09-480-070A-43	Sequence 43, Appl
40	454	82.7	109	US-09-490-153-28	Sequence 28, Appl
41	454	82.7	109	US-09-490-153-43	Sequence 43, Appl
42	454	82.7	109	US-09-490-324-28	Sequence 28, Appl
43	454	82.7	109	US-09-490-324-43	Sequence 43, Appl
44	453	82.5	108	US-08-652-816A-4	Sequence 4, Appl
45	452	82.3	107	US-08-276-852-105	Sequence 105, App

ALIGNMENTS

RESULT 1

US-08-812-586-45

Sequence 45, Application US/08812586

Patent No. 6048704

GENERAL INFORMATION:

APPLICANT: Martin David Tilson

TITLE OF INVENTION: PRIORITD AND RECOMBINANT ANTIGENIC

TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)

TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESS: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/812,586

FILING DATE: 07-MAR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/53862-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 233 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-812-586-45

Query Match 94.4%; Score 518; DB 3; Length 233;

Best Local Similarity 96.2%; Pred. No. 4, 1e-41;

Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTRASQGISWLAHQHGRKPKLLIYSASSLSGCVSRF 60

DB 23 ELTQSPSSVASVGDRTVITTRASQGISWLAHQHGRKPKLLIYSASSLSGCVSRF 82

Qy 61 SGGSGTDFSLTISLQPEDSATYCCQANSFPYTGQTKVEIKR 106
Db 83 SGGSGTDFSLTISLQPEDSATYCCQANSFPYTGQTKVEIKR 128

RESULT 2

US-09-535-832A-42
; Sequence 42, Application US/09535832A
; Patent No. 6537769
; GENERAL INFORMATION:
; APPLICANT: Tilson, Martin David
; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
; TITLE OF INVENTION: With Abdominal Aortic Aneurysm (AAA) Disease, and
; TITLE OF INVENTION: Diagnostic and Therapeutic use Thereof
; FILE REFERENCE: 53862-AZ
; CURRENT APPLICATION NUMBER: US/09/535, 832A
; CURRENT FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-832A-42

Query Match 94.4%; Score 518; DB 4; Length 233;
Best Local Similarity 96.2%; Pred. No. 4.1e-41;
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVASVGDRTVITTCRASQGISLWLYOHQPKKLIYASASSLQSGVPSRF 60
Db 23 ELTQSPSSVASVGDRTVITTCRASQGISLWLYOHQPKKLIYASASSLQSGVPSRF 82
Qy 61 SGGSGTDFSLTISLQPEDSATYCCQANSFPYTGQTKVEIKR 106
Db 83 SGGSGTDFSLTISLQPEDSATYCCQANSFPYTGQTKVEIKR 128

RESULT 3

US-09-859-053-30
; Sequence 30, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. 6803039uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIN AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859, 053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-30

Query Match 86.5%; Score 475; DB 4; Length 236;
Best Local Similarity 88.7%; Pred. No. 4.4e-37;
Matches 94; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVASVGDRTVITTCRASQGISLWLYOHQPKKLIYASASSLQSGVPSRF 60
Db 25 QMTQSPSSVASVGDRTVITTCRASQGISLWLYOHQPKKLIYASASSLQSGVPSRF 84
Qy 61 SGGSGTDFSLTISLQPEDSATYCCQANSFPYTGQTKVEIKR 106

Db 85 SGGSGTDFSLTISLQPEDSATYCCQANSFPYTGQTKVEIKR 130

RESULT 4

US-07-934-373C-3
; Sequence 3, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9861

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-07-934-373C-3

Query Match 84.9%; Score 466; DB 2; Length 109;
Best Local Similarity 84.9%; Pred. No. 1.3e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVASVGDRTVITTCRASQGISLWLYOHQPKKLIYASASSLQSGVPSRF 60
Db 3 QMTQSPSSLASVGDRTVITTCRASQDVSYLWYQKPKKLIYASASSLQSGVPSRF 62
Qy 61 SGGSGTDFSLTISLQPEDSATYCCQANSFPYTGQTKVEIKR 106
Db 63 SGGSGTDFSLTISLQPEDSATYCCQANSFPYTGQTKVEIKR 108

RESULT 5

US-08-437-642B-3
; Sequence 3, Application US/08437642B
; Patent No. 6034297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.

Qy 1 ELTQSPSSVASVGDRTVITTCRASQGISLWLYOHQPKKLIYASASSLQSGVPSRF 60
Db 25 QMTQSPSSVASVGDRTVITTCRASQGISLWLYOHQPKKLIYASASSLQSGVPSRF 84
Qy 61 SGGSGTDFSLTISLQPEDSATYCCQANSFPYTGQTKVEIKR 106


```
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-3

Query Match      84.9%; Score 466; DB 3; Length 109;
Best Local Similarity 84.9%; Pred. No. 1.3e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Cy 1 ELTQSPSSVASVGDRTTTCRASQGISLWLYQHOGKAPKLLIYSASSLSQGVSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSLASVGDRTTTCRASQDVSSYLAWYQKRGKAPKLLIYAASLSQGVSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Cy 61 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGQGTVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SGSGSGTDFTLTISLQPEDPATYCCQYNSLPYTFGQGTVEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
US-08-146-206C-3
Sequence 3, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-3

Query Match      84.9%; Score 466; DB 4; Length 109;
Best Local Similarity 84.9%; Pred. No. 1.3e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Cy 1 ELTQSPSSVASVGDRTTTCRASQGISLWLYQHOGKAPKLLIYSASSLSQGVSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSLASVGDRTTTCRASQDVSSYLAWYQKRGKAPKLLIYAASLSQGVSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Cy 61 SGSGYGTDFSLTISLQPEDSATYCCQANSFPYTFGQGTVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SGSGSGTDFTLTISLQPEDPATYCCQYNSLPYTFGQGTVEIKR 108
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RESULT 7
US-09-705-686-3
Sequence 3, Application US/09705686
Patent No. 6639055
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
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?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 109 amino acids
?      TYPE: Amino Acid
?      TOPOLOGY: Linear
?      SEQUENCE DESCRIPTION: SPQ ID NO: 3
US-09-705-666-3

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Query Match	84.9%	Score 466;	DB 4;	Length 109;
Best Local Similarity	84.9%	Pred. No. 1.3e-36;		
Matches 90;	Conservative 9;	Mismatches 7;	Indels 0;	Gaps 0;

QY 1 ELTGPSSVSA SVGDRVTITCTASQGSISSLWAWQHQPCKAPKLLIYSASSLQSGVPSRF 60
:::|||||:|||||:|||||:|||||:|||||:
Dd 3 QMTGPSSLSASVGDRVITICTASQDVSSYLAWYQQPKPAFKLLIYAASSLSLEGVPSRF 62

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QY      61 SGGSGYGDPSLTITSSIQFEDSATYCCQANSFPTFGQGTKEIKR 106
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Db      63 SGGSGTDFLTITISSIQEDPATYCCQYNLSPTTFGQGTKEIKR 109

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RESULT 8
US-09-705-392A-3
; Sequence 3, Application US/09705392A

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1  APPLICANT: Carter, Paul J.
2  Presta, Leonard G.
3  TITLE OF INVENTION: Method for Making Humanized Antibodies
4  NUMBER OF SEQUENCES: 36
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE: Genentech, Inc.
7  STREET: 1 DNA Way
8  CITY: South San Francisco
9  STATE: California
10 COUNTRY: USA
11 ZIP: 94080
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: WinPatIn (Genentech)
18
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/09/705,392A
21 FILING DATE: 02-No. 6719971-2002
22 CLASSIFICATION: <Unknown>
23
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 08/146206
26 FILING DATE: 17-NOV-1993
27 APPLICATION NUMBER: 07/715272
28 FILING DATE: 14-JUN-1991
29
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Lee, Wendy M.
32 REGISTRATION NUMBER: 40,378
33 REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: 650/225-1994
36 TELEFAX: 650/952-9881
37
38 INFORMATION FOR SEQ ID NO: 3:
39
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 109 amino acids
42 TYPE: Amino Acid
43 TOPOLOGY: linear
44
45 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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Qy	1	ELTSPSSVSA	SVGDRTVITTCRASGSGISMTLAWYOHGQKAPKLLIYASSISQSGVPSRF	60
		:::>:::		
Db	3	QMTSPSSLSVSGGRVITTCRASGDVSSSYLAWYQOKGKPKLLIYASSISQSGVPSRF	62	
		:::>:::		
Matches	90;	Conservative	9;	Mismatches 7; Indels 0; Gaps 0;
Query Match	84.9%;	Score 466;	DB 4;	Length 109;
Best Local Similarity	84.9%;	Pred. No. 1,3e-36;		

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QY      61 SGGSGYGTDFSLTITSSLDGEDSATYYCCQANSPYTFGGQGTKEIKR 106
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      63 SGGSGGTDFLTITSSLDGEDFATYYCCQYNSSPYTFGGQGTKEIKR 108
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RESULT 9
US-09-705-398-3
; Sequence 3, Application US/09705398
; Patent No. 6800738

Matches	90, Conservative	9, Mismatches	7, Indels	0, Gaps
QY	1	ELTQSPSSVSVASVDRVTITTCRA	SOGSISMLAWTQHOHQKAPKLLIYASASSIOSGVPRF	60
Db	3	QMTQSPSSLSASVGRVTITTCRA	SQDVSYLAWTQOQKQKAPKLLIYASASSIOSGVPRF	62
QY	61	SGSGYGVNDFSLTISLSLOPES	ATSATYYCOQANSFPTTFGGGTVEIKR	106
Db	63	SGSSGSGNDFLLTISLSLOPES	ATATYYCOQYNLPTTFGGGTVEIKR	108

RESULT 10

RESULT 10
PCT-US93-07832-3
Sequence 3, Application PC/TUS9307832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd

```
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-07832-3

Query Match      84.9%; Score 466; DB 5; Length 109;
Best Local Similarity 84.9%; Pred. No. 1.3e-36;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Cy 1 ELTQSPSSVASVGDRTVITICRASQGISWLMWYOHQPGKAPKLLIYASASSLQSGVPSRF 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSLSASVGDRTVITICRASQDVSYLAWYQQRKPKLLIYAAASSLQSGVPSRF 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Cy 61 SSGSGYDTSLTITSLQFEDSATYCCQANSFPYTFGGQTKVEIKR 106
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SSGSGYDFTLTITSLQPEDPATYCCQVNSLPYTFGGQTKVEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-09-240-274-40
; Sequence 40, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 109
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US-09-240-274-40
Query Match      84.3%; Score 463; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 2.5e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Cy 1 ELTQSPSSVASVGDRTVITICRASQGISWLMWYOHQPGKAPKLLIYASASSLQSGVPSRF 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 ELTQSPSSLSASVGDRTVITICRASQGISWLMWYQQRKPKLLIYAAASSLQSGVPSRF 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Cy 61 SSGSGYDTSLTITSLQFEDSATYCCQANSFPYTFGGQTKVEIKR 106
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SSGSGYDTSLTITSLQPEDPATYCCQVNSLPYTFGGQTKVEIKR 107
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-08-276-852-104
; Sequence 104, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-852-104

Query Match      83.8%; Score 460; DB 1; Length 107;
Best Local Similarity 85.8%; Pred. No. 4.8e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Cy 1 ELTQSPSSVASVGDRTVITICRASQGISWLMWYOHQPGKAPKLLIYASASSLQSGVPSRF 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 ELTQSPSSLSASVGDRTVITICRASQGISWLMWYQQRKPKLLIYAAASSLQSGVPSRF 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 61 SSGSGYDFSLTISLQPEDSATYVCOQANSFYTFQGTVEIKR 106
Db 61 SSGSGYDFSLTISLQPEDPATYVCOQSYSTPYTFQGTVEIKR 106

RESULT 13

US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbos, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Query Match 83.8%; Score 460; DB 1; Length 107;
Best Local Similarity 85.8%; Pred. No. 4.8e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSAVGDRTYITTCRASQGISISWLAHYOHQPGAKPKLLIYSASSLSQGVSRF 60
Db 1 ELTQSPSSLSASVGDRTYITTCRASQGISISYLMWYQKPGAKPKLLIYAASSLQGVSRF 60
QY 61 SSGSGYDFSLTISLQPEDSATYVCOQANSFYTFQGTVEIKR 106
Db 61 SSGSGYDFSLTISLQPEDPATYVCOQSYSTPYTFQGTVEIKR 106

RESULT 14

US-08-899-575-104
; Sequence 104, Application US/08899575

; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbos, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRI452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-104

Query Match 83.8%; Score 460; DB 1; Length 107;
Best Local Similarity 85.8%; Pred. No. 4.8e-36;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSAVGDRTYITTCRASQGISISWLAHYOHQPGAKPKLLIYSASSLSQGVSRF 60
Db 1 ELTQSPSSLSASVGDRTYITTCRASQGISISYLMWYQKPGAKPKLLIYAASSLQGVSRF 60
QY 61 SSGSGYDFSLTISLQPEDSATYVCOQANSFYTFQGTVEIKR 106
Db 61 SSGSGYDFSLTISLQPEDPATYVCOQSYSTPYTFQGTVEIKR 106

RESULT 15

PCT-US95-08743-104
; Sequence 104, Application PC/TUS9508743
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

US-08-899-575-104
; Sequence 104, Application US/08899575

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/08743
 FILING DATE: 11-JUL-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/276,852
 FILING DATE: 18-JUL-1994
 INFORMATION FOR SEQ ID NO: 104:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULAR TYPE: protein
 PCT-US95-08743-104

Query Match 83.8%; Score 460; DB 5; Length 107;
 Best Local Similarity 85.8%; Pred. No. 4.8e-36;
 Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY	1	ELTQSPSSVSAVGDRVTITCRASOGISWLAWYOHQKAPKLLIYSASSLSGVP	SRF	60
DB	1	ELTQSPSSLSASVGDRTITCRASQSISSYLNWYQKPKLLIYASSLSGVP	SRF	60
QY	61	SGSGGTDFELTISLSQFEDSATYCCQANSFYTFGQGTKVEIKR		106
DB	61	SGSGSGTDFLTITSLQPEDFATYCCQSYSTPYTFGQGTKLEIKR		106

Search completed: July 26, 2005, 09:30:02
 Job time: 21.0758 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 09:07:26 ; Search time 13.6515 Seconds
(without alignments)
747.095 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549

Sequence: 1 ELTQSPSSVSAVGDVRLT.....QANSPFYFGGTKEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	84.2	117	2	S46376 Ig kappa chain V-J
2	462	84.2	125	2	S40316 Ig kappa chain - h
3	459	83.6	125	2	S40333 Ig kappa chain V-J
4	455	82.9	125	2	S40336 Ig kappa chain V-J
5	454.5	82.8	124	2	S40336 Ig kappa chain V-J
6	454	82.7	130	2	S40368 Ig kappa chain - h
7	451	82.1	128	2	S46372 Ig kappa chain var
8	451	82.1	131	2	S40352 Ig kappa chain V-J
9	450	82.0	105	2	S36266 Ig kappa chain V-J
10	447	81.4	127	2	S40367 Ig kappa chain V-J
11	446	81.2	108	2	S19674 Ig kappa chain V r
12	445	81.1	117	2	S38646 Ig kappa chain V r
13	445	81.1	117	2	S46371 Ig kappa chain V-J
14	444	80.9	123	2	S40331 Ig kappa chain - h
15	444	80.9	132	2	S40334 Ig kappa chain - h
16	443	80.7	108	2	S49047 Ig kappa chain V r
17	441	80.3	108	2	S47182 Ig kappa chain - h
18	441	80.3	109	2	S31998 Ig kappa chain - h
19	441	80.3	124	2	S40318 Ig kappa chain V r
20	439.5	80.1	108	2	S30521 Ig kappa chain V r
21	439	80.0	129	2	S40369 Ig kappa chain V r
22	437	79.6	107	2	S36264 Ig kappa chain - h
23	435.5	79.3	108	2	S34007 Ig kappa chain V r
24	435	79.2	108	1	K1HUBN Ig kappa chain V-I
25	434.5	79.1	107	2	S36275 Ig kappa chain V
26	434	79.1	108	1	K1HUMS Ig kappa chain V-I
27	434	79.1	108	2	S44122 Ig kappa chain V r
28	433	78.9	117	2	S21527 Ig kappa chain pre
29	432	78.7	108	2	S36283 Ig lambda chain V

30	431.5	78.6	107	2	S47183 Ig kappa chain - h
31	431	78.5	107	2	S36262 Ig lambda chain V
32	428	78.0	107	2	S36269 Ig lambda chain V
33	427	77.8	109	2	S31981 Ig kappa chain - h
34	426.5	77.7	107	1	K1HUMR Ig kappa chain V-I
35	426	77.6	108	2	S36277 Ig lambda chain V
36	426	77.6	109	2	S31979 Ig kappa chain - h
37	426	77.6	110	2	PN0535 Ig kappa chain V r
38	426	77.6	122	2	S40370 Ig kappa chain - h
39	426	77.6	141	2	A49334 Ig kappa chain V-I
40	424	77.2	107	2	I69017 anti-HIV envelope
41	424	77.2	108	1	K1HUMK Ig kappa chain V-I
42	424	77.2	129	1	K1HUMK Ig kappa chain pre
43	423	77.0	108	1	K1HUGL Ig kappa chain V-I
44	423	77.0	108	1	K1HUMU Ig kappa chain V-I
45	423	77.0	126	2	S40335 Ig kappa chain V-J

ALIGNMENTS

RESULT 1
S46376
Ig kappa chain V-J region (713-14) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46376, S38649, P.; Zouali, M.
R:Benjamin, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re-
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46376
A:Molecule type: mRNA
A:Residues: 1-117 <BEN>
A:Cross-references: EMBL:Z27177; NID:9415969; PIDN:CAA81701.1; PID:9415970
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:25-99/Domain: immunoglobulin homology <IMV>

Query Match 84.2%; Score 462; DB 2; Length 117;
Best Local Similarity 84.9%; Pred. No. 2.5e-32;
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSAVGDVRLTICRAGGISMLAWYQHOGKAPKLLIYASSLQGVPERF 60
Db 12 QMTQSPSSVSAISDRVLTICRASQDISMLAWIQKRPKALLIYASSLQGVPLRF 71

Qy 61 SGSGVGTDFSLITISLQFEDSATYCCOANSFPYTFGGTKEIKR 106
Db 72 SGSGSGTDFLTITISLQPEPDATYCCOANSFPRGFGTKEIKR 117

RESULT 2
S40316
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40316
R:Klein, R.; Jaenichen, R.; Zachau, H. G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080691; PMID:8258341
A:Accession: S40316
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72426
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:31-105/Domain: immunoglobulin homology <IMV>

Query Match 84.2%; Score 462; DB 2; Length 125;
Best Local Similarity 85.8%; Pred. No. 2.7e-32;

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Matches 91; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSAVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSGVSRRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 18 QLTQSPSSVSAVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYHISLSLGVSRRF 77
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 SSGSGYGFDSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 78 SSGSGYGFDSLTISLQFEDPATYCCQANSFPYTFGGTKVEIKR 123

RESULT 3
S40333
Ig kappa chain V-J region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40333
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40333
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-125 <KLE>
A/Cross-references: EMBL:X72443; NID:9441354; PIDN:CAAS1111.1; PID:9441355
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-108/Domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 459; DB 2; Length 125;
Best Local Similarity 82.9%; Pred. No. 4.8e-32;
Matches 87; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSAVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSGVSRRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 QMTQSPPTLSAVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYASLSGVSRRF 80
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 SSGSGYGFDSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 SSGSGYGFDSLTISLQFEDPATYCCQANSFPYTFGGTKVEIKR 125

RESULT 4
S40349
Ig kappa chain V-J region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C/Accession: S40349
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40349
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-125 <KLE>
A/Cross-references: EMBL:X72459; NID:9441386; PIDN:CAAS1127.1; PID:9441387
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/33-107/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 455; DB 2; Length 125;
Best Local Similarity 84.9%; Pred. No. 1e-31;
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSAVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSGVSRRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QLTQSPSSVSAVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYDASSLSGVSRRF 79
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 SSGSGYGFDSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 SSGSGYGFDSLTISLQFEDPATYCCQANSFPYTFGGTKVEIKR 125
```

```
Matches 90; Conservative 10; Mismatches 6; Indels 1; Gaps 1;

Qy 1 ELTQSPSSVSAVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSGVSRRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 18 QLTQSPSSVSAVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYAASTLSGVSRRF 77
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 SSGSGYGFDSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 78 SSGSGYGFDSLTISLQFEDPATYCCQANSFPYTFGGTKVEIKR 124

RESULT 5
S40336
Ig kappa chain V-J region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40336
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40336
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-124 <KLE>
A/Cross-references: EMBL:X72446; NID:9441360; PIDN:CAAS1114.1; PID:9441361
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/31-105/Domain: immunoglobulin homology <IMM>

Query Match 82.8%; Score 454.5; DB 2; Length 124;
Best Local Similarity 84.1%; Pred. No. 1.1e-31;
Matches 90; Conservative 10; Mismatches 6; Indels 1; Gaps 1;

Qy 1 ELTQSPSSVSAVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSGVSRRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 18 QLTQSPSSVSAVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYAASTLSGVSRRF 77
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 SSGSGYGFDSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 78 SSGSGYGFDSLTISLQFEDPATYCCQANSFPYTFGGTKVEIKR 124

RESULT 6
S40368
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40368
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40368
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-130 <KLE>
A/Cross-references: EMBL:X72478; NID:9441424; PIDN:CAAS1146.1; PID:9441425
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/33-107/Domain: immunoglobulin homology <IMM>

Query Match 82.7%; Score 454; DB 2; Length 130;
Best Local Similarity 83.0%; Pred. No. 1.3e-31;
Matches 88; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSAVGDRTVITTCRASQGISWLAHYQHOPGKAPKLLIYSASSLSGVSRRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QMTQSPPTLSAVGDRTVITTCRASQDVAGLAHYQHOPGKAPKLLIYASLSGVSRRF 79
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 SSGSGYGFDSLTISLQFEDSATYCCQANSFPYTFGGTKVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 SSGSGYGFDSLTISLQFEDPATYCCQANSFPYTFGGTKVEIKR 125

RESULT 7
S46372
IG light chain variable region (VJ) - human
C/Species: Homo sapiens (man)
C/Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C/Accession: S46372
R/Bensimon, C.; Chastagner, P.; Zouali, M.
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 08:52:21 ; Search time 66.6515 Seconds

(without alignments)
814.391 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549
Sequence: 1 ELTQSPSSVASVGDVRLTIF.....QQANSPFYFGQTKVEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	88.0	236	2	O6GMX8
2	444	80.9	236	2	O6GMW1
3	443	80.7	236	2	O6PIH7
4	437	79.6	108	2	O9UL70
5	437	79.6	108	2	O9UL77
6	435	79.2	108	1	KV1V_HUMAN
7	434	79.1	108	1	KV1S_HUMAN
8	434	79.1	108	2	O9UL79
9	429	78.1	236	2	O6GMX9
10	427	77.8	244	2	O65ZC8
11	426.5	77.7	107	2	KV1D_HUMAN
12	426.5	77.7	107	2	O96SA9
13	426	77.6	234	2	O7Z473
14	425	77.4	236	2	O7Z3Y4
15	424	77.2	108	1	KV1R_HUMAN
16	424	77.2	129	1	KV1W_HUMAN
17	424	77.0	236	2	O6PIT5
18	423	77.0	108	1	KV1G_HUMAN
19	423	77.0	108	1	KV1H_HUMAN
20	423	77.0	240	2	O65ZC9
21	419	76.3	108	1	KV1F_HUMAN
22	419	76.3	108	1	KV1L_HUMAN
23	416	75.8	108	1	KV1O_HUMAN
24	416	75.8	236	2	O6GMX0
25	416	75.8	236	2	O6PIH4
26	413	75.2	108	1	KV1B_HUMAN
27	411.5	75.0	107	2	O9UL81
28	410	74.7	108	1	KV1M_HUMAN
29	408	74.3	108	1	KV1E_HUMAN
30	406	74.0	108	1	KV1A_HUMAN
31	405	73.8	108	1	KV1P_HUMAN

32	402	73.2	117	1	KV1I_HUMAN	P01601 homo sapien
33	401	73.0	108	1	KV1N_HUMAN	P01606 homo sapien
34	401	73.0	108	1	KV1Y_HUMAN	P80362 homo sapien
35	394	71.8	117	1	KV1J_HUMAN	P01602 homo sapien
36	393	71.6	108	1	KV1C_HUMAN	P01595 homo sapien
37	391	71.2	108	1	KV1K_HUMAN	P01603 homo sapien
38	385	70.1	108	1	KV1Q_HUMAN	P01609 homo sapien
39	385	70.1	129	1	KV1X_HUMAN	P04432 homo sapien
40	383	69.8	108	1	KV5S_MOUSE	P01652 mus musculus
41	382	69.6	108	2	O9UL83	O9UL83 homo sapien
42	380	69.2	108	1	KV5Q_MOUSE	P01650 mus musculus
43	376	68.5	108	1	KV5T_MOUSE	P01653 mus musculus
44	374	68.1	236	2	O7ES98	O7ES98 mus musculus
45	373	67.9	108	1	KV5K_MOUSE	P01644 mus musculus

ALIGNMENTS

RESULT 1
O6GMX8 PRELIMINARY; PRT; 236 AA.
AC O6GMX8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bork S.S., Lequellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smalins D.B., Scherch A., Schein J.B.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -
DR InterPro; IPR003599; IG
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00654; CI-set; I.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
Query Match 88.0%; Score 483; DB 2; Length 236;
Best Local Similarity 87.7%; Pred. No. 7.5e-41;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
QY 1 ELTQSPSSVASGVDRVTITTCRASQGISSWLAWQHPGKAPKLLIYASASSLQSGVPSRF 60
DB 25 QMTQSPSSVASGVDRVTITTCRASQGISSWLAWQHPGKAPKLLIYASASSLQSGVPSRF 84
QY 61 SSGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFQGTKEIKR 106
DB 85 SSGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFQGTKEIKR 130
RESULT 2
ID 06GMM1 PRELIMINARY; PRT; 236 AA.
AC 06GMM1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whitting R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.M., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791.1; AAH3791.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003596; IG_v.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00407; IG; 1.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BF6EA087AFAC437 CRC64;

Query Match 80.9%; Score 444; DB 2; Length 236;
Best Local Similarity 82.1%; Pred. No. 6.8e-37;
Matches 87; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
QY 1 ELTQSPSSVASGVDRVTITTCRASQGISSWLAWQHPGKAPKLLIYASASSLQSGVPSRF 60
DB 25 QMTQSPSSVASGVDRVTITTCRASQGISSWLAWQHPGKAPKLLIYASASSLQSGVPSRF 84
QY 61 SSGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFQGTKEIKR 106
DB 85 SSGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFQGTKEIKR 130
RESULT 3
ID 06PIH7 PRELIMINARY; PRT; 236 AA.
AC 06PIH7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whitting R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.M., Young A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -.
DR HSP; P01607; IAR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003596; IG_v.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;
Query Match 80.7%; Score 443; DB 2; Length 236;
Best Local Similarity 83.0%; Pred. No. 8.5e-37;
Matches 88; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

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Qy 1 ELTQSPSSVSVASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 QLTQSPSFLSASVGDRTVITTCRASQGISWLAWYQKRGKAPNLLIYAASLSQGVPSRF 84
Qy 61 SSGSGYGFDFSLTISLSQPEDSATYCCQANSFPYTFGGGTVEIKR 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 SSGSGSGTDFLTITSLQPEDPATYCCQQLNSPPTFGGTVEIKR 130

RESULT 4
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70
AC Q9UL70;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
    (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
    fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IBMW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCC437 CRC64;

Query Match 79.6%; Score 437; DB 2; Length 108;
Best Local Similarity 80.2%; Pred. No. 1.5e-36;
Matches 85; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSVASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSFLSASVGDRTVITTCRASQGISWLAWYQKRGKAPNLLIYAASLSQGVPSRF 62
Qy 61 SSGSGYGFDFSLTISLSQPEDSATYCCQANSFPYTFGGGTVEIKR 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SSGSGSGTDFLTITSLQPEDPATYCCQKNSAPPTFGGTVEIKR 108

RESULT 5
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70
AC Q9UL70;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
    (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
    fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; IBMW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 79.6%; Score 437; DB 2; Length 108;
Best Local Similarity 81.1%; Pred. No. 1.5e-36;
Matches 86; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSVASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSFLSASVGDRTVITTCRASQGISWLAWYQKRGKAPNLLIYAASLSQGVPSRF 62
Qy 61 SSGSGYGFDFSLTISLSQPEDSATYCCQANSFPYTFGGGTVEIKR 106
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SSGSGSGTDFLTITSLQPEDPATYCCQSYSTSWTFGGGTVEIKR 108

RESULT 6
KVIV_HUMAN STANDARD; PRT; 108 AA.
ID KVIV_HUMAN
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
RA Dwyer F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; KIHUEN.
DR HSSP; P80362; IWTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KM Amyloid; Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1
FT DOMAIN 23
FT DOMAIN 24
FT DOMAIN 34
FT DOMAIN 35
FT DOMAIN 49
FT DOMAIN 50
FT DOMAIN 56
FT DOMAIN 57
FT DOMAIN 88
FT DOMAIN 89
FT DOMAIN 97
FT DOMAIN 98
FT DISULFID 98
FT NON_TER 23
FT SEQUENCE 108 AA; 11840 MW; CD3PD944FE96FD37 CRC64;

Query Match 79.2%; Score 435; DB 1; Length 108;
Best Local Similarity 78.3%; Pred. No. 2.4e-36;
Matches 83; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ELTQSPSSVSVASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
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[illegible]

DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98271139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Benney S.M.,
RA Young D.C.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR PIR; S23638; S23638.
DR PIR; S30521; S30521.
DR PIR; S34090; S34090.
DR HSSP; P01607; IBMW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR NON_TER 1
FT TER 1
FT 108 108
SQ SEQUENCE 108 AA; 11787 MW; DBS645F19724FBAE CRC64;

Query Match 79.1%; Score 434; DB 2; Length 108;
Best Local Similarity 81.0%; Pred. No. 3e-36;
Matches 85; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Qy 2 LTQSPSSVASVGEGRVITTCRASGCTISMLAWMOHQGKAPKLLIYASASSLOSVPSPRS 61
Db 4 MTQSPSLASSTGRTVITSCMSQGISLYLAWYQKQKAPKELLITYASTLQSGVSPRS 63
62 GSGYGTDFSLTISLQFEDSATYVCCQANSPFYFGGTKEIKR 106
64 GSGGCTDFTLTISCLQSEDPRTYCCQGYSPFPFGGTKEIKR 108

RESULT 9
OG6GMX9 PRELIMINARY; PRT; 236 AA.
AC OG6GMX9;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Hypoetical protein.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Fellingsold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schutler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rudin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carantini P., Prange C.,
RA Raha S.S., Loeblano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schermer A., Schein J.E.,
RA Jones S.J., Maitra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC073763; AAH73763.1; -
DR InterPro; IPR003599; Ig_1.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; Ig_2.
DR SMART; SM00407; Ig_c1; 1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CF7 CRC64;

Query Match 78.1%; Score 429; DB 2; Length 236;
Best Local Similarity 78.3%; Pred. No. 2.2e-35;
Matches 83; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 ELTOSPSVSASVGDRTVITCRASQGISSWLAWYOHQPGKPKLLIYSASSLSQGVPSRF 60
DB 25 QMTOSPSLSASVGHRTVITCRASQNVSRWLAWYQGRPEKPKSLIYATSSLSHGVSRRF 84
QY 61 SGSGYGDPSLTSSLOFEDSATYCCOANSFPYTFGCGTVEIKR 106
DB 85 SGSGSGTDFLTSSLOPEDPATYCCOQYNTPPLTFGGTVEIKR 130

RESULT 10
ID Q65ZC8 PRELIMINARY; PRT; 244 AA.
AC Q65ZC8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scfv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97362799; PubMed=9219263;
RA Kontersmann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies";
RL Nat. Biotechnol. 15:628-631(1997).
DR EMBL; Y13057; CAAT73500.1; -
DR InterPro; IPR003599; Ig_1.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; Ig_2.
DR SMART; SM00406; IgV_2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1 1
FT NON_TER 244 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 77.8%; Score 427; DB 2; Length 244;
Best Local Similarity 75.5%; Pred. No. 3.7e-35;
Matches 80; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTOSPSVSASVGDRTVITCRASQGISSWLAWYOHQPGKPKLLIYSASSLSQGVPSRF 60

DB 139 QMTOSPSLTASIGDRVITCRASEGTHLAWYQGRKPKLLIYSASSLSGAPSRF 198
QY 61 SGSGYGDPSLTSSLOFEDSATYCCOANSFPYTFGCGTVEIKR 106
DB 199 SGSGSGTDFLTSSLOPDPATYCCOQYSNTPPLTFGGTVEIKR 244

RESULT 11
ID KVID HUMAN STANDARD; PRT; 107 AA.
AC P01596;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region CAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75075135; PubMed=4216454;
RA Milstein C.P., Deverson E.V.;
RT "Primary structure of kappa light chain from a human myeloma protein";
RL Eur. J. Biochem. 49:377-391(1974).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2) marker.
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.
DR PIR; A01864; KIHUAR.
DR HSSP; P80362; IWTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006935; P:immune response; NAS.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Direct protein sequencing; Glycoprotein; Immunoglobulin V region.
FT CARBOHYD 28 28
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;

Query Match 77.7%; Score 426.5; DB 1; Length 107;
Best Local Similarity 76.4%; Pred. No. 1.7e-35;
Matches 81; Conservative 15; Mismatches 9; Indels 1; Gaps 1;

QY 1 ELTOSPSVSASVGDRTVITCRASQGISSWLAWYOHQPGKPKLLIYSASSLSQGVPSRF 60
DB 3 QMTOSPSLTASVGDRAVITCRASQNVSRWLAWYQGRKPKLLIYSASSLSHGVSRRF 62
QY 61 SGSGYGDPSLTSSLOFEDSATYCCOANSFPYTFGCGTVEIKR 106
DB 63 SGSGSGTDFLTSSLPBBERATYCCOQYNTPFTFGGTVEIKR 107

RESULT 12
ID Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-mycosin immunoglobulin kappa light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB6785.1; -.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSSP; P01607; 1BWW.
DR InterPro; IPR007110; Ig_1like.
DR SMART; SM00406; IGV_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;

Query Match 77.7%; Score 426.5; DB 2; Length 107;
Best Local Similarity 82.1%; Pred. No. 1.7e-35;
Matches 87; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
Db 3 QMTQSPSSVASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 62
QY 61 GSGGYGTFSLTISLSQFEDSATYCCQANSFPYTFGGGTVEIKR 106
Db 63 GSGSGTDFTLTISLSQFEDSATYCCQANSFPYTFGGGTVEIKR 107

RESULT 13
Q72473 PRELIMINARY; PRT; 234 AA.
ID Q72473
AC Q72473;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshyuk S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunnaracne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
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RC TISSUE=Lung;
RA Strausberg R.;
RT Submitted (JUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -.
DR HSSP; P01834; 1HEZ.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003066; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-sect; 1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 77.6%; Score 426; DB 2; Length 234;
Best Local Similarity 78.1%; Pred. No. 4.5e-35;
Matches 82; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 2 LTQSPSSVASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 61
Db 24 MTQSPSSVASVGDRTVITTCRASQGISWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 63
QY 62 GSGGYGTFSLTISLSQFEDSATYCCQANSFPYTFGGGTVEIKR 106
Db 84 GSASGTFSLTISLSQFEDSATYCCQANSFPYTFGGGTVEIKR 128

RESULT 14
Q723Y4 PRELIMINARY; PRT; 236 AA.
ID Q723Y4
AC Q723Y4;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshyuk S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunnaracne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -.
DR HSSP; P01834; 1HEZ.
DR InterPro; IPR007110; Ig_1like.
```


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PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgG Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 41; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgG Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergenic patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific Fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The Fabs
CC - or a vaccine against a type I allergy is useful for diagnosing a type
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific Fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgG antibodies to Phi p 2. The present sequence represents the human IgG
CC Fab, clone 100 light chain protein of the invention
XX
SQ Sequence 106 AA;
Query Match 96.0%; Score 527; DB 5; Length 106;
Best Local Similarity 97.2%; Pred. No. 6,7e-30;
Matches 103; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 ELTQSPSSVASVGDRTYITCRASQGISWLAWYQHQPGRAPKLLIYSASLSQGVPSRF 60
Db 1 ELTQSPSSVASVGDRTYITCRASQGISWLAWYQHQPGRAPKLLIYSASLSQGVPSRF 60
QY 61 SSGSGYGTDFSLTISLSLPEDSATYCCQANSFYTFGGGTKEIKR 106
Db 61 SSGSGYGTDFSLTISLSLPEDSATYCCQANSFYTFGGGTKEIKR 106
Db
RESULT 2
ID AAB03713 standard; protein; 233 AA.
XX
AC AAB03713;
XX
DT 04-OCT-2000 (first entry)
XX
DE Immunoglobulin kappa amino acid sequence fragment.
XX
KM Aortic aneurysm-associated antigen protein; AAP; microfibrillar protein;
KM abdominal aortic aneurysm disease; treatment; detect; tolerance;
KM immunoglobulin kappa; IgK.
XX
OS Unidentified.
XX
PN US6048704-A.
XX
PD 11-APR-2000.
XX
PE 07-MAR-1997; 97US-00812586.
XX
PR 07-MAR-1996; 96US-0012976P.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Tilson MD;
XX
DR WPI; 2000-316895/27.
XX
XX Isolated microfibrillar protein for alleviating abdominal aortic aneurysm
PT disease is purified from human aortic tissue and binds immunoreactively
PT with immunoglobulin.
XX
PS Example 3; Col 29-31; 70pp; English.

XX
CC The present invention relates to an isolated microfibrillar protein of
CC approximately 40kD. The protein is isolated from human aortic tissue and
CC binds immunoreactively with immunoglobulin purified from human abdominal
CC aortic aneurysm (AAA) tissue. The protein is referred to as aortic
CC aneurysm-associated antigenic protein (AAP). The protein is capable of
CC forming a disulphide bonded dimer. The protein is immunoreactive with
CC human kappa immunoglobulin. Also included in the invention are
CC recombinantly produced human AAA proteins. AAP shows regions of homology
CC with the bovine microfibril associated glycoprotein MFAP-4 and also with
CC fibrinogen and vitronectin. The isolated microfibrillar protein is useful
CC for alleviating abdominal aortic aneurysm (AAA) disease and detecting the
CC presence of AAA-associated immunoglobulin bound to the human aortic
CC tissue. Antibodies directed against AAP can be used to detect AAA
CC disease. The recombinant protein can be used to induce tolerance to
CC antigenic AAA protein in the subject e.g. human. This sequence represents
CC an immunoglobulin kappa amino acid sequence. The sequence shares homology
CC with the AAP of the invention, it was used to identify and characterise
XX
SQ Sequence 233 AA;
Query Match 94.4%; Score 518; DB 3; Length 233;
Best Local Similarity 96.2%; Pred. No. 5,7e-29;
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 ELTQSPSSVASVGDRTYITCRASQGISWLAWYQHQPGRAPKLLIYSASLSQGVPSRF 60
Db 23 ELTQSPSSVASVGDRTYITCRASQGISWLAWYQHQPGRAPKLLIYSASLSQGVPSRF 82
QY 61 SSGSGYGTDFSLTISLSLPEDSATYCCQANSFYTFGGGTKEIKR 106
Db 83 SSGSGYGTDFSLTISLSLPEDSATYCCQANSFYTFGGGTKEIKR 128
Db
RESULT 3
ID ADB72874 standard; protein; 233 AA.
XX
AC ADB72874;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human AAA-associated immunoglobulin related polypeptide, SEQ ID No:42.
XX
KM Human; aortic tissue; immunoreactive; abdominal aortic aneurysm;
KM AAA-associated immunoglobulin 40kDa protein.
XX
OS Homo sapiens.
XX
PN US6537769-B1.
XX
PD 25-MAR-2003.
XX
PE 28-MAR-2000; 2000US-00535832.
XX
PR 07-MAR-1996; 96US-0012976P.
XX
PR 07-MAR-1997; 97US-00812586.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Tilson MD;
XX
DR WPI; 2003-687181/65.
XX
XX Purified protein useful in diagnosing abdominal aortic aneurysm disease
PT in subject, e.g. human, contains specified amino acids.
XX
PS Disclosure; Col 73-74; 67pp; English.
XX
XX The present invention relates to the isolation of a protein approximately
CC 40kDa which is purified from human aortic tissue. The protein is
CC immunoreactive with abdominal aortic aneurysms (AAA)-associated

immunoglobulin. The protein is useful for diagnosing AAA disease in a subject, e.g. human, by administering the protein or a composition comprising the protein. The inventive protein is capable of forming a disulphide-bonded dimer of 80 kDa. The present sequence of unknown CC function is given in the Sequence Listing but is not mentioned elsewhere in the specification.

XX Sequence 233 AA;

Query Match 94.4%; Score 518; DB 7; Length 233;
Best Local Similarity 96.2%; Pred. No. 5.7e-23;
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVCDRTVITTCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
23 ELTQSPSSVASVCDRTVITTCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 82

QY 61 SGSGCYGTFPSLTITSSLPEDSATYTCQANSFPYTFQGTVEIKR 106
83 SGSGCYGTFPSLTITSSLPEDSATYTCQANSFPYTFQGTVEIKR 128

RESULT 4
ADP22406
ID ADP22406 standard; protein; 107 AA.

XX ADP22406;

DT 09-SEP-2004 (first entry)

XX Human anti-TNFA antibody light chain variable region SEQ ID NO:312.

human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;
anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
antibacterial; antiinflammatory; antiporiatic; antirheumatic;
eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;
TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
bladder cancer; lung cancer; glioblastoma; stomach cancer;
endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
prostate cancer; immuno-mediated inflammatory disease;
rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
septic shock; cachexia; anorexia; multiple sclerosis.

XX Homo sapiens.

OS WO2004050683-A2.

PN 17-JUN-2004.

PD 02-DEC-2003; 2003WO-US038281.

PF 02-DEC-2002; 2002US-0430729P.

PR 02-DEC-2002; 2002US-0430729P.

XX (ABGE-) ABGENIX INC.

PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
PI Haak-Frendscho M, Rathnaswami P, Pigott C, Liang ML, Lee R;
PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;
PI WPI; 2004-480601/45.

XX New recombinant human monoclonal antibody that specifically binds to
PT Tumor Necrosis factor-alpha, useful for treating neoplastic disease such
PT as cancer, or immuno-mediated inflammatory diseases such as rheumatoid
PT arthritis.

XX Example 10; SEQ ID NO 312; 213pp; English.

XX The present invention describes a human monoclonal antibody (I) that
CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the

two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC (M1) the level of TNFA in a patient sample, comprising contacting with
CC (1), and detecting the level of binding between the antibody and TNFA in
CC the sample; (2) a composition comprising the antibody or its functional
CC fragment and a carrier; (3) treating (M2) an animal suffering from a
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC animal in need of treatment for the disease by administering the human
CC monoclonal antibody of (1); and (4) inhibiting (M3) TNFA induced
CC apoptosis in an animal by selecting an animal in need of treatment for
CC TNFA induced apoptosis by administering the human monoclonal antibody of
CC (1). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC antibacterial, antiinflammatory, antiporiatic, antirheumatic, eating-
CC disorder, immunomodulator, immunosuppressive, nephrotropic,
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC as a TNFA antagonist. The antibody (I) is useful in the preparation of
CC medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence represents a human anti-TNFA
CC antibody light chain variable region, which is used in the
CC exemplification of the present invention.

XX Sequence 107 AA;

Query Match 89.4%; Score 491; DB 8; Length 107;
Best Local Similarity 90.5%; Pred. No. 2.3e-27;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVCDRTVITTCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 60
3 QMTQSPSSVASVCDRTVITTCRASQGISSWLAWYQHOPGKAPKLLIYSASSLSQGVPSRF 62

QY 61 SGSGCYGTFPSLTITSSLPEDSATYTCQANSFPYTFQGTVEIKR 105
63 SGSGCYGTFPSLTITSSLPEDSATYTCQANSFPYTFQGTVEIKR 107

RESULT 5
ADP22216
ID ADP22216 standard; protein; 107 AA.

XX ADP22216;

DT 09-SEP-2004 (first entry)

XX Human anti-TNFA antibody heavy chain variable region SEQ ID NO:122.

human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;
anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
antibacterial; antiinflammatory; antiporiatic; antirheumatic;
eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;
TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
bladder cancer; lung cancer; glioblastoma; stomach cancer;
endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
prostate cancer; immuno-mediated inflammatory disease;
rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
septic shock; cachexia; anorexia; multiple sclerosis.

XX Homo sapiens.

OS WO2004050683-A2.

PN 17-JUN-2004.

PD 02-DEC-2003; 2003WO-US038281.

QY	Matches	93:	Conservative	7:	Mismatches	5:	Indels	0:	Gaps	0:
QY	1	ELTQSPSSVSA	YVGRVITTCRASGIGIS	SWLAWYOHQKGA	PKLLIYASSLSQSV	PERF	60			
DB	3	QMTQSPSSVSA	YVGRVITTCRASGIGIS	SWLAWYOHQKGA	PKLLIYASSLSQSV	PERF	62			
QY	61	SGSGGTDPS	LTISLQPEDSATY	YCOQANSFP	YPYFGGQTK	EIK	105			
DB	63	SGSGGTDPS	LTISLQPEDSATY	YCOQANSFP	YPYFGGQTK	EIK	107			
		RESULT 7								
		ABJ36940								
XX		ABJ36940	standard; protein; 223	AA.						
XX		ABJ36940;								
XX		01-MAY-2003	(first entry)							
DE		Anti-CD40	monoclonal antibody related protein	SEQ ID NO 66.						
KW		Antiallergic; haemostatic; immunomodulator; cyostatic; antibody;								
KW		human CD40; IL-12; IPS; lipopolysaccharide; IFNgamma; interferon gamma;								
KW		dendritic cell; high G28-5; CD95 expression; high G28-5; B cell line;								
KW		immunoadaptor; anti-tumour agent; immunosuppressant; allergy;								
KW		autoimmune disease; coagulation factor VIII inhibitor; anti-CD40.								
XX		Unidentified.								
OS		WO20028186-A1.								
PN		07-NOV-2002.								
PD		26-APR-2002; 2002WO-JP004292.								
XX		27-APR-2001; 2001WO-US013672.								
XX		11-MAY-2001; 2001JP-00142482.								
PR		05-OCT-2001; 2001JP-00310535.								
PR		26-OCT-2001; 2001US-00040244.								
XX		(KIRI) KIRIN BEER KK.								
XX		Mikayama T, Yoshida H, Force WR, Chen X, Takahashi N;								
PI		WP1; 2003-120463/11.								
DR		N-PSDB; ABT31882.								
PT		Anti-CD40 monoclonal antibody with antagonist/agonist activity to CD40.								
PT		or functional fragment, is useful in the treatment of e.g. autoimmune								
XX		diseases or cancer.								
XX		Claim 15; Page 60; 94pp; Japanese.								
PS		The invention relates to an antibody to human CD40, or its functional								
XX		fragment, has at least one of the following properties: acting on								
CC		dendritic cells to produce IL-12 in the presence of IPS								
CC		(lipopolysaccharide) and IFNgamma (interferon gamma); acting on dendritic								
CC		cells to activate maturity of the dendritic cells with high G28-5								
CC		antibody; and activating CD95 expression with high G28-5 antibody against								
CC		B cell line. Such antibodies or functional fragments can be used as								
CC		immunoadaptors, anti-tumour agents, immunosuppressants, and as remedies								
CC		for autoimmune diseases, allergy or coagulation factor VIII inhibitors								
CC		syndrome. This sequence represents a protein relating to the anti-CD40								
CC		monoclonal antibody of the invention								
XX		Sequence 223 AA;								
QY	Query Match	88.2%;	Score 484;	DB 6;	Length 223;					
QY	Best Local Similarity	87.7%;	Pred. No. 1.4e-26;							
QY	Matches	93;	Conservative	7;	Mismatches	5;	Indels	0;	Gaps	0;
QY	1	ELTQSPSSVSA	YVGRVITTCRASGIGIS	SWLAWYOHQKGA	PKLLIYASSLSQSV	PERF	60			
QY	1	ELTQSPSSVSA	YVGRVITTCRASGIGIS	SWLAWYOHQKGA	PKLLIYASSLSQSV	PERF	60			

[illegible]

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Db      23 QMTQSPSSVSASVDGRVTITCRASQVTSWLAHYQKPGKAPKLLITYAASSLSGVSRRF 82
QY      61 SSGSGYGFDFSLTISLQFEDSATYYCOQANSFPYTFGQGTKEIKR 106
Db      83 SSGSGGTFDFLTITISLQPEDFATYYCOQANSFPPTFGQGTKEIKR 128

RESULT 9
ADP03922
ID      ADP03922 standard; protein; 107 AA.
XX
AC      ADP03922;
XX
DT      29-JUL-2004 (first entry)
XX
DE      Murine-expressed anti-human CA IX monoclonal antibody VL protein -SEQ 62.
XX
KW      monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW      cytosol; colorectal neoplasm; renal cell carcinoma;
KW      cervical intraepithelial squamous neoplasia;
KW      cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KW      gene therapy; murine; mouse; human; light chain variable domain.
XX
OS      Unidentified.
XX
PN      WO2003048328-A2.
XX
PD      12-JUN-2003.
XX
PF      02-DEC-2002; 2002MO-US038550.
XX
PR      03-DEC-2001; 2001US-0337275P.
XX
PA      (ABGE-) ABGENIX INC.
XX
PI      Gudas J, Foltz I, Handa M, Gallo M;
XX
DR      WPI; 2003-523295/49.
XX
PT      New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT      colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT      intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS      Claim 3; SEQ ID NO 62; 89pp; English.
XX
CC      The invention relates to a novel isolated monoclonal antibody (mAb)
CC      comprising a heavy chain polypeptide and light chain polypeptide having a
CC      sequence chosen from one of 53 fully defined amino acid sequences given
CC      in the specification, where the antibody specifically binds carbonic
CC      anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC      demonstrates cytosolic activity and may be useful for treating a tumour,
CC      such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC      cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC      tumour or breast cancer, possibly via gene therapy. The current sequence
CC      is that of a murine-expressed anti-human CA IX monoclonal antibody VL
CC      (light chain variable domain) protein of the invention. The protein was
CC      generated via the introduction of the human CA IX protein into a
CC      transgenic mouse strain.
XX
SQ      Sequence 107 AA;

Query Match      87.2%; Score 479; DB 7; Length 107;
Best Local Similarity 88.6%; Pred. No. 1.6e-26;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY      1 ELTQSPSSVSASVDGRVTITCRASQVTSWLAHYQKPGKAPKLLITYAASSLSGVSRRF 60
Db      3 QMTQSPSSVSASVDGRVTITCRASQVTSWLAHYQKPGKAPKLLITYAASSLSGVSRRF 62

QY      61 SSGSGYGFDFSLTISLQFEDSATYYCOQANSFPYTFGQGTKEIKR 105
Db      63 SSGSGGTFDFLTITISLQPEDFATYYCOQANSFPPTFGQGTKEIKR 107

RESULT 10
ADP03994
ID      ADP03994 standard; protein; 107 AA.
XX
AC      ADP03994;
XX
DT      29-JUL-2004 (first entry)
XX
DE      Murine-expressed anti-human CA IX monoclonal antibody VL protein SEQ 164.
XX
KW      monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW      cytosol; colorectal neoplasm; renal cell carcinoma;
KW      cervical intraepithelial squamous neoplasia;
KW      cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KW      gene therapy; murine; mouse; human; light chain variable domain.
XX
OS      Unidentified.
XX
PN      WO2003048328-A2.
XX
PD      12-JUN-2003.
XX
PF      02-DEC-2002; 2002MO-US038550.
XX
PR      03-DEC-2001; 2001US-0337275P.
XX
PA      (ABGE-) ABGENIX INC.
XX
PI      Gudas J, Foltz I, Handa M, Gallo M;
XX
DR      WPI; 2003-523295/49.
XX
PT      New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT      colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT      intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS      Example 2; SEQ ID NO 164; 89pp; English.
XX
CC      The invention relates to a novel isolated monoclonal antibody (mAb)
CC      comprising a heavy chain polypeptide and light chain polypeptide having a
CC      sequence chosen from one of 53 fully defined amino acid sequences given
CC      in the specification, where the antibody specifically binds carbonic
CC      anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC      demonstrates cytosolic activity and may be useful for treating a tumour,
CC      such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC      cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC      tumour or breast cancer, possibly via gene therapy. The current sequence
CC      is that of a murine-expressed anti-human CA IX monoclonal antibody VL
CC      (light chain variable domain) protein of the invention. The protein was
CC      generated via the introduction of the human CA IX protein into a
CC      transgenic mouse strain.
XX
SQ      Sequence 107 AA;

Query Match      87.2%; Score 479; DB 7; Length 107;
Best Local Similarity 88.6%; Pred. No. 1.6e-26;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY      1 ELTQSPSSVSASVDGRVTITCRASQVTSWLAHYQKPGKAPKLLITYAASSLSGVSRRF 60
Db      3 QMTQSPSSVSASVDGRVTITCRASQVTSWLAHYQKPGKAPKLLITYAASSLSGVSRRF 62

QY      61 SSGSGYGFDFSLTISLQFEDSATYYCOQANSFPYTFGQGTKEIKR 105
Db      63 SSGSGGTFDFLTITISLQPEDFATYYCOQANSFPPTFGQGTKEIKR 107

RESULT 11
AA65571
ID      AA65571 standard; protein; 107 AA.
XX
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Db      23 QMTQSPSSVSASVDGRVTITCRASQVTSWLAHYQKPGKAPKLLITYAASSLSGVSRRF 82
QY      61 SSGSGYGFDFSLTISLQFEDSATYYCOQANSFPYTFGQGTKEIKR 106
Db      83 SSGSGGTFDFLTITISLQPEDFATYYCOQANSFPPTFGQGTKEIKR 128

RESULT 10
ADP03994
ID      ADP03994 standard; protein; 107 AA.
XX
AC      ADP03994;
XX
DT      29-JUL-2004 (first entry)
XX
DE      Murine-expressed anti-human CA IX monoclonal antibody VL protein SEQ 164.
XX
KW      monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW      cytosol; colorectal neoplasm; renal cell carcinoma;
KW      cervical intraepithelial squamous neoplasia;
KW      cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KW      gene therapy; murine; mouse; human; light chain variable domain.
XX
OS      Unidentified.
XX
PN      WO2003048328-A2.
XX
PD      12-JUN-2003.
XX
PF      02-DEC-2002; 2002MO-US038550.
XX
PR      03-DEC-2001; 2001US-0337275P.
XX
PA      (ABGE-) ABGENIX INC.
XX
PI      Gudas J, Foltz I, Handa M, Gallo M;
XX
DR      WPI; 2003-523295/49.
XX
PT      New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT      colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT      intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS      Example 2; SEQ ID NO 164; 89pp; English.
XX
CC      The invention relates to a novel isolated monoclonal antibody (mAb)
CC      comprising a heavy chain polypeptide and light chain polypeptide having a
CC      sequence chosen from one of 53 fully defined amino acid sequences given
CC      in the specification, where the antibody specifically binds carbonic
CC      anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC      demonstrates cytosolic activity and may be useful for treating a tumour,
CC      such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC      cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC      tumour or breast cancer, possibly via gene therapy. The current sequence
CC      is that of a murine-expressed anti-human CA IX monoclonal antibody VL
CC      (light chain variable domain) protein of the invention. The protein was
CC      generated via the introduction of the human CA IX protein into a
CC      transgenic mouse strain.
XX
SQ      Sequence 107 AA;

Query Match      87.2%; Score 479; DB 7; Length 107;
Best Local Similarity 88.6%; Pred. No. 1.6e-26;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY      1 ELTQSPSSVSASVDGRVTITCRASQVTSWLAHYQKPGKAPKLLITYAASSLSGVSRRF 60
Db      3 QMTQSPSSVSASVDGRVTITCRASQVTSWLAHYQKPGKAPKLLITYAASSLSGVSRRF 62

QY      61 SSGSGYGFDFSLTISLQFEDSATYYCOQANSFPYTFGQGTKEIKR 105
Db      63 SSGSGGTFDFLTITISLQPEDFATYYCOQANSFPPTFGQGTKEIKR 107

RESULT 11
AA65571
ID      AA65571 standard; protein; 107 AA.
XX
```


AC	AA065571;	
XX		
DT	30-NOV-2001 (first entry)	
XX		
DE	Amino acid sequence of protein seq Id No. 96.	
XX		
KM	Gene library; immunoglobulin; antibody library; human.	
XX		
OS	Homo sapiens.	
XX		
PN	MO200162907-A1.	
PD	30-AUG-2001.	
XX		
PF	22-FEB-2001; 2001WO-JP001298.	
PR	22-FEB-2000; 2000JP-00050543.	
XX		
PA	(MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.	
PI	Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M,	
PI	Okuno Y, Shiraki K;	
XX	WPI: 2001-565420/63.	
DR	N-PSDB; AAH47735.	
PT	Producing gene libraries and antibody libraries, involves selecting a	
PT	light chain that binds to a heavy chain product to produce a functional	
PT	formation, and producing a gene library of the light chain variable	
PT	regions.	
XX		
PS	Examples; p 172; 181pp; Japanese.	
XX		
CC	The invention relates to producing gene libraries, comprising	
CC	immunoglobulin light and heavy variable region. The method involves	
CC	selecting light chain that binds with the heavy chain product to produce	
CC	a functional conformation, producing a gene library comprising a	
CC	collection of these light chain variable genes, and combining with gene	
CC	library of heavy chain variable genes. The method is used for production	
CC	of gene and antibody libraries	
XX		
SQ	Sequence 107 AA;	
	Query Match 87.1%; Score 478; DB 4; Length 107;	
	Best Local Similarity 88.6%; Pred. No. 1.9e-26;	
	Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0	
QY	1 ELTQSPSSVASVGDRTVTTTCRASGIGSSWLAHYOHQPKAPKLLIYASSLSQGVSPRF 60	
	::: : : : : : : : : :	
DB	3 QMTQSPSSVSASVGDRTVTTTCRASGIGSSWLAHYOHQPKAPKLLIYASSLSQGVSPRF 62	
QY	61 SSGSGGTDPSLTITSLQPEDSATYVCCOANSPRYFFGGGTKEIK 105	
	: : : : : : : : :	
DB	63 SSGSGGTDPSLTITSLQPEDSATYVCCOANSPRYFFGGGTKEIK 107	
RESULT 12		
ID	ADP03924 standard; protein; 107 AA.	
AD	ADP03924;	
XX		
DT	29-JUL-2004 (first entry)	
XX		
DE	Murine-expressed anti-human CA IX monoclonal antibody VL protein -SEQ 64.	
XX		
KM	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;	
KM	cytostatic; colorectal neoplasm; renal cell carcinoma;	
KM	cervical intraepithelial squamous neoplasia;	
KM	cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;	
XX	gene therapy; murine; mouse; human; light chain variable domain.	
OS	Unidentified.	

XX	WO2003048328-A2.
PN	
PD	12-JUN-2003.
PX	
PF	02-DEC-2002; 2002WO-USO38550.
XX	
PR	03-DEC-2001; 2001US-0337275P.
XX	
PA	(ABGE-) ABGENIX INC.
XX	
PI	Gudas J, Foltz I, Handa M, Gallo M;
XX	
DR	WPI; 2003-523295/49.
XX	
PT	New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PP	colorectal neoplasm, colorectal tumors, cervical carcinoma, cervical
PT	intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX	
PS	Claim 3; SEQ ID NO 64; 89pp; English.
XX	
CC	The invention relates to a novel isolated monoclonal antibody (mAb)
CC	comprising a heavy chain polypeptide and light chain polypeptide having a
CC	sequence chosen from one of 53 fully defined amino acid sequences given
CC	in the specification, where the antibody specifically binds carbonic
CC	anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC	demonstrates cytostatic activity and may be useful for treating a tumour,
CC	such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC	cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC	tumour or breast cancer, possibly via gene therapy. The current sequence
CC	is that of a murine-expressed anti-human CA IX monoclonal antibody VL
CC	(light chain variable domain) protein of the invention. The protein was
CC	generated by the introduction of the human CA IX protein into a
CC	transgenic mouse strain.
XX	
SQ	Sequence 107 AA:
	Query Match 87.1%; Score 478; DB ?; Length 107;
	Best Local Similarity 87.6%; Pred. No. 1.9e-26;
	Matches 92; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
OY	1 ELTSPSSVSAASVGDRVTITCRASQGTSWLAWYQHOPKAPKLLIYSASSLSGVSRSRF 60
DB	3 QMTSPSSVSAASVGDRVTITCRASQGTSWLAWYQHOPKAPKLLIYSASSLSGVSRSRF 62
OY	61 SGSGVGTDFSLTISLQEDSATYYCCQANSFPFTFGGTVEIK 105
DB	63 SGSGSGTDFTLTISLQEDPATYYCQQANSFPTFGGTIRLEIK 107
	RESULT 13
	ADP03989
	ID ADP03989 standard; protein; 107 AA.
XX	
AC	ADP03989;
XX	
DT	29-JUL-2004 (first entry)
DE	Murine-expressed anti-human CA IX monoclonal antibody VL protein SEQ 159.
XX	
KM	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW	Cyostatic; colorectal neoplasm; renal cell carcinoma;
KW	cervical intraepithelial squamous neoplasia;
KW	cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX	gene therapy; murine; mouse; human; light chain variable domain.
XX	
OS	Unidentified.
XX	
PN	WO2003048328-A2.
XX	
PD	12-JUN-2003.
XX	
PF	02-DEC-2002; 2002WO-USO38550.

```
XX 03-DEC-2001; 2001US-0337275P.
PR (ABGE-) ABGENIX INC.
PA
XX Gudäs J, Foltz I, Handa M, Gallo M;
XX WPI; 2003-523295/49.
DR
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Example 2; SEQ ID NO 159; 89pp; English.
PS
XX The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VL
CC (light chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 107 AA;
Query Match 87.1%; Score 478; DB 7; Length 107;
Best Local Similarity 87.6%; Pred. No. 1.9e-26;
Matches 92; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
QY 1 ELTQSPSSVASVGDVRYTITCRASQGISWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 60
Db 3 QMTQSPSSVASVGDVRYTITCRASQGISWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 62
QY 61 SGSGYGTDFSLTITSSLOFEDSATYTCQANSFPYTGQGTKEIK 105
Db 63 SGSGSGTGFLLTITSSLOPEDFATYTCQANSFPITFGGTRLEIK 107
RESULT 14
ADP03921
ID ADP03921 standard; protein; 107 AA.
XX
AC ADP03921;
XX
XX 29-JUL-2004 (first entry)
XX
XX Murine-expressed anti-human CA IX monoclonal antibody VL protein -SEQ 61.
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW cytosolic; colorectal neoplasm; renal cell carcinoma;
KW cervical intraepithelial squamous neoplasia;
KW cervical intraepithelial glandular neoplasia;
KW gene therapy; murine; mouse; human; light chain variable domain.
XX
XX Unidentified.
OS
XX
XX WO2003048328-A2.
XX
XX 12-JUN-2003.
XX
XX 02-DEC-2002; 2002WO-US038550.
XX
XX 03-DEC-2001; 2001US-0337275P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudäs J, Foltz I, Handa M, Gallo M;
```

```
XX WPI; 2003-523295/49.
DR
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Claim 3; SEQ ID NO 61; 89pp; English.
PS
XX The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VL
CC (light chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 107 AA;
Query Match 87.1%; Score 478; DB 7; Length 107;
Best Local Similarity 87.6%; Pred. No. 1.9e-26;
Matches 92; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
QY 1 ELTQSPSSVASVGDVRYTITCRASQGISWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 60
Db 3 QMTQSPSSVASVGDVRYTITCRASQGISWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 62
QY 61 SGSGYGTDFSLTITSSLOFEDSATYTCQANSFPYTGQGTKEIK 105
Db 63 SGSGSGTGFLLTITSSLOPEDFATYTCQANSFPITFGGTRLEIK 107
RESULT 15
ABP45870
ID ABP45870 standard; protein; 244 AA.
XX
AC ABP45870;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv SEQ ID 1881.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
OS
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX
XX 17-OCT-2000; 2000US-0240816P.
XX
XX 16-MAR-2001; 2001US-0276284P.
XX
XX 21-MAR-2001; 2001US-0277379P.
XX
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
```

XX WPI; 2002-114799/15.

DR Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.

PT Claim 1; Page 2646-2647; 3148pp; English.

XX
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX

XX Sequence 244 AA;

Query Match 87.1%; Score 478; DB 5; Length 244;
Best Local Similarity 88.6%; Pred. No. 3.9e-26;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 LTQSPSSVSASVGRVITTCASQGISISWLAHYOHQPKAKKLITYASSLQSGVPSRFS 61
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
140 WTQSPSTLSASVGRVITTCASQGISISWLAHYOHQPKAKKLITYASSLQSGVPSRFS 199
QY 62 GSGYGTDFSLTISLQFEDSATYCCQANSPPYTFGQGTKEIKR 106
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
200 GSGSGTDFSLTISLQFEDSATYCCQANSPPYTFGQGTKEIKR 244

Search completed: July 26, 2005, 09:19:23
Job time : 81.3394 secs

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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:26:32 ; Search time 67.4545 Seconds

(without alignments)
611.274 Million cell updates/sec

Title: US-10-027-725A-12

Perfect score: 549

Sequence: 1 ELTQSPSSVSAVSDRVITF.....COANSFPTFGGTVKEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/prodata/2/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB.pep.*
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- 12: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/prodata/2/pubppaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/2/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/2/pubppaa/US10C_PUBCOMB.pep.*
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- 17: /cgn2_6/prodata/2/pubppaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/prodata/2/pubppaa/US10F_NEW_PUB.pep.*
- 19: /cgn2_6/prodata/2/pubppaa/US11_PUBCOMB.pep.*
- 20: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep.*
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- 22: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	549	100.0	106	US-10-027-725A-12	Sequence 12, App1
2	493	89.8	107	US-10-891-658-80	Sequence 80, App1
3	491	89.4	107	US-10-727-155-312	Sequence 312, App1
4	491	89.4	129	US-10-910-901-20	Sequence 20, App1
5	489	89.1	236	US-10-910-901-12	Sequence 12, App1
6	488	88.9	108	US-10-938-353-109	Sequence 109, App1
7	487	88.7	107	US-10-727-155-122	Sequence 122, App1
8	486	88.5	107	US-10-938-353-117	Sequence 117, App1
9	485	88.3	107	US-10-982-359-67	Sequence 67, App1
10	484	88.2	223	US-10-693-629-66	Sequence 66, App1
11	483	88.0	129	US-10-910-901-19	Sequence 19, App1

12	482	87.8	107	15	US-10-309-762-159	Sequence 159, App
13	481	87.6	107	15	US-10-292-088-105	Sequence 105, App
14	481	87.6	129	17	US-10-910-901-17	Sequence 17, App1
15	479	87.2	107	15	US-10-309-762-62	Sequence 62, App1
16	479	87.2	107	15	US-10-309-762-164	Sequence 164, App
17	478	87.1	107	15	US-10-309-762-61	Sequence 61, App1
18	478	87.1	107	15	US-10-309-762-61	Sequence 64, App1
19	478	87.1	244	10	US-09-880-748-1881	Sequence 1881, Ap
20	478	87.1	244	15	US-10-293-418-1881	Sequence 1881, Ap
21	477	86.9	107	17	US-10-638-265-76	Sequence 76, App1
22	477	86.9	107	17	US-10-893-576-177	Sequence 177, App
23	477	86.9	129	17	US-10-893-576-24	Sequence 24, App1
24	477	86.9	212	18	US-10-513-725-7	Sequence 7, App1
25	475	86.5	236	9	US-09-859-053-30	Sequence 30, App1
26	475	86.5	236	16	US-10-625-105-30	Sequence 30, App1
27	475	86.5	236	18	US-10-800-250-30	Sequence 30, App1
28	474	86.3	107	14	US-10-041-860-43	Sequence 43, App1
29	474	86.3	107	14	US-10-041-860-218	Sequence 218, App
30	474	86.3	107	16	US-10-665-383-64	Sequence 64, App1
31	474	86.3	236	17	US-10-910-901-16	Sequence 16, App1
32	473.5	86.2	106	15	US-10-309-762-84	Sequence 84, App1
33	472	86.0	107	15	US-10-309-762-60	Sequence 60, App1
34	472	86.0	107	15	US-10-309-762-63	Sequence 63, App1
35	471	85.8	236	17	US-10-910-901-4	Sequence 4, App1
36	468.5	85.3	108	14	US-10-041-860-357	Sequence 357, App
37	468	85.2	234	15	US-10-292-088-24	Sequence 24, App1
38	467	85.1	107	16	US-10-703-714-4	Sequence 4, App1
39	467	85.1	107	16	US-10-703-714-8	Sequence 8, App1
40	467	85.1	107	16	US-10-703-714-16	Sequence 16, App1
41	467	85.1	134	16	US-10-473-287-47	Sequence 47, App1
42	466	84.9	108	10	US-09-920-262A-8	Sequence 8, App1
43	466	84.9	108	17	US-10-912-994-8	Sequence 8, App1
44	466	84.9	108	17	US-10-975-683-8	Sequence 8, App1
45	466	84.9	109	16	US-10-835-641-3	Sequence 3, App1

ALIGNMENTS

RESULT 1
US-10-027-725A-12
Sequence 12, Application US/10027725A
Publication No. US20030082659A1
GENERAL INFORMATION:
APPLICANT: Flicker, Sabine
TITLE OR INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
FILE REFERENCE: 25401-4
CURRENT APPLICATION NUMBER: US/10/027, 725A
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/259, 436
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 106
TYPE: PRT
ORGANISM: Homo sapiens
US-10-027-725A-12

Query Match 100.0%; Score 549; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.4e-40;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELTQSPSSVSAVSDRVITTCRASQGISWLAWOHPGKAPKLLIYSASSLSQGVSRF 60
DB 1 ELTQSPSSVSAVSDRVITTCRASQGISWLAWOHPGKAPKLLIYSASSLSQGVSRF 60
QY 61 SSGSGYGFSLITSLQFEDSATYCCOANSFPTFGGTVKEIKR 106
DB 61 SSGSGYGFSLITSLQFEDSATYCCOANSFPTFGGTVKEIKR 106

RESULT 2

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US-10-891-658-80
; Sequence 80, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapien
US-10-891-658-80
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Query Match      89.8%; Score 493; DB 17; Length 107;
Best Local Similarity 90.5%; Pred. No. 1.1e-35;
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Db      3 QMTQSPSSVASVGDRTVITTCRASQGISIMLAWYQHKGKAPKLLIYAASSLQGVPSRF 62

Qy      61 SSGSGYGFDTLTSSLOFEDSATYCCQANSFPYTFGQGTVEIK 105
Db      63 SSGSGYGFDTLTSSLOFEDPATYCCQANSFPWTFGQGTVEIK 107
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RESULT 3
US-10-727-155-312
; Sequence 312, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaapal S. Kang
; APPLICANT: Jaapal S. Kang
; APPLICANT: Larry Green
; APPLICANT: Xiaofeng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendescho
; APPLICANT: Palaniswami Rathnaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenko
; APPLICANT: Rafiaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Olajuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR AND USES THEREOF
; FILE REFERENCE: AGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-312
```

```
Query Match      89.4%; Score 491; DB 17; Length 107;
Best Local Similarity 90.5%; Pred. No. 1.6e-35;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      1 ELTQSPSSVASVGDRTVITTCRASQGISSWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 60
Db      3 QMTQSPSSVASVGDRTVITTCRASQGISIMLAWYQHKGKAPKLLIYAASSLQGVPSRF 62

Qy      61 SSGSGYGFDTLTSSLOFEDSATYCCQANSFPYTFGQGTVEIK 105
Db      63 SSGSGYGFDTLTSSLOFEDPATYCCQANSFPWTFGQGTVEIK 107
```

```
RESULT 4
US-10-910-901-20
; Sequence 20, Application US/10910901
; Publication No. US20050054019A1
; GENERAL INFORMATION:
; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO C-MET
; FILE REFERENCE: ABX-PF5
; CURRENT APPLICATION NUMBER: US/10/910,901
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 20
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-901-20
```

```
Query Match      89.4%; Score 491; DB 17; Length 129;
Best Local Similarity 90.5%; Pred. No. 2e-35;
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      1 ELTQSPSSVASVGDRTVITTCRASQGISSWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 60
Db      25 QMTQSPSSVASVGDRTVITTCRASQGISIMLAWYQHKGKAPKLLIYAASSLQGVPSRF 84

Qy      61 SSGSGYGFDTLTSSLOFEDSATYCCQANSFPYTFGQGTVEIK 105
Db      85 SSGSGYGFDTLTSSLOFEDPATYCCQANSFPWTFGQGTVEIK 129
```

```
RESULT 5
US-10-910-901-12
; Sequence 12, Application US/10910901
; Publication No. US20050054019A1
; GENERAL INFORMATION:
; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO C-MET
; FILE REFERENCE: ABX-PF5
; CURRENT APPLICATION NUMBER: US/10/910,901
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-901-12
```

```
Query Match      89.1%; Score 489; DB 17; Length 236;
Best Local Similarity 89.6%; Pred. No. 5.3e-35;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy      1 ELTQSPSSVASVGDRTVITTCRASQGISSWLAWYOHQPGKAPKLLIYASASSLQGVPSRF 60
Db      25 QMTQSPSSVASVGDRTVITTCRASQGISIMLAWYQHKGKAPKLLIYAASSLQGVPSRF 84
```

QY 61 SGGSGYGFSLTISLQFEDSATYCCOANSFPYTFQGTKEIKR 106
DB 85 SGGSGGTFLLTISLQSEDFATYCCOANSFPITFGTKVEIKR 130

RESULT 6

US-10-938-353-109
; Sequence 109, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
; APPLICANT: FOLTZ, IAN
; APPLICANT: HAAK-FRENDSCHO, MARY
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: LOW, JOSEPH EDWIN
; APPLICANT: MOBLEY, JAMES LESLIE
; TITLE OF INVENTION: ANTIBODIES TO M-CSF
; FILE REFERENCE: ABX-PF4
; CURRENT APPLICATION NUMBER: US/10/938,353
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/502,163
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 109
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-353-109

Query Match 88.9%; Score 488; DB 17; Length 108;
Best Local Similarity 88.7%; Pred. No. 3e-35;
Matches 94; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTITTCRASQGISWLAHYOHOPGKAPKLLIYASASSLQGVPSRF 60
DB 3 QMTQSPSSVASVGDRTITTCRASQGISWLAHYOHOPGKAPKLLIYASASSLQGVPSRF 62
QY 61 SGGSGYGFSLTISLQFEDSATYCCOANSFPYTFQGTKEIKR 106
DB 63 SGGSGGTFLLTISLQSEDFATYCCOANSFPITFGTKVEIKR 108

RESULT 7

US-10-727-155-122
; Sequence 122, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendescho
; APPLICANT: Palaniswami Rathnaswami
; APPLICANT: Craig Pigot
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Marchulenchio
; APPLICANT: Katiela Paggioli
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FILE REFERENCE: AGENIX 073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-122

Query Match 88.7%; Score 487; DB 17; Length 107;
Best Local Similarity 89.5%; Pred. No. 3.7e-35;
Matches 94; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTITTCRASQGISWLAHYOHOPGKAPKLLIYASASSLQGVPSRF 60
DB 3 QMTQSPSSVASVGDRTITTCRASQGISWLAHYOHOPGKAPKLLIYASASSLQGVPSRF 62
QY 61 SGGSGYGFSLTISLQFEDSATYCCOANSFPYTFQGTKEIKR 105
DB 63 SGGSGGTFLLTISLQSEDFATYCCOANSFPITFGTKVEIKR 107

RESULT 8

US-10-938-353-117
; Sequence 117, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
; APPLICANT: FOLTZ, IAN
; APPLICANT: HAAK-FRENDSCHO, MARY
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: LOW, JOSEPH EDWIN
; APPLICANT: MOBLEY, JAMES LESLIE
; TITLE OF INVENTION: ANTIBODIES TO M-CSF
; FILE REFERENCE: ABX-PF4
; CURRENT APPLICATION NUMBER: US/10/938,353
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/502,163
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 117
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-353-117

Query Match 88.5%; Score 486; DB 17; Length 108;
Best Local Similarity 89.6%; Pred. No. 4.5e-35;
Matches 95; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTITTCRASQGISWLAHYOHOPGKAPKLLIYASASSLQGVPSRF 60
DB 3 QMTQSPSSVASVGDRTITTCRASQGISWLAHYOHOPGKAPKLLIYASASSLQGVPSRF 62
QY 61 SGGSGYGFSLTISLQFEDSATYCCOANSFPYTFQGTKEIKR 106
DB 63 SGGSGGTFLLTISLQSEDFATYCCOANSFPITFGTKVEIKR 108

RESULT 9

US-10-982-359-67
; Sequence 67, Application US/10982359
; Publication No. US20050112694A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Zhou, Hongxing
; TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
; FILE REFERENCE: 3492-A
; CURRENT APPLICATION NUMBER: US/10/982,359
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/518,166
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 77

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: 63 light chain variable region
US-10-982-359-67

Query Match      88.3%; Score 485; DB 17; Length 107;
Best Local Similarity 88.6%; Pred. No. 5.5e-35;
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASLSQGVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGYGFDFSLTISLQFEDSATYCCOQANSFPTFGQGTVEIK 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SSGSGYGFDFSLTISLQFEDSATYCCOQANSFPTFGQGTVEIK 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-10-693-629-66
; Sequence 66, Application US/10693629
; Publication No. US20040120948A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: MIKAYAMA, Toshifumi
; APPLICANT: YOSHIDA, Hitoshi
; APPLICANT: FORCE, Walker, R.
; APPLICANT: CHEN, Xingjie
; APPLICANT: TAKAHASHI, Nobuaki
; TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY
; FILE REFERENCE: 021286-0306473
; CURRENT APPLICATION NUMBER: US/10/693,629
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US09/844,684
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP2001/142482
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: JP2001/310535
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US10/040,244
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-693-629-66

Query Match      88.2%; Score 484; DB 16; Length 223;
Best Local Similarity 87.7%; Pred. No. 1.4e-34;
Matches 93; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 QMTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASLSQGVPSRF 84
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGYGFDFSLTISLQFEDSATYCCOQANSFPTFGQGTVEIK 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 SSGSGYGFDFSLTISLQFEDSATYCCOQANSFPTFGQGTVEIK 130
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-10-910-901-19
; Sequence 19, Application US/10910901
; Publication No. US20050054019A1
; GENERAL INFORMATION:
```

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; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO C-MET
; FILE REFERENCE: ABX-BF5
; CURRENT APPLICATION NUMBER: US/10/910,901
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 19
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-901-19

Query Match      88.0%; Score 483; DB 17; Length 129;
Best Local Similarity 88.6%; Pred. No. 9.8e-35;
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 QMTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASLSQGVPSRF 84
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGYGFDFSLTISLQFEDSATYCCOQANSFPTFGQGTVEIK 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 SSGSGYGFDFSLTISLQFEDSATYCCOQANSFPTFGQGTVEIK 129
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-10-309-762-159
; Sequence 159, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Handa, Masahisa
; APPLICANT: Poltz, Ian
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-159

Query Match      87.8%; Score 482; DB 15; Length 107;
Best Local Similarity 88.6%; Pred. No. 1e-34;
Matches 93; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSVASVGDRTVITTCRASQGISWLAHYOHQPGKAPKLLIYASASLSQGVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGYGFDFSLTISLQFEDSATYCCOQANSFPTFGQGTVEIK 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SSGSGYGFDFSLTISLQFEDSATYCCOQANSFPTFGQGTVEIK 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-10-292-088-105
; Sequence 105, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
```



```
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-105
```

```
Query Match      87.6%; Score 481; DB 15; Length 107;
Best Local Similarity 89.5%; Pred. No. 1.2e-34;
Matches 94; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSVASVGDRTVITCRASQGISWLAHYQHOPGKAPKLLIYASASSLQSGVPSRF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSVASVGDRTVITCRASQGISWLAHYQHOPGKAPKLLIYASASSLQSGVPSRF 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQTKVEIK 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SGSGSGTDFLTITISLQPEDPATYCCQANSFPLTFGGTKVEIK 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 14
US-10-910-901-17
; Sequence 17, Application US/10910901
; Publication No. US20050054019A1
; GENERAL INFORMATION:
; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO C-MET
; FILE REFERENCE: ABX-PF5
; CURRENT APPLICATION NUMBER: US/10/910,901
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-901-17
```

```
Query Match      87.6%; Score 481; DB 17; Length 129;
Best Local Similarity 89.5%; Pred. No. 1.5e-34;
Matches 94; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSVASVGDRTVITCRASQGISWLAHYQHOPGKAPKLLIYASASSLQSGVPSRF 60
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Db 25 QMTQSPSSVASVGDRTVITCRASQGISWLAHYQHOPGKAPKLLIYASASSLQSGVPSRF 84
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQTKVEIK 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 SGSGSGTDFLTITISLQPEDPATYCCQANSFPLTFGGTKVEIK 129
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 15
US-10-309-762-62
; Sequence 62, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Poltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
```

```
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-62
```

```
Query Match      87.2%; Score 479; DB 15; Length 107;
Best Local Similarity 88.6%; Pred. No. 1.8e-34;
Matches 93; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 ELTQSPSSVASVGDRTVITCRASQGISWLAHYQHOPGKAPKLLIYASASSLQSGVPSRF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSVASVGDRTVITCRASQGISWLAHYQHOPGKAPKLLIYASASSLQSGVPSRF 62
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGSGYGTDFSLTISLQFEDSATYCCQANSFPYTFGQTKVEIK 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SGSGSGTDFLTITISLQPEDPATYCCQANSFPLTFGGTKVNIK 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

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Search completed: July 26, 2005, 10:05:21
Job time : 68.6212 secs
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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:09:56 ; Search time 20.0758 Seconds
(without alignments)
394.147 Million cell updates/sec

Title: US-10-027-725A-11

Perfect score: 1 ELTQSPSSLSASVCDRTVIT.....QQSTTYLTFRSGTKLEIKR 106

Sequence: 1 ELTQSPSSLSASVCDRTVIT.....QQSTTYLTFRSGTKLEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	484	88.5	107	1	US-08-276-852-104
2	484	88.5	107	1	US-08-899-575-104
3	484	88.5	107	1	US-08-899-575-104
4	484	88.5	107	5	PCT-US95-08743-104
5	483	88.3	107	3	US-09-240-274-33
6	480	87.8	107	3	US-09-240-274-156
7	476	87.0	107	1	US-08-276-852-105
8	476	87.0	107	1	US-08-899-575-105
9	476	87.0	107	1	US-08-899-575-105
10	476	87.0	107	5	PCT-US95-08743-105
11	475	86.8	107	3	US-09-240-274-115
12	475	86.8	107	3	US-09-240-274-176
13	474	86.7	107	3	US-09-240-274-179
14	473.5	86.6	108	3	US-09-240-274-32
15	473.5	86.6	108	3	US-09-240-274-43
16	473	86.5	107	3	US-09-240-274-37
17	472.5	86.4	108	3	US-09-240-274-167
18	472	86.3	107	3	US-09-240-274-38
19	472	86.3	107	3	US-09-240-274-39
20	472	86.3	107	3	US-09-240-274-162
21	471	86.1	107	3	US-09-240-274-158
22	469	85.7	107	3	US-09-240-274-44
23	468	85.6	108	2	US-08-379-057-29
24	467	85.4	240	4	US-09-192-854-2
25	464.5	84.9	108	3	US-09-240-274-163
26	463	84.6	104	1	US-08-276-852-106
27	463	84.6	104	1	US-08-899-575-106

28	463	84.6	104	1	US-08-899-575-106	Sequence 106, App
29	463	84.6	104	5	PCT-US95-08743-106	Sequence 106, App
30	461	84.3	108	3	US-09-025-769B-14	Sequence 14, App1
31	461	84.3	108	4	US-09-490-070A-14	Sequence 14, App1
32	461	84.3	108	4	US-09-490-153-14	Sequence 14, App1
33	461	84.3	108	4	US-09-490-324-14	Sequence 14, App1
34	459	83.9	107	1	US-08-300-386A-66	Sequence 66, App1
35	459	83.9	107	3	US-08-931-645-66	Sequence 66, App1
36	459	83.9	107	3	US-09-240-274-168	Sequence 168, App
37	459	83.9	107	5	PCT-US95-11235-66	Sequence 66, App1
38	457	83.5	107	3	US-09-240-274-36	Sequence 36, App1
39	457	83.5	109	3	US-09-157-370-3	Sequence 3, App1
40	457	83.5	214	4	US-09-472-087-71	Sequence 71, App1
41	456.5	83.5	108	1	US-08-276-852-109	Sequence 109, App
42	456.5	83.5	108	1	US-08-899-575-109	Sequence 109, App
43	456.5	83.5	108	1	US-08-899-575-109	Sequence 109, App
44	456.5	83.5	108	3	US-09-240-274-41	Sequence 41, App1
45	456.5	83.5	108	5	PCT-US95-08743-109	Sequence 109, App

ALIGNMENTS

RESULT 1
US-08-276-852-104
Sequence 104, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESS: The Scripps Research Institute, Office of
ADDRESS: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-104

Query Match 88.5%; Score 484; DB 1; Length 107;
Best Local Similarity 88.7%; Pred. No. 2e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITTCRAROSISTYLNWYQOKGKAPKLLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGRVITTCRASQSSISYLNWYQOKGKAPKLLIYASSLQSGVPSRF 60

QY 61 SSGSGTEFTLTISNLQFEDFASYYCOQSYTTLYTFSGGTLEIKR 106
DB 61 SSGSGTDFLTLTISLQPEDFATYYCOQSYSTPYTFGGTLEIKR 106

RESULT 2
US-08-899-575-104
Sequence 104, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-104

Query Match 88.5%; Score 484; DB 1; Length 107;
Best Local Similarity 88.7%; Pred. No. 2e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITTCRAROSISTYLNWYQOKGKAPKLLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGRVITTCRASQSSISYLNWYQOKGKAPKLLIYASSLQSGVPSRF 60

QY 61 SSGSGTEFTLTISNLQFEDFASYYCOQSYTTLYTFSGGTLEIKR 106
DB 61 SSGSGTDFLTLTISLQPEDFATYYCOQSYSTPYTFGGTLEIKR 106

RESULT 3
US-08-899-575-104
Sequence 104, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-104

Query Match 88.5%; Score 484; DB 1; Length 107;
Best Local Similarity 88.7%; Pred. No. 2e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVITTCRAROSISTYLNWYQOKGKAPKLLIWSASNLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGRVITTCRASQSSISYLNWYQOKGKAPKLLIYASSLQSGVPSRF 60

QY 61 SSGSGTEFTLTISNLQFEDFASYYCOQSYTTLYTFSGGTLEIKR 106
DB 61 SSGSGTDFLTLTISLQPEDFATYYCOQSYSTPYTFGGTLEIKR 106

RESULT 4
PCT-US95-08743-104
Sequence 104, Application PC/TUS9508743

```

; GENERAL INFORMATION:
; APPLICANT: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-104

Query Match      88.5%; Score 484; DB 5; Length 107;
Best Local Similarity 88.7%; Pred. No. 2e-36;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGDRTVITTCRASQISITVLMWYQOKRGKAPKLLIYASNLQSGVPSRF 60
DB 1 ELTOSPSLSASVGDRTVITTCRASQISITVLMWYQOKRGKAPKLLIYASNLQSGVPSRF 60
QY 61 SGGSGGTFTLTISNLQFEDPASYCCOOSYTTLYTFGSGTLEIKR 106
DB 61 SGGSGGTFTLTISNLQFEDPASYCCOOSYTTLYTFGSGTLEIKR 106
DB 62 SGGSGGTFTLTISNLQFEDPASYCCOOSYTTLYTFGSGTLEIKR 107

RESULT 5
US-09-240-274-33
; Sequence 33, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-240-274-33

Query Match      88.3%; Score 483; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.4e-36;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGDRTVITTCRASQISITVLMWYQOKRGKAPKLLIYASNLQSGVPSRF 60
DB 2 ELTOSPSLSASVGDRTVITTCRASQISITVLMWYQOKRGKAPKLLIYASNLQSGVPSRF 61
QY 61 SGGSGGTFTLTISNLQFEDPASYCCOOSYTTLYTFGSGTLEIKR 106
DB 62 SGGSGGTFTLTISNLQFEDPASYCCOOSYTTLYTFGSGTLEIKR 107
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RESULT 6
US-09-240-274-156
; Sequence 156, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-156

Query Match      87.8%; Score 480; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 4.5e-36;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGDRTVITTCRASQISITVLMWYQOKRGKAPKLLIYASNLQSGVPSRF 60
DB 2 ELTOSPSLSASVGDRTVITTCRASQISITVLMWYQOKRGKAPKLLIYASNLQSGVPSRF 61
QY 61 SGGSGGTFTLTISNLQFEDPASYCCOOSYTTLYTFGSGTLEIKR 106
DB 62 SGGSGGTFTLTISNLQFEDPASYCCOOSYTTLYTFGSGTLEIKR 107
DB 62 SGGSGGTFTLTISNLQFEDPASYCCOOSYTTLYTFGSGTLEIKR 107

RESULT 7
US-08-276-852-105
; Sequence 105, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Bardas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSER: The Scripps Research Institute, Office of
; ADDRESSER: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-105

Query Match 87.0%; Score 476; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 1e-35;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRAROSISTYLNMYQOKPGKAPKLLIWSASNLQGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITCRAROSISTYLNMYQOKPGKAPKLLIWSASNLQGVPSRF 60

QY 61 SGGSGGTFFLTITSLNLFEDFASYCCOQSYTTLVTFSGTKLEIKR 106
Db 61 SGGSGGTDFLTITSLQPEDFATYCCOQSYSTPQTFGGTLEIKR 106

RESULT 8
US-08-899-575-105
Sequence 105, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbias, Carlos F
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSER: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-105

Query Match 87.0%; Score 476; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 1e-35;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRAROSISTYLNMYQOKPGKAPKLLIWSASNLQGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITCRAROSISTYLNMYQOKPGKAPKLLIWSASNLQGVPSRF 60

QY 61 SGGSGGTFFLTITSLNLFEDFASYCCOQSYTTLVTFSGTKLEIKR 106
Db 61 SGGSGGTDFLTITSLQPEDFATYCCOQSYSTPQTFGGTLEIKR 106

RESULT 9
US-08-899-575-105
Sequence 105, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbias, Carlos F
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSER: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-105

Query Match 87.0%; Score 476; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 1e-35; Indels 0; Gaps 0;
Matches 93; Conservative 8; Mismatches 5;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLMWYQKRGKAPKLLIWSASNLQGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLMWYQKRGKAPKLLIWSASNLQGVPSRF 60
QY 61 SGGSGGTFTLTITSLNLOPEDFASYYCOOSYTTLYTFSGTKLEIKR 106
DB 61 SGGSGGTFTLTITSLNLOPEDFATYYCOOSYSTPQTFQGTLEIKR 106

RESULT 10
PCT-US95-08743-105
Sequence 105, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08743-105

Query Match 87.0%; Score 476; DB 5; Length 107;
Best Local Similarity 87.7%; Pred. No. 1e-35; Indels 0; Gaps 0;
Matches 93; Conservative 8; Mismatches 5;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLMWYQKRGKAPKLLIWSASNLQGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLMWYQKRGKAPKLLIWSASNLQGVPSRF 60
QY 61 SGGSGGTFTLTITSLNLOPEDFASYYCOOSYTTLYTFSGTKLEIKR 106
DB 61 SGGSGGTFTLTITSLNLOPEDFATYYCOOSYSTPQTFQGTLEIKR 106

RESULT 11
US-09-240-274-175
Sequence 175, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 175
LENGTH: 107

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-175

Query Match 86.8%; Score 475; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.3e-35; Indels 0; Gaps 0;
Matches 91; Conservative 11; Mismatches 4;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLMWYQKRGKAPKLLIWSASNLQGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITTCRASQISSTYLMWYQKRGKAPKLLIWSASNLQGVPSRF 61
QY 61 SGGSGGTFTLTITSLNLOPEDFASYYCOOSYTTLYTFSGTKLEIKR 106
DB 62 SGGSGGTFTLTITSLNLOPEDFATYYCOOSYSTPQTFQGTLEIKR 107

RESULT 12
US-09-240-274-176
Sequence 176, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 176
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-240-274-176

Query Match 86.8%; Score 475; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.3e-35; Indels 0; Gaps 0;
Matches 91; Conservative 11; Mismatches 4;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLMWYQKRGKAPKLLIWSASNLQGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITTCRASQISSTYLMWYQKRGKAPKLLIWSASNLQGVPSRF 61
QY 61 SGGSGGTFTLTITSLNLOPEDFASYYCOOSYTTLYTFSGTKLEIKR 106
DB 62 SGGSGGTFTLTITSLNLOPEDFATYYCOOSYSTPQTFQGTLEIKR 107

RESULT 13
US-09-240-274-179
Sequence 179, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 179
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-179

Query Match 86.7%; Score 474; DB 3; Length 107;
Best Local Similarity 85.8%; Pred. No. 1.5e-35;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITCRARQSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
DB 2 ELTQSPSSLSASVGDVVTITCRARQSISTYLMWYQKPGKAPKLLIYAASSLQGVPSRF 61
QY 61 SSGSGGTEFTLTISNLFQEDFASYYCOQSYTT-LYTFGSGTKLEIKR 106
DB 62 SSGSGGTEFTLTISNLFQEDFATYYCOQSYSTPPTFGQGTKEIKR 107

RESULT 14

US-09-240-274-32
Sequence 32, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 101
US-09-240-274-32

Query Match 86.6%; Score 473.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 1.7e-35;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDVVTITCRARQSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
DB 2 ELTQSPSSLSASVGDVVTITCRARQSISTYLMWYQKPGKAPKLLIYAASSLQGVPSRF 61
QY 61 SSGSGGTEFTLTISNLFQEDFASYYCOQSYTT-LYTFGSGTKLEIKR 106
DB 62 SSGSGGTEFTLTISNLFQEDFATYYCOQSYSTPPTFGQGTKEIKR 108

RESULT 15
US-09-240-274-43
Sequence 43, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 112
US-09-240-274-43

Query Match 86.6%; Score 473.5; DB 3; Length 108;
Best Local Similarity 87.9%; Pred. No. 1.7e-35;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDVVTITCRARQSISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
DB 2 ELTQSPSSLSASVGDVVTITCRARQSISTYLMWYQKPGKAPKLLIYAASSLQGVPSRF 61
QY 61 SSGSGGTEFTLTISNLFQEDFASYYCOQSYTT-LYTFGSGTKLEIKR 106
DB 62 SSGSGGTEFTLTISNLFQEDFATYYCOQSYSTPPTFGQGTKEIKR 108

Search completed: July 26, 2005, 09:30:01
Job time: 21.0758 secs

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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:07:26 ; Search time 13.6515 Seconds

(without alignments)
747.095 Million cell updates/sec

Title: US-10-027-725A-11

Perfect score: 547

Sequence: 1 ELTQSPSLASVGDRTVIT.....QQSYTLTYFGSGTKLEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79:.*
2: p1r1:.*
3: p1r2:.*
4: p1r3:.*
5: p1r4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	468	85.6	108	2 B49047	Ig kappa chain V r
2	465	85.0	108	2 S47182	Ig kappa chain - h
3	465	85.0	127	2 S40367	Ig kappa chain V-J
4	464	84.8	109	2 S31998	Ig kappa chain - h
5	462	84.5	123	2 S40331	Ig kappa chain - h
6	457	83.5	122	2 S40370	Ig kappa chain - h
7	455	83.0	108	2 S44122	Ig kappa chain V r
8	454	83.0	108	2 S31977	Ig kappa chain - h
9	453	82.8	129	1 K1HUKK	Ig kappa chain pre
10	451	82.4	109	2 S31981	Ig kappa chain - h
11	449	82.1	108	2 S31978	Ig kappa chain V-I
12	447	81.7	108	2 K1HUBB	Ig kappa chain V r
13	446	80.1	117	2 S46371	Ig kappa chain - h
14	438	80.1	117	2 S46371	Ig kappa chain V-J
15	437.5	80.0	106	2 PC2397	anti-tetanus toxin
16	437	79.9	107	2 S36264	Ig lambda chain V
17	437	79.9	108	1 K1HUKK	Ig kappa chain V-I
18	437	79.9	120	2 S46370	Ig kappa chain V-J
19	436	79.7	109	2 S31979	Ig kappa chain - h
20	434	79.3	129	2 S52793	Ig kappa chain V r
21	433	79.0	128	2 S46372	Ig light chain var
22	432	79.0	109	2 S31980	Ig kappa chain - h
23	432	79.0	125	2 S40350	Ig kappa chain - h
24	431	78.8	109	2 S31983	Ig kappa chain - h
25	429	78.4	129	2 S52792	Ig kappa chain V r
26	429	78.4	132	2 S40334	Ig kappa chain - h
27	428	78.2	109	2 S32001	Ig kappa chain - h
28	428	78.2	122	2 S40314	Ig kappa chain - h

30	428	78.2	132	2 S38646	Ig kappa chain V r
31	427.5	78.2	125	2 S40315	Ig kappa chain - h
32	427	78.1	125	2 S40349	Ig kappa chain V-J
33	425.5	77.8	124	2 S40336	Ig kappa chain V-J
34	424.5	77.6	107	2 S36275	Ig kappa chain V
35	424	77.5	108	1 K1HUKK	Ig kappa chain V-I
36	424	77.5	125	2 S40333	Ig kappa chain V-J
37	421.5	77.1	108	2 S30521	Ig kappa chain V r
38	419	76.6	116	2 A27594	Ig kappa chain pre
39	419	76.6	117	2 S24206	Ig kappa chain V r
40	418	76.4	109	2 UN0296	Ig kappa chain V-J
41	418	76.4	129	2 S40369	Ig kappa chain - h
42	417.5	76.3	108	2 S34007	Ig kappa chain V r
43	417	76.2	126	2 S40335	Ig kappa chain V-J
44	416	76.1	108	1 K1HUKK	Ig kappa chain V-I
45	416	76.1	108	1 K1HUKK	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

B49047
Ig kappa chain V region (monoclonal strictional autoantibody StrAB SA-1A) - human (fragm
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B49047
R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A:Title: Human monoclonal strictional autoantibodies isolated from thymic B lymphocytes
A:Reference number: A49047; MUID:92387224; PMID:1516616
A:Accession: B49047
A>Status: Preliminary
A:Molecule type: nucleic acid
A:Residues: 1-108 <VIC>
A:Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
A:Experimental source: thymic B lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBI:113208, NCBI:113209)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 468; DB 2; Length 108;
Best Local Similarity 84.9%; Pred. No. 4; 1e-34;
Matches 90; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVITTCRAQISITLYNMYQKRGKPKLLMSASNLQGVSRF 60
Db 3 QMTQSPSLASVGDRTVITTCRAQISITLYNMYQKRGKPKLLIYAASLQGVSRF 62
QY 61 SGSGSGTEFTLTISNLQEPDPAASYCCOOSYTLTYFGSGTKLEIKR 106
Db 63 SGSGSGTEFTLTISNLQEPDPAASYCCOOSYTLTYFGSGTKLEIKR 108

RESULT 2

S47182
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
R:McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Wetman, A.P.
submitted to the EMBL Data Library, June 1994
A:Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien
A:Reference number: S47181
A:Accession: S47182
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <MC1>
A:Cross-references: EMBL:X79786; NID:9506422; PIDN:CA56182.1; PID:9506423
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

```
Query Match      85.0%; Score 465; DB 2; Length 108;
Best Local Similarity 85.8%; Pred. No. 7.5e-34;
Matches 91; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGGTEFTLTISNLOPEDFASYYCOQSYTTLYTFGSGTKLEIKR 106
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SSGSGGTEFTLTISNLOPEDFATYYCOQSYTPTTSGGTRLEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
S40367
Ig kappa chain V-J-C region - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40367
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40367
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-127 <KLE>
A/Cross-references: EMBL:X72477
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/33-107/Domain: immunoglobulin homology <IMM>

Query Match      85.0%; Score 465; DB 2; Length 127;
Best Local Similarity 84.0%; Pred. No. 8.8e-34;
Matches 89; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QMTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGGTEFTLTISNLOPEDFASYYCOQSYTTLYTFGSGTKLEIKR 106
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 SSGSGGTEFTLTISNLOPEDFATYYCOQSYTPTTSGGTRLEIKR 125
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
S31998
Ig kappa chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S31998
R/Portiano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31998
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <POR>
A/Cross-references: EMBL:Z15081; NID:G38501; PIDN:CAA78790.1; PID:G38502
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match      84.8%; Score 464; DB 2; Length 109;
Best Local Similarity 85.7%; Pred. No. 9.3e-34;
Matches 90; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 MTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 62 GSGSGTEFTLTISNLOPEDFASYYCOQSYTTLYTFGSGTKLEIKR 106
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
Db 64 GSGSGTEFTLTISNLOPEDFATYYCOQSYTPTTSGGTRLEIKR 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
S40331
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40331
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40331
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-123 <KLE>
A/Cross-references: EMBL:X72441; NID:G441350; PIDN:CAA51109.1; PID:G441351
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/32-106/Domain: immunoglobulin homology <IMM>

Query Match      84.5%; Score 462; DB 2; Length 123;
Best Local Similarity 84.8%; Pred. No. 1.6e-33;
Matches 89; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 19 QMTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 78
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGGTEFTLTISNLOPEDFASYYCOQSYTTLYTFGSGTKLEIKR 105
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 79 SSGSGGTEFTLTISNLOPEDFATYYCOQSYTPTTSGGTRLEIKR 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
S40370
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40370
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40370
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-122 <KLE>
A/Cross-references: EMBL:X72480; NID:G441428; PIDN:CAA51148.1; PID:G441429
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/30-104/Domain: immunoglobulin homology <IMM>

Query Match      83.5%; Score 457; DB 2; Length 122;
Best Local Similarity 84.9%; Pred. No. 4.2e-33;
Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 17 QLTQSPSSLSASVGDRTVITTCRAQSISTYLNWYQKPGKAPKLLIWSASNLQSGVPSRF 76
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGGTEFTLTISNLOPEDFASYYCOQSYTTLYTFGSGTKLEIKR 106
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 77 SSGSGGTEFTLTISNLOPEDFATYYCOQSYTPTTSGGTRLEIKR 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
S44122
Ig kappa chain V region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
```

Accession: S44122
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, P.K.
submitted to the EMBL Data Library, March 1994
A:Description: Idiotype vaccination against human B-cell lymphoma: rescue of variable n
A:Reference number: S44105
A:Accession: S44122
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <HAM>
A:Cross-references: EMBL:Z31390; NID:G472976; PIDN:CA83265.1; PID:G940533
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 455; DB 2; Length 108;
Best Local Similarity 84.0%; Pred. No. 5.6e-33;
Matches 89; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

Oy 1 ELTQSPSSLSASVGDRTVTTCRAROSISTYLNWYQQKRGKPKLLINSASLTQSGVPSRF 60
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 3 QMTQSPSSLASVGDRTVTTCRASQSISSYLNWYQQKRGKPKLLIYSASSLTQSGVPSRF 62

Oy 61 SGSGSGTEFTLTISNLQEDPASYYCOQSYYTLTYFGSGTKLEIKR 106
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 63 SGSGSGTDFTLTITSLQPEDPATYYCOQSYYTPMTFGGTVEIKR 108

RESULT 8
S31977

Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S31977
R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL data library, June 1992
A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A:Reference number: S31977
A:Accession: S31977
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <POR>
A:Cross-references: UNIPROT:Q96SA9; EMBL:Z15073
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 454; DB 2; Length 108;
Best Local Similarity 84.8%; Pred. No. 6.8e-33;
Matches 89; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Oy 2 LTQSPSSLSASVGDRVTTCRAROSISTYLNWYQQKPKAPRLTIWSASNTQSGVPSRF 61
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 4 MTQSSGSSLSASVGDRTVTTCRASGISAYLNWYQQKPKAKRLTIYSASSLTQSGVPSRF 63

Oy 62 GSGSGTEFTLTISNLQEDPASYYCOQSYYTLTYFGSGTKLEIKR 106
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 64 GSGSGTDFTLTITSLQPEDPATYYCOQSYYTVDFDGHGTKEIKR 108

RESULT 9
K1HWMK

Ig kappa chain precursor V-I region (Walker) - human
C:Species: Homo sapiens (man)
C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C:Accession: A01883
R:Klobeck, H.G.; Combariato, G.; Zachau, H.G.
Nucleic Acids Res. 12, 6995-7006, 1984
A>Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cell
A:Reference number: A93534; MUID:85014148; PMID:6091049
A:Accession: A01883
A:Molecule type: DNA
A:Residues: 1-129 <KLO>
A:Cross-references: UNIPROT:P04431

A:Note: the sequence was determined from the differentiated gene

A:Genetic: GDB:IGKVI

A:Gene: GDB:IGKVI

A:Cross-references: GDB:136264

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into larger complexes.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-129/Product: Ig kappa chain V-I region (walker) #status predicted <MAT>

F:23-45/Region: framework 1

F:38-112/Domain: immunoglobulin homology <IMM>

F:46-56/Region: complementarity-determining 1

F:57-71/Region: framework 2

F:72-78/Region: complementarity-determining 2

F:79-110/Region: framework 3

F:111-119/Region: complementarity-determining 3

F:120-129/Region: framework 4

F:45-110/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 82.8%; Score 453; DB 1; Length 129;

Matches 88; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 EITQSPSSISASVGDRTITTCRAPQSISTYLMNYOQKPGAPKLLIMSASNLQGVPSRF 60

DB 25 QMTQSPSSISASVGDRTITTCRAPQSISYLMNYOQKPGAPKLLIYAASLQGVTSRF 84

QY 61 SSGSGTEFTLTISNLQFEDPASYYCOOSYTTLYTSGSGTKLEIK 105

DB 85 SSGSGTDFTLTISLQPEDSATYYCOOSYTTLYTSGSGTKLEIK 129

RESULT 10

S31981

Ig kappa chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence _revision 06-Jan-1995 #text_change 21-Jan-2000

C:Accession: S31981

R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992

A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as A:Reference number: S31977

A:Accession: S31981

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-109 <POR>

A:Cross-references: EMBL:Z15077; NID:g38493; PIDN:CAA78786.1; PID:g38494

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 82.4%; Score 451; DB 2; Length 109;

Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 2 LTQSPSSISASVGDRTITTCRAPQSISTYLMNYOQKPGAPKLLIMSASNLQGVPSRF 61

DB 4 MTQSPSSISASVGDRTITTCRAPQSISYLMNYOQKPGAPKLLIHASTLESQVPSRF 63

QY 62 SSGSGTEFTLTISNLQFEDPASYYCOOSYTTLYTSGSGTKLEIK 106

DB 64 SSGSGTDFTLTISLQPEDSATYYCOOSYTPFTFGGTKLEIKR 108

RESULT 11

S31978

Ig kappa chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence _revision 06-Jan-1995 #text_change 21-Jan-2000

C:Accession: S31978

R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.

submitted to the EMBL Data Library, June 1992
A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A;Reference number: S31977
A;Accession: S31978
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-109 <PDR>
A;Cross-references: EMBL:Z55074; NID:938487; PIDN:CAA7873.1; PID:938488
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.4%; Score 451; DB 2; Length 109;
Best Local Similarity 82.9%; Pred. No. 1.3e-32;
Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 2 LTQSPSSLSASVGDVRYITTCRAQOSISTYINWYQQRKGA PKKLIWSASNLQSGVPSRF 61
Db 4 LTQSPSSLSASVGDVRYITTCRAQOSISTYINWYQQRKGA PKKLIWSASNLQSGVPSRF 63
Qy 62 GSGSGTEFTLTISNLQPEDFASYYCOOSYTTLYTFGSGTKLEIKR 106
Db 64 GSGSGTEFTLTISNLQPEDFATYYCOQSYTTPYFGGTYKLEIKR 108

RESULT 12

KIHDD
Ig kappa chain V-I region (Dee) - human (tentative sequence)

C;Species: Homo sapiens (man)
C;Date: 24-Apr-1994 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01865
R;Milestone: C.P.; Deverson, E.V.
Biochem. J. 123, 945-958, 1971
A;Title: The amino acid sequence of a human kappa light chain.
A;Reference number: A01865; MUID:72053133; PMID:5124396
A;Accession: A01865
A;Molecule type: protein
A;Residues: 1-108 <MTL>
A;Cross-references: UNIPROT:P01597
A;Note: the C region of this chain as the inv (3) marker
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status Predicted

Query Match 82.1%; Score 449; DB 1; Length 108;
Best Local Similarity 80.2%; Pred. No. 1.9e-32;
Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDVRYITTCRAQOSISTYINWYQQRKGA PKKLIWSASNLQSGVPSRF 60
Db 3 ZMTQSPSSLSASVGDVRYITTCRAQOSYVKNYINWYQQRKGA PKKLIWSASNLQSGVPSRF 62
Qy 61 GSGSGTEFTLTISNLQPEDFASYYCOOSYTTLYTFGSGTKLEIKR 106
Db 63 GSGSGTEFTLTISNLQPEDFATYYCOQSYTTPYFGGTYKLEIKR 108

RESULT 13

S19674
Ig kappa chain V region (clone alpha-TEL9) - human

C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19674
R;Marks: J.D.; Hoogenboom, H.R.; Bonnert, T.P.; Mc Cafferty, J.; Griffiths, A.D.; Winter, J.; Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage

A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19674
A;Molecule type: mRNA
A;Residues: 1-108 <MAR>
A;Cross-references: EMBL:X61642; NID:937860; PIDN:CAA43823.1; PID:91335386
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 447; DB 2; Length 108;
Best Local Similarity 83.8%; Pred. No. 2.8e-32;
Matches 88; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 2 LTQSPSSLSASVGDVRYITTCRAQOSISTYINWYQQRKGA PKKLIWSASNLQSGVPSRF 61
Db 4 LTQSPSSLSASVGDVRYITTCRAQOSISTYINWYQQRKGA PKKLIWSASNLQSGVPSRF 63
Qy 62 GSGSGTEFTLTISNLQPEDFASYYCOOSYTTLYTFGSGTKLEIKR 106
Db 64 GSGSGTEFTLTISNLQPEDFATYYCOQSYTTPYFGGTYKLEIKR 108

RESULT 14

S40317
Ig kappa chain - human

C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40317
R;Milestone: R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:828341
A;Accession: S40317
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-129 <KLE>
A;Cross-references: EMBL:X72427; NID:9441322; PIDN:CAA51095.1; PID:9441323
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 446; DB 2; Length 129;
Best Local Similarity 81.0%; Pred. No. 4e-32;
Matches 85; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDVRYITTCRAQOSISTYINWYQQRKGA PKKLIWSASNLQSGVPSRF 60
Db 24 QMTQSPSSLSASVGDVRYITTCRAQOSISTYINWYQQRKGA PKKLIWSASNLQSGVPSRF 83
Qy 61 GSGSGTEFTLTISNLQPEDFASYYCOOSYTTLYTFGSGTKLEIKR 105
Db 84 GSGSGTEFTLTISNLQPEDFATYYCOQSYTTPYFGGTYKLEIKR 128

RESULT 15

S46371
Ig kappa chain V-J region (T24-3) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S46371; S38645
R;Benjamin, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rearrangement
A;Reference number: S46369; MUID:94333975; PMID:8039491
A;Accession: S46371
A;Molecule type: mRNA
A;Residues: 1-117 <BEN>
A;Cross-references: EMBL:Z27172; NID:9415959; PIDN:CAA8196.1; PID:9415960
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;23-97/Domain: immunoglobulin homology <IMM>

Query Match 80.1%; Score 438; DB 2; Length 117;

Best Local Similarity 80.6%; Pred. No. 1.8e-31;
Matches 87; Conservative 10; Mismatches 9; Indels 2; Gaps 1;

Qy	1	ELTQSPSSLSASVGDVYITTCRAROSISTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF	60
Db	10	QMTQSPSTLSASVGDVYITTCRASRISITWLAWYQOKPGKAPKLLIYKASTLBSGVPSRF	69
Qy	61	SGSGSGTEFTLTISNLOFEDFASYCOO--SYTTLYTEGSGTKLEIKR	106
Db	70	SGSGSGTEFTLTISLQPDDEPATYCCQYNSYFPPTFGGCTKLEIKR	117

Search completed: July 26, 2005, 09:27:50
Job time : 13.6515 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 08:52:21 ; Search time 66.6515 Seconds

(without alignments)
814.391 Million cell updates/sec

Title: US-10-027-725A-11

Sequence: 1 ELTQSPSSLSASVGDRTVIT.....QQSYTTLVTFGSGTKLEIKR 106

Scoring table: ELTQSPSSLSASVGDRTVIT.....QQSYTTLVTFGSGTKLEIKR 106

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	85.4	108	Q9UL77	Q9UL77 homo sapien
2	465.5	85.1	107	Q96SA9	Q96SA9 homo sapien
3	453	82.8	129	KV1W_HUMAN	P04431 homo sapien
4	449	82.1	108	KV1E_HUMAN	P01597 homo sapien
5	448.5	82.0	107	Q9UL81	Q9UL81 homo sapien
6	437	79.9	108	KV1H_HUMAN	P01600 homo sapien
7	433	79.2	236	Q6GMX8	Q6GMX8 homo sapien
8	431	78.8	236	Q6GMW1	Q6GMW1 homo sapien
9	430	78.6	236	Q6GMX0	Q6GMX0 homo sapien
10	428	78.2	236	Q6PIH7	Q6PIH7 homo sapien
11	424	77.5	108	KV1N_HUMAN	P01606 homo sapien
12	423	77.3	234	Q7Z473	Q7Z473 homo sapien
13	416	76.1	108	KV1B_HUMAN	P01594 homo sapien
14	416	76.1	108	KV1O_HUMAN	P01607 homo sapien
15	414	75.7	108	Q9UL70	Q9UL70 homo sapien
16	413.5	75.6	107	KV1D_HUMAN	P01596 homo sapien
17	413	75.3	129	Q9UL79	Q9UL79 homo sapien
18	412	75.3	109	KV1X_HUMAN	P04432 homo sapien
19	411.5	75.2	109	KV1T_HUMAN	P01612 homo sapien
20	411	75.1	108	KV1S_HUMAN	P01611 homo sapien
21	408	74.6	108	KV1V_HUMAN	P04430 homo sapien
22	408	74.6	236	Q7Z3Y4	Q7Z3Y4 homo sapien
23	407	74.4	108	KV1F_HUMAN	P01598 homo sapien
24	403	73.7	108	KV1A_HUMAN	P01608 homo sapien
25	402	73.5	108	KV1G_HUMAN	P01593 homo sapien
26	402	73.5	108	KV1I_HUMAN	P01599 homo sapien
27	401	73.3	108	KV1J_HUMAN	P01604 homo sapien
28	401	73.3	108	KV1Y_HUMAN	P08362 homo sapien
29	401	73.3	236	Q6PIT5	Q6PIT5 homo sapien
30	399	72.9	108	KV1R_HUMAN	P01610 homo sapien
31	398	72.8	236	Q6GMX9	Q6GMX9 homo sapien

32	397	72.6	244	2	Q65ZC8	Q65ZC8 homo sapien
33	396	72.4	108	1	KV1C_HUMAN	P01595 homo sapien
34	395	72.2	108	1	KV1M_HUMAN	P01605 homo sapien
35	395	72.2	236	2	Q6PIH4	Q6PIH4 homo sapien
36	394	72.0	240	2	Q65ZC9	Q65ZC9 homo sapien
37	393	71.8	108	1	KV1K_HUMAN	P01603 homo sapien
38	387	70.7	238	2	Q9QYF0	Q9QYF0 synthetic c
39	384	70.2	108	1	KV1Q_HUMAN	P01609 homo sapien
40	384	70.2	108	1	KV5M_MOUSE	P01646 mus musculu
41	383	70.0	117	1	KV1J_HUMAN	P01602 homo sapien
42	377	68.9	117	1	KV1I_HUMAN	P01601 homo sapien
43	375	68.6	108	1	KV5N_MOUSE	P01647 mus musculu
44	374	68.4	108	1	KV5K_MOUSE	P01644 mus musculu
45	374	68.4	116	2	Q96PF6	Q96PF6 homo sapien

ALIGNMENTS

RESULT 1									
ID	Q9UL77	PRELIMINARY;	PRT;	108	AA.				
AC	Q9UL77;								
DT	01-MAY-2000 (TREMBlrel. 13, Created)								
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)								
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)								
DE	Myosin-reactive immunoglobulin light chain variable region (Fragment).								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.								
OX	NCBI_Taxid:9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE:98277139; PubMed:9614934; DOI:10.1006/clin.1998.4531;								
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,								
RA	Young D.C.;								
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal								
RT	fetus.";								
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).								
DR	EMBL; AF035037; AAD56273.1; -.								
DR	PIR; B49047; B49047.								
DR	PIR; S34083; S34083.								
DR	HSSP; P01607; IBMW.								
DR	InterPro; IPR007110; Ig-like.								
DR	InterPro; IPR003596; Ig_v.								
DR	SMART; SM00406; IG_v.1.								
DR	PROSITE; PS50835; IG_LIKE; 1.								
FT	NON_TER								
FT	SEQUENCE								
SO	SEQUENCE								
Query Match									
Best Local Similarity 84.0%; Pred. No. 7.1e-41;									
Matches 89; Conservative 12; Mismatches 5; Indels 0; Gaps 0;									
Qy	1	ELTQSPSSLSASVGDRTVITTCRAQOSTITLNTQYQKRGAKLLISASNLGCVSRF	60						
Db	3	QMTQSPSSLSASVGDRTVITTCRASQSSISYLNWYQKRGAPNLLIYAASLSGVSRRF	62						
Qy	61	SGSGSGEFTLTISNLOFEDPASYYCOQSYTTLVTFGSGTKLEIKR	106						
Db	63	SGSGSGEFTLTISNLOFEDPASYYCOQSYTTLVTFGSGTKLEIKR	108						
RESULT 2									
ID	Q96SA9	PRELIMINARY;	PRT;	107	AA.				
AC	Q96SA9;								
DT	01-DEC-2001 (TREMBlrel. 19, Created)								
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)								
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)								
DE	Anti-streptococcal/anti-myosin immunoglobulin kappa light chain								

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DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.B., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mycosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AB86785.1; -.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSSP; P01607; 1BWM.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 85.1%; Score 465.5; DB 2; Length 107;
Best Local Similarity 85.8%; Pred. No. 1e-40; 3; Indels 1; Gaps 1;
Matches 91; Conservative 11; Mismatches 3;

QY 1 ELTQSPSSLSASVGDRTITTCRAQSISTYLNWYQKPGKAPKLLIMASNLGVSRSF 60
Db 3 QMTQSPSSLSASVGDRTITTCRAQSISTYLNWYQKPGKAPKLLIYAASLSGVSRSF 62
61 SSGSGGTFFLTITSLNLOFEDPASYYCOQSTYTTLYTSGSKLEIKR 106
63 SSGSGGTFFLTITSLNLOFEDPASYYCOQSTYTTLYTSGSKLEIKR 107

RESULT 3
KVLE_HUMAN STANDARD; PRT; 129 AA.
ID KVLE_HUMAN STANDARD; PRT; 129 AA.
AC P0431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combrici G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC -----
DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; KIHDMK.
DR HSSP; P01607; 1BWM.

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DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 23 129
FT DOMAIN 23 45
FT DOMAIN 46 56
FT DOMAIN 57 71
FT DOMAIN 72 78
FT DOMAIN 79 110
FT DOMAIN 111 119
FT DOMAIN 120 129
FT DISULFID 45 110
FT NON_TER 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07DAFC2F9 CRC64;

Query Match 82.8%; Score 453; DB 1; Length 129;
Best Local Similarity 83.8%; Pred. No. 2.5e-39; 7; Indels 0; Gaps 0;
Matches 88; Conservative 10; Mismatches 7;

QY 1 ELTQSPSSLSASVGDRTITTCRAQSISTYLNWYQKPGKAPKLLIMASNLGVSRSF 60
Db 25 QMTQSPSSLSASVGDRTITTCRAQSISTYLNWYQKPGKAPKLLIYAASLSGVSRSF 84
61 SSGSGGTFFLTITSLNLOFEDPASYYCOQSTYTTLYTSGSKLEIKR 105
85 SSGSGGTFFLTITSLNLOFEDPASYYCOQSTYTTLYTSGSKLEIKR 129

RESULT 4
KVLE_HUMAN STANDARD; PRT; 108 AA.
ID KVLE_HUMAN STANDARD; PRT; 108 AA.
AC P01597;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region DEE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72053133; PubMed=5124396;
RA Mistein C.P., Deveron E.V.;
RT "The amino acid sequence of a human kappa light chain."
RL Biochem. J. 123:945-958(1971).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
DR PIR; A01865; KIHUDE.
DR HSSP; P01607; 1BWM.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88

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FT  NON_TER      108      108
SQ  SEQUENCE      108 AA; 11661 MW; BDD6B350017F1E51 CRC64;

Query March
Best Local Similarity 82.1%; Score 449; DB 1; Length 108;
Matches 85; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY  1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQQRKPKLLMSASNLQSGVPSRF 60
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB  3 ZMTQSPSSLSASVGDRTVITTCRARSISYLNWYQQRKPKPKYLLIFASLSKGVPSRF 62
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

QY  61 SGGSGGTFFLTITISNLOFEDPASVYCCQSYTTLYTFSSGTYLEIKR 106
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB  63 SGGSGGTDFLTITISGLLPEDFATVYCCQSYTTPYTFPGTKEVEMTR 108
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

RESULT 5
Q9UL81 PRELIMINARY; PRT; 107 AA.
ID  Q9UL81;
AC  Q9UL81;
DT  01-MAY-2000 (TREMBlrel. 13, Created)
DT  01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE  01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE  Myosin-reactive immunoglobulin light chain variable region
    (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Betney S.M.,
RA  Young D.C.;
RT  "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT  fetus.";
RL  Clin. Immunol. Immunopathol. 87:184-192(1998).
DR  EMBL; AF035033; AAD56269.1; -
DR  HSSP; P01607; IBMW
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003596; Ig_v.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PSS0835; IG_LIKE; 1.
FT  NON_TER      1
FT  NON_TER      107
SQ  SEQUENCE      107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query March
Best Local Similarity 82.0%; Score 448.5; DB 2; Length 107;
Matches 87; Conservative 11; Mismatches 7; Indels 1; Gaps 1;

QY  1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQQRKPKLLMSASNLQSGVPSRF 60
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB  3 QMTQSPSSLSASVGDRTVITTCRARSISYLNWYQQRKPKPKYLLIFASLSKGVPSRF 62
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

QY  61 SGGSGGTFFLTITISNLOFEDPASVYCCQSYTTLYTFSSGTYLEIKR 106
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB  63 SGGSGGTDFLTITISGLLPEDFATVYCCQSYTTPYTFPGTKEVEMTR 107
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

RESULT 6
KV1H_HUMAN STANDARD; PRT; 108 AA.
ID  KV1H_HUMAN
AC  P01600;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DE  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Ig kappa chain V-I region Hau.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]

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RP  SEQUENCE.
RX  MEDLINE=71032830; PubMed=4097974;
RA  Watanabe S., Hilschmann N.;
RT  "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT  chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT  subgroups.";
RL  Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC  -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC  -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR  PIR; A01868; KIHUHU.
DR  PDB; 1FEU; X-ray; L=1-108.
DR  GO; GO:0005576; C:extracellular; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PSS0835; IG_LIKE; 1.
KW  3D-structure; Bence-Jones protein; Direct protein sequencing;
KW  Immunoglobulin V region.
FT  DOMAIN 1 23 Framework-1.
FT  DOMAIN 24 34 Complementarity-determining-1.
FT  DOMAIN 35 49 Framework-2.
FT  DOMAIN 50 56 Complementarity-determining-2.
FT  DOMAIN 57 88 Framework-3.
FT  DOMAIN 89 97 Complementarity-determining-3.
FT  DOMAIN 98 107 Framework-4.
FT  DISULFID 23 88 By similarity.
FT  NON_TER      108
SQ  SEQUENCE      108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query March
Best Local Similarity 79.9%; Score 437; DB 1; Length 108;
Matches 83; Conservative 16; Mismatches 7; Indels 0; Gaps 0;

QY  1 ELTQSPSSLSASVGDRTVITTCRARSISTYLNWYQQRKPKLLMSASNLQSGVPSRF 60
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB  3 QMTQSPSSLSASVGDRTVITTCRARSISYLNWYQQRKPKPKYLLIFASLSKGVPSRF 62
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

QY  61 SGGSGGTFFLTITISNLOFEDPASVYCCQSYTTLYTFSSGTYLEIKR 106
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
DB  63 SGGSGGTDFLTITISGLLPEDFATVYCCQSYTTPYTFPGTKEVEMTR 108
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

RESULT 7
Q6GMX8 PRELIMINARY; PRT; 236 AA.
ID  Q6GMX8
AC  Q6GMX8;
DT  05-JUL-2004 (TREMBlrel. 27, Created)
DT  05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE  05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE  Hypothetical protein.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  TISSUE=Primary B-Cells;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Scheffen C.F., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marisica K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA  Bosak S.A., McEwan P.O., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Huijck S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN
RP
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC073764; AAH73764.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003066; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; C1-sec; 1.
DR Pfam: PF07654; Ig; 2.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00406; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PSS0835; IG LIKE; 2.
DR PROSITE: PSS0230; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E1AB6559EFC9 CRC64;

Query Match 79.2%; Score 433; DB 2; Length 236;
Best Local Similarity 77.4%; Pred. No. 6,1e-37;
Matches 82; Conservative 17; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTYITTCRAQOSISTYLMYQOKPGKAPKLLMSASNLQSGVPSRF 60
Db 25 QMTQSPSSLSASVGDRTYITTCRAQOSISMLAWQOKPGKAPKLLIYAASLSQGVPSRF 84
QY 61 SGSGSGTFFLTITSLNLOFEDPASYCOQSYTTLTYTSGSKLEIKR 106
Db 85 SGSGSGTFFLTITSLNLOFEDPASYCOQAHSPFTFGPKTKVDIKR 130

RESULT 8
Q6GKMI PRELIMINARY; PRT; 236 AA.
AC Q6GKMI;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN
RP
RC TISSUE=Primary B-Cells;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bock S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN
RP
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC073791; AAH73791.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003066; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; C1-sec; 1.
DR Pfam: PF07654; Ig; 2.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00406; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PSS0835; IG LIKE; 2.
DR PROSITE: PSS0230; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BF6A087AFA437 CRC64;

Query Match 78.8%; Score 431; DB 2; Length 236;
Best Local Similarity 79.2%; Pred. No. 9,8e-37;
Matches 84; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTYITTCRAQOSISTYLMYQOKPGKAPKLLMSASNLQSGVPSRF 60
Db 25 QMTQSPSSLSASVGDRTYITTCRAQOSISMDLWYQOKPGKAPKLLIYAASLSQGVPSRF 84
QY 61 SGSGSGTFFLTITSLNLOFEDPASYCOQSYTTLTYTSGSKLEIKR 106
Db 85 SGSGSGTFFLTITSLNLOFEDPASYCOQAHSPFTFGPKTKVDIKR 130

RESULT 9
Q6GKXO PRELIMINARY; PRT; 236 AA.
AC Q6GKXO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN
RP
RC TISSUE=Spleen;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bock S.A., McEwan P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073775; AAH3775.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; Ig; 2.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_1.
DR Hypothetical protein_
KM SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8 CRC64;
SQ
Query Match 78.6%; Score 430; DB 2; Length 236;
Best Local Similarity 77.4%; Pred. No. 1,3e-36;
Matches 82; Conservative 13; Mismatches 11; Indels 0; Gaps 0;
Qy 1 ELTSPSPSLASVGDRTVITTCRAQSISTYLNWYQKRGKAPKLLMSASNLGSGVPSRF 60
Db 25 QLTSPSPFLASVGDRTVITTCRASQGISSTYLNWYQKRGKAPNLLIYAASLTGSGVPSRF 84
Qy 61 SGSSGSGTEFTLTISNLQPEDPASYCCOQSYTTLYTPSGGTLEIKR 106
Db 85 SGSSGSGTEFTLTISNLQPEDPASYCCOQSYTTLYTPSGGTLEIKR 130
RESULT 10
ID Q6PIH7 PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg H., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshlyuk S., Carlini P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Mair M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strauberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -.
DR HSSP; P01607; IAK2.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Ig; 1.
DR PROSITE; PSS0835; IG_LIKE; 2.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_1.
DR Hypothetical protein_
KM SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;
SQ
Query Match 78.2%; Score 428; DB 2; Length 236;
Best Local Similarity 80.2%; Pred. No. 2e-36;
Matches 85; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
Qy 1 ELTSPSPSLASVGDRTVITTCRAQSISTYLNWYQKRGKAPKLLMSASNLGSGVPSRF 60
Db 25 QLTSPSPFLASVGDRTVITTCRASQGISSTYLNWYQKRGKAPNLLIYAASLTGSGVPSRF 84
Qy 61 SGSSGSGTEFTLTISNLQPEDPASYCCOQSYTTLYTPSGGTLEIKR 106
Db 85 SGSSGSGTEFTLTISNLQPEDPASYCCOQSYTTLYTPSGGTLEIKR 130
RESULT 11
ID KVIN_HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
chain".
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
macroglobulin.
CC PIR: A01872; KIHOU.
DR HSSP; P01607; IEMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 2 34 Complementarity-determining-1.
FT DOMAIN 3 35 Framework-2.
FT DOMAIN 4 49 Complementarity-determining-2.
FT DOMAIN 50 56 Complementarity-determining-3.
FT DOMAIN 57 88 Complementarity-determining-4.
FT DOMAIN 89 97 Framework-3.
FT DOMAIN 98 107 Framework-4.

FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283D4A24105827E CRC64;
Query Match 77.5%; Score 424; DB 1; Length 108;
Best Local Similarity 68.9%; Pred. No. 2.2e-36;
Matches 73; Conservative 25; Mismatches 8; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITTCRAQOSISTYLMWYQKPKAKPKLLMSASNLGSPSRF 60
DB 3 QMTZSPSSLSASVGBRVITTCRASZITSSYLBWYZKRGKAPBLLIYAASHLSGVSRRF 62
QY 61 GSGSGTFFLTITSLNLOFEDFASYYCOOSTYTLTPSSGRTLEIKR 106
DB 63 GSGSGTFFLTITSLTPZBPAFYCCZSYSPPTFGZGRLZIKR 108
RESULT 12
Q72473 PRELIMINARY; PRT; 234 AA.
AC Q72473;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshitsuki S., Carninci P., Prange C.,
RA Raha S.S., Loughlano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosnak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalek U., Smaluk D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC056256; AAHS6256.1; -;
DR HSSP: P01834; 1HEZ.
DR InterPro: IPR007110; Ig-1like.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; C1-sect; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG_LIKE; 2.
DR PROSITE: PSS0290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BCOF CRC64;
Query Match 77.3%; Score 423; DB 2; Length 234;
Best Local Similarity 78.1%; Pred. No. 6.6e-36;

Matches 82; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
QY 2 LTQSPSSLSASVGDRTVITTCRAQOSISTYLMWYQKPKAKPKLLMSASNLGSPSRF 61
DB 24 MTQSPSSLSASVGDRTVITTCRAQOSIGSYLMWYQKPKAKPKLLIYAASHLSGVSRRF 83
QY 62 GSGSGTFFLTITSLNLOFEDFASYYCOOSTYTLTPSSGRTLEIKR 106
DB 84 GSGSGTFFLTITSLCLQSEDFATYYCCQYYTYPTFGQTKVEIKR 128
RESULT 13
KV1B_HUMAN STANDARD; PRT; 108 AA.
ID KV1B_HUMAN
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-1 region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Haischmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlgamer H., Schiffer M., Bpp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the Bence-
RT Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -1- MISCELLANEOUS: The structure of the V region was determined by
CC molecular replacement methods using the known structure of the V
CC region of the kappa chain RL.
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR: A91653; K1H0U0.
DR PDB: 1JVS; X-ray; A=1-107.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-1like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; IGV; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 2 34 Complementarity-determining-1.
FT DOMAIN 3 35 Framework-2.
FT DOMAIN 4 49 Complementarity-determining-2.
FT DOMAIN 5 56 Complementarity-determining-3.
FT DOMAIN 6 88 Complementarity-determining-4.
FT DOMAIN 7 97 Framework-3.
FT DOMAIN 8 107 Complementarity-determining-3.
FT DISULFID 23 88 By similarity.
FT STRAND 4 5
FT STRAND 10 13
FT STRAND 15 16
FT STRAND 19 25
FT STRAND 30 31
FT STRAND 33 38
FT STRAND 40 41
FT STRAND 44 49
FT STRAND 50 52

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FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108
SQ SEQUENCE 108 AA; 11939 MW; E801187EE6F6FB9 CRC64;

Query Match 76.1%; Score 416; DB 1; Length 108;
Best Local Similarity 76.4%; Pred. No. 1.5e-35;
Matches 81; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARQSIQTYLWYQKPGKAPKLLIWSASNLQSGVPSRF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSLSASVGDRTVITTCQASQDISDYLNWYQKPGKAPKLLIYDASVLSGVSF 62
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGGSGSGTEFLTITSNLOFEDPASVYCCOQSYTTLTYTSGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SGGSGSGHFTFTTISLQPEDIAITYCCQYDYLFWTFQGTKEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
KV10_HUMAN STANDARD; PRT; 108 AA.
ID KV10_HUMAN
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Iq kappa chain V-I region Rel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type I-chain; subgroup I (Bence-Jones protein Rel); isolation
RT and characterization of the cryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191 (1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein Rel refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952 (1975).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91663; KIHURE.
DR PDB; 1AR2; X-ray; @=1-107.
DR PDB; 1BMW; X-ray; A/B=1-107.
DR PDB; 1REI; X-ray; A/B=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.

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FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DISULFID 98 107 Framework-4.
FT STRAND 10 13
FT STRAND 15 16
FT TURN 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 76.1%; Score 416; DB 1; Length 108;
Best Local Similarity 75.5%; Pred. No. 1.5e-35;
Matches 80; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRARQSIQTYLWYQKPGKAPKLLIWSASNLQSGVPSRF 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QMTQSPSSLSASVGDRTVITTCQASQDISDYLNWYQKPGKAPKLLIYDASVLSGVSF 62
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SGGSGSGTEFLTITSNLOFEDPASVYCCOQSYTTLTYTSGSGTKLEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 SGGSGSGHFTFTTISLQPEDIAITYCCQYDYLFWTFQGTKEIKR 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70
AC Q9UL70;
DT 01-MAY-2000 (TREMBlRel. 13, Created)
DT 01-MAY-2000 (TREMBlRel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlRel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; 1BMW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 108
FT NON_TER 108

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SO SEQUENCE 108 AA; 1163 MW; B7BEDC3E41FCCA37 CRC64;

Query Match	75.7%;	Score 414;	DB 2;	Length 108;
Best local Similarity	77.4%;	Pred No 2	4e-35.	

Best Local Similarity 77.4%; Pred. No. 2.4e-35;
Matches 82; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

Matches 82; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

0Y 1 ELTQSPSSLASVGDVTTTCRARQISITLYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60

db 3 QMTQSPSSLSASVGDRVITTCRASQGISNTLAWYQQKPKSLIYAASITLQGVPSRF 62

61 SGGSGTEFTLTISNLQFEDFASYYCQDSYTTLYTFGSGTKLEIKR 106

Db 63 SGGSGTDFLTISLQPEDVATYYCQKNSAPRTFGPGTKLEIKR 108

Search completed: July 26, 2005, 09:26:20
Job time: 67.6515 sec

Job time : 67.6515 secs

PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 40; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to Phl p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific Fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The Fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific Fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to Phl p 2. The present sequence represents the human IgG
CC Fab, clone 60 light chain protein of the invention
XX
SQ Sequence 106 AA:
Query Match 98.2%; Score 537; DB 5; Length 106;
Best Local Similarity 99.1%; Pred. No. 5.8e-30;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ELTQSPSLASVGDRTYTCRAROSISTYLNWYQKRGKAPKLLIMASNLQGVPSRF 60
Db 1 ELTQSPSLASVGDRTYTCRAROSISTYLNWYQKRGKAPKLLIMASNLQGVPSRF 60
QY 61 SSGSGGTFTLTISNLOFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106
Db 61 SSGSGGTFTLTISNLOFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106
RESULT 2
ID AAR54260 standard; protein; 107 AA.
XX
AC AAR54260;
XX
DT 25-MAR-2003 (revised)
DT 10-NOV-1994 (first entry)
XX
DE Anti-HIV gp120 immunoglobulin light chain variable region b22.
XX
XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KM neutralisation; monoclonal antibody; kappa light chain; variable region;
KM framework; complementarity determining region.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..21
FT /label= FR1
FT 22..33
FT /label= CDR1
FT 34..48
FT /label= FR2
FT 49..55
FT /label= CDR2
FT 56..87
FT /label= FR3
FT 88..95
FT /label= CDR3
FT 96..107
FT /label= FR4
XX
PN WO9407922-A1.
XX

PD 14-APR-1994.
XX
XX 30-SEP-1993; 93WO-US009328.
PF
XX 30-SEP-1992; 92US-00954148.
PR
XX (SCRI) SCRIIPS RES INST.
PA
PI Burton DR, Barbas CF, Lerner RA;
PI
XX WPI; 1994-135516/16.
DR
XX New human monoclonal antibodies neutralising HIV - react with gp120 or
PT gp120 and nucleic acid encoding them, useful for in vivo or in vitro
PT diagnosis and for passive immuno-therapy.
XX
XX Claim 5; Page 189; 248pp; English.
PS
XX Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
CC using primers specific for heavy and light chain variable regions. The
CC amplification products were inserted into a dicistronic vector to produce
CC a library of fragments. E.coli XLI Blue cells were transformed with the
CC library. Filamentous phage were produced which expressed the Mab regions
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
CC immunoreactive clones. The light chain VK region sequence AAR54260
CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 107 AA:
Query Match 88.5%; Score 484; DB 2; Length 107;
Best Local Similarity 88.7%; Pred. No. 2.2e-26;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
QY 1 ELTQSPSLASVGDRTYTCRAROSISTYLNWYQKRGKAPKLLIMASNLQGVPSRF 60
Db 1 ELTQSPSLASVGDRTYTCRAROSISTYLNWYQKRGKAPKLLIMASNLQGVPSRF 60
QY 61 SSGSGGTFTLTISNLOFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106
Db 61 SSGSGGTFTLTISNLOFEDFASYYCOQSYTTLTYFGSGTKLEIKR 106
RESULT 3
ID AAM01283 standard; protein; 107 AA.
XX
AC AAM01283;
XX
DT 29-JAN-1997 (first entry)
DT
XX
DE VL region of HIV neutralising Mab, clone b22 and B35.
XX
XX Heavy chain; light chain; variable region; VH; monoclonal antibody; Mab;
KM HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KM virus infectivity assay; precursor gp160; immunocompetence; human;
KM anti-HIV antibody; detection; HIV infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..21
FT /label= FR1
FT 22..32
FT /label= CDR1
FT 33..47
FT /label= FR2
FT 48..54
FT /label= CDR2
FT 55..86
FT /label= FR3
FT 87..95
FT /label= CDR3
FT 96..107
FT /label= FR4
XX
PN Region
FT


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FT      /label= FR4
XX      MO9602273-A1.
XX      01-FEB-1996.
XX      11-JUL-1995; 95MO-US008743.
XX      18-JUL-1994; 94US-00276852.
XX      (SCRI ) SCRIPPS RES INST.
XX      Burton DR, Barbas CF, Lerner RA;
XX      WPI, 1996-179601/18.
XX      Monoclonal antibody binding to VI/V2 loop of HIV gp120 - used in passive
XX      immuno-therapy and detection of HIV infection.
XX      Example: Fig 11; 366pp; English.
XX      The sequences given in AAW01261-92 represent the light chain variable
XX      regions (VL) of a series of monoclonal antibodies (Mab's) which are
XX      immunoreactive with HIV glycoprotein gp120 and are capable of
XX      neutralising HIV. This sequence represents the sequence of the JK2 gene
XX      clones, b22 and B35. A Mab containing this VL sequence has the capacity
XX      to reduce HIV infectivity titre in an in vivo virus infectivity assay by
XX      50 % at a concentration of less than 700 ng of antibody/ml, and binds
XX      mature gp120 preferentially over the precursor gp160. The Mab may be used
XX      for determining immunocompetence of a human anti-HIV antibody and in the
XX      detection of HIV infection
XX      Sequence 107 AA;
SQ
Query Match      88.5%; Score 484; DB 2; Length 107;
Best Local Similarity 88.7%; Pred. No. 2.6e-26;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY      1 ELTQSPSSLSASVGDRTVITTCARQOSISTYLNWYQOKRGKAPKLIWASNLQGVPSRF 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      1 ELTQSPSSLSASVGDRTVITTCARQOSISTYLNWYQOKRGKAPKLIWASNLQGVPSRF 60

QY      61 SSGSGTEFTLTISNLQPEDFASYCCOOSYTTLYTFGSGTKLEIKR 106
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      61 SSGSGTEFTLTISNLQPEDFASYCCOOSYTTLYTFGSGTKLEIKR 106

RESULT 4
AAV98244
ID      AAV98244 standard; protein; 107 AA.
AC      AAV98244;
XX
XX      04-JUL-2000 (first entry)
XX
XX      Anti-gp120 antibody light chain variable region from clone b22.
DE
XX      Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
XX      human immunodeficiency virus type 1; HIV-1; infectivity titre;
XX      passive immunotherapy; reduce severity; HIV-induced disease;
XX      immunocompetence; active immunisation.
XX
XX      Homo sapiens.
XX
XX      AU9948754-A.
XX
XX      17-FEB-2000.
XX
XX      16-SEP-1999; 99AU-00048754.
XX
XX      16-SEP-1999; 99AU-00048754.
XX
XX      (SCRI ) SCRIPPS RES INST.

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XX      Burton DR, Barbas CF, Lerner RA;
XX      WPI, 2000-246867/22.
XX      Human neutralizing monoclonal antibodies to human immunodeficiency virus
XX      (HIV) used for providing passive immunotherapy to HIV are specific for
XX      glycoprotein-120.
XX      Example 9; Fig 11; 374pp; English.
XX      This sequence represents a fragment of the antibodies of the invention.
XX      The invention relates to the production of an anti-HIV (human
XX      immunodeficiency virus) glycoprotein (gp) -120 monoclonal antibody capable
XX      of reducing an HIV infectivity titre in an in vitro virus infectivity
XX      assay by 50% at a concentration of less than 70 ng/ml. The method for the
XX      production of the antibody comprises: (a) providing a first
XX      polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
XX      (which does not comprise the sequence represented by AAV98206) and a
XX      second polynucleotide encoding a light chain immunoglobulin amino acid
XX      sequence; (b) inserting the first and second polynucleotide sequences
XX      into a host cell; (c) maintaining the host cell in conditions which allow
XX      the amino acid sequences encoded by the polynucleotides to be expressed
XX      in the host cell; and (d) isolating the antibody comprising the heavy and
XX      light chain immunoglobulin amino acid sequences from the host cell. The
XX      anti-HIV gp-120 monoclonal antibody is used for providing passive
XX      immunotherapy to HIV in a human. They can be administered to high-risk
XX      patients to reduce the likelihood and/or severity of HIV-induced disease
XX      and to patients who are already HIV-infected. The antibodies are used for
XX      neutralising field isolates which provides information about the
XX      immunocompetence of an immune response in HIV patients, for detecting HIV
XX      in a biological fluid or tissue sample e.g. by radioimmunoassay, for
XX      producing anti-idiotypic antibodies which can be used for active
XX      immunisation and to screen human monoclonal antibodies to identify those
XX      with the same binding specificity and to monitor the course of HIV
XX      disease therapy by measuring the changes in concentration of HIV present
XX      in the body or in body fluids by immunoassay. The anti-HIV gp-120
XX      monoclonal antibodies are encoded by a human polynucleotide sequence and
XX      when used in vivo for diagnosis and immunotherapy of HIV-induced disease
XX      reduce the problems of significant host immune response to the antibodies
XX      associated with monoclonal antibodies of xenogeneic or chimeric
XX      derivation
XX      Sequence 107 AA;
SQ
Query Match      88.5%; Score 484; DB 3; Length 107;
Best Local Similarity 88.7%; Pred. No. 2.6e-26;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY      1 ELTQSPSSLSASVGDRTVITTCARQOSISTYLNWYQOKRGKAPKLIWASNLQGVPSRF 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      1 ELTQSPSSLSASVGDRTVITTCARQOSISTYLNWYQOKRGKAPKLIWASNLQGVPSRF 60

QY      61 SSGSGTEFTLTISNLQPEDFASYCCOOSYTTLYTFGSGTKLEIKR 106
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      61 SSGSGTEFTLTISNLQPEDFASYCCOOSYTTLYTFGSGTKLEIKR 106

RESULT 5
AAV95135
ID      AAV95135 standard; protein; 107 AA.
AC      AAV95135;
XX
XX      30-JUN-2000 (first entry)
XX
XX      Anti-gp120 antibody light chain variable region from clone b22.
DE
XX      Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
XX      reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
XX      glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
XX
XX      Homo sapiens.

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XX AU9948756-A.
 PN 17-FEB-2000.
 PD 16-SEP-1999; 99AU-00048756.
 XX 16-SEP-1999; 99AU-00048756.
 PR 16-SEP-1999; 99AU-00048756.
 XX (SCRI) SCRIPPS RES INST.
 PA Burton DR, Barbas CF, Lerner RA;
 XX WPI; 2000-293393/26.
 DR
 PT Novel human monoclonal antibodies which immunoreact with and neutralize
 XX human immunodeficiency virus useful for treating HIV infections.
 PT
 XX Example 9; Fig 11; 366pp; English.
 PS
 XX The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralizes HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50%, at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
 CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantage of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV
 CC
 XX Sequence 107 AA;
 SQ
 Query Match 88.5%; Score 484; DB 3; Length 107;
 Best Local Similarity 88.7%; Pred. No. 2.6e-26;
 Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ELTQSPSLASVGDRTVITTCRARSISTYLNWYQKPGKAPKLIWSASNLQSGVPSRF 60
 DB 1 ELTQSPSLASVGDRTVITTCRARSISTYLNWYQKPGKAPKLIWAASSLQSGVPSRF 60
 QY 61 SSGSGTEFTLTISNLQFEDFASYYCOOSYTTLYTFGSGTKLEIKR 106
 DB 61 SSGSGGIDFTLTISLQPEDFATYYCOOSYSTLTFTFGGTKLEIKR 106
 RESULT 6
 AAG93590
 ID AAG93590 standard; protein; 107 AA.
 AC AAG93590;
 XX 14-SEP-2001 (first entry)
 XX Human anti-Rh(D) chain I02 protein sequence.
 DE Human anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW

KW red blood cell; Rh phenotype; diagnosis; therapeutic.
 XX Homo sapiens.
 OS US6255455-B1.
 XX 03-JUL-2001.
 PD 29-JAN-1999; 99US-00240274.
 XX 29-JAN-1999; 99US-00240274.
 PF 11-OCT-1996; 96US-0028550P.
 XX 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA
 XX Siegel DL;
 PI
 XX WPI; 2001-388931/41.
 DR N-PSDB; AAH68647.
 XX
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX Claim 1; Col 43; 162pp; English.
 PS
 XX The present invention describes an isolated Rh(D) binding protein.
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (II) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determining the Rh phenotype of human red blood cells.
 CC AA668615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention
 XX
 XX Sequence 107 AA;
 SQ
 Query Match 88.3%; Score 483; DB 4; Length 107;
 Best Local Similarity 87.7%; Pred. No. 3.1e-26;
 Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ELTQSPSLASVGDRTVITTCRARSISTYLNWYQKPGKAPKLIWSASNLQSGVPSRF 60
 DB 2 ELTQSPSLASVGDRTVITTCRARSISTYLNWYQKPGKAPKLIWAASSLQSGVPSRF 61
 QY 61 SSGSGTEFTLTISNLQFEDFASYYCOOSYTTLYTFGSGTKLEIKR 106
 DB 62 SSGSGGIDFTLTISLQPEDFATYYCOOSYSTLTFTFGGTKLEIKR 107
 RESULT 7
 ABO27397
 ID ABO27397 standard; protein; 107 AA.
 AC ABO27397;
 XX 12-SEP-2003 (first entry)
 XX Anti-Rh(D) chain I02.
 DE Human, Rh(D) binding protein; blood typing; blood product; antibody;
 XX magnetically activated cell sorting.
 KW Homo sapiens.
 OS US2003040605-A1.
 XX 27-FEB-2003.
 PD

PF 04-MAY-2001; 2001US-00848798.
XX
XX 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-0088404S.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
XX
XX WPI; 2003-512273/48.
DR N-PSDB; ACD45311.
XX
XX New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
XX
XX Claim 4; Page 26; 187pp; English.
XX
XX The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents the amino acid sequence of a human anti-Rh(D) chain
XX
SQ Sequence 107 AA;

Query Match 88.3%; Score 483; DB 6; Length 107;
Best Local Similarity 87.7%; Pred. No. 3,1e-26;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ELTQSPSLASVGDRTITTCRAQSISTYLMWYQKPKKLIASNLQSGVPSRF 60
Db 2 ELTQSPSLASVGDRTITTCRAQSISTYLMWYQKPKKLIYAASLRGVSFRF 61
61 SGGSGGTEFTLTISNLQFEDFASYCCQOQSYTTLYTFGSGTKLEIKR 106
62 SGGSGGTDFTLTISLQPEDFATYCCQOQSYTTLYTFGSGTKLEIKR 107
Db

RESULT 8
AAG93644
ID AAG93644 standard; protein; 107 AA.
XX
XX AAG93644;
XX
XX 14-SEP-2001 (first entry)
XX
XX Human anti-Rh(D) antibody clone SH13 protein sequence.
XX
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
XX Homo sapiens.
XX
XX US6255455-B1.
XX
XX 03-JUL-2001.
XX
XX 29-JAN-1999; 99US-00240274.
XX
XX 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-0088404S.
PR 10-APR-1998; 98US-0081380P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
XX
XX WPI; 2001-388931/41.
DR N-PSDB; AAH68701.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in

PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX Claim 1; Col 68; 162pp; English.
XX
XX The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
XX Sequence 107 AA;

Query Match 87.8%; Score 480; DB 4; Length 107;
Best Local Similarity 87.7%; Pred. No. 5e-26;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Oy 1 ELTQSPSLASVGDRTITTCRAQSISTYLMWYQKPKKLIASNLQSGVPSRF 60
Db 2 ELTQSPSLASVGDRTITTCRAQSISTYLMWYQKPKKLIYAASLRGVSFRF 61
61 SGGSGGTEFTLTISNLQFEDFASYCCQOQSYTTLYTFGSGTKLEIKR 106
62 SGGSGGTDFTLTISLQPEDFATYCCQOQSYTTLYTFGSGTKLEIKR 107
Db

RESULT 9
ABO27451
ID ABO27451 standard; protein; 107 AA.
XX
XX ABO27451;
XX
XX 12-SEP-2003 (first entry)
XX
XX Anti-Rh(D) light chain SH13.
XX
XX Human; RH(D) binding protein; blood typing; blood product; antibody;
KW magnetically activated cell sorting.
XX
XX Homo sapiens.
XX
XX US2003040605-A1.
XX
XX 27-FEB-2003.
XX
XX 04-MAY-2001; 2001US-00848798.
XX
XX 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-0088404S.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
XX
XX WPI; 2003-512273/48.
DR N-PSDB; ACD45365.
XX
XX New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
XX
XX Claim 4; Page 50; 187pp; English.
XX
XX The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,

CC including typing of blood or blood products. The present sequence
CC represents the amino acid sequence of a human anti-Rh(D) chain
XX
SQ Sequence 107 AA;

Query Match 87.8%; Score 480; DB 6; Length 107;
Best Local Similarity 87.7%; Pred. No. 5e-26;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTSPSSLSASVGDRTITTCRASQISITLYLWYQOKPGKAPKLLIMASNLQSGVPSRF 60
Db 2 ELTSPSSLSASVGDRTITTCRASQISITLYLWYQOKPGKAPKLLIMASNLQSGVPSRF 61

QY 61 SGGSGTEFTLLTISNLOFEDPASYCCQSYTTLYTFGSGTKLEIKR 106
Db 62 SGGSGTEFTLLTISNLOFEDPASYCCQSYTTLYTFGSGTKLEIKR 107

RESULT 10

AAR54261
ID AAR54261 standard; protein; 107 AA.

AC AAR54261;

DT 25-MAR-2003 (revised)
DT 10-NOV-1994 (first entry)

DE Anti-HIV gp120 immunoglobulin light chain variable region b27.

XX Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain; variable region;
KW framework; complementarity determining region.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..21 /label= FR1

FT Region 22..33 /label= CDR1

FT Region 34..48 /label= FR2

FT Region 49..55 /label= FR2

FT Region 56..87 /label= CDR2

FT Region 88..95 /label= FR3

FT Region 96..107 /label= CDR3

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

CC amplification products were inserted into a dicistronic vector to produce
CC a library of fragments. E.coli XL1 Blue cells were transformed with the
CC library. Filamentous phage were produced which expressed the Mab regions
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
CC immunoreactive clones. The light chain VK region sequence AAR54261
CC neutralises HIV gp120. (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 107 AA;

Query Match 87.0%; Score 476; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 9.4e-26;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTSPSSLSASVGDRTITTCRASQISITLYLWYQOKPGKAPKLLIMASNLQSGVPSRF 60
Db 1 ELTSPSSLSASVGDRTITTCRASQISITLYLWYQOKPGKAPKLLIMASNLQSGVPSRF 60

QY 61 SGGSGTEFTLLTISNLOFEDPASYCCQSYTTLYTFGSGTKLEIKR 106
Db 61 SGGSGTEFTLLTISNLOFEDPASYCCQSYTTLYTFGSGTKLEIKR 106

RESULT 11

AAW01284
ID AAW01284 standard; protein; 107 AA.

AC AAW01284;

DT 29-JAN-1997 (first entry)

DE VL region of HIV neutralising Mab, clone b27.

XX Heavy chain; light chain; variable region; VH; monoclonal antibody; Mab;
KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..21 /label= FR1

FT Region 22..32 /label= CDR1

FT Region 33..47 /label= FR2

FT Region 48..54 /label= CDR2

FT Region 55..86 /label= FR3

FT Region 87..95 /label= CDR3

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

FT Region 96..107 /label= FR4

Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in passive
immuno-therapy and detection of HIV infection.
Example; Fig 11; 366pp; English.

XX The sequences given in AAW01261-92 represent the light chain variable
CC regions (VL) of a series of monoclonal antibodies (Mab's) which are
CC immunoreactive with HIV glycoprotein gp120 and are capable of
CC neutralising HIV. This sequence represents the sequence of the JK2 gene
CC clone, b27. A Mab containing this VL sequence has the capacity to reduce
CC HIV infectivity titre in an in vitro virus infectivity assay by 50 % at a
CC concentration of less than 700 ng of antibody/ml, and binds mature gp120
CC preferentially over the precursor gp160. The Mab may be used for
CC determining immunocompetence of a human anti-HIV antibody and in the
CC detection of HIV infection
CC
XX
SQ Sequence 107 AA;
Query Match 87.0%; Score 476; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 9.4e-26;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
Dy 1 ELTQSPSSLASVGVDRVTITCRARQSIISTYLNWYQQRKGAKPKLLIWSASNLQSGVPSRF 60
1 ELTQSPSSLASVGVDRVTITCRARQSIISTYLNWYQQRKGAKPKLLIWSASNLQSGVPSRF 60
Dy 61 SGSGSGTEFTLTISNLQPEDPASYCCOQSYTTLTYTPSGTKLEIKR 106
61 SGSGSGTEFTLTISNLQPEDPASYCCOQSYTTLTYTPSGTKLEIKR 106
Db
RESULT 12
AA98245
ID AAY98245 standard; protein; 107 AA.
AC AAY98245;
XX
XX 04-JUN-2000 (first entry)
DT
DE Anti-gp120 antibody light chain variable region from clone B27.
XX
KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
KW passive immunotherapy; reduce severity; HIV-induced disease;
KW immunocompetence; active immunisation.
XX
OS Homo sapiens.
XX
XX AU9948754-A.
XX
XX 17-FEB-2000.
XX
XX 16-SEP-1999; 99AU-00048754.
XX
XX 16-SEP-1999; 99AU-00048754.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 2000-246867/22.
XX
XX Human neutralizing monoclonal antibodies to human immunodeficiency virus
XX (HIV) used for providing passive immunotherapy to HIV are specific for
XX glycoprotein-120.
XX
XX Example 9; Fig 11; 374pp; English.
XX
XX This sequence represents a fragment of the antibodies of the invention.
XX The invention relates to the production of an anti-HIV (human
XX immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
XX of reducing an HIV infectivity titre in an in vitro virus infectivity
XX assay by 50% at a concentration of less than 70 ng/ml. The method for the
XX production of the antibody comprises: (a) providing a first
XX polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
XX (which does not comprise the sequence represented by AAY98206) and a
XX second polynucleotide encoding a light chain immunoglobulin amino acid

CC sequence; (b) inserting the first and second polynucleotide sequences
CC into a host cell; (c) maintaining the host cell in conditions which allow
CC the amino acid sequences encoded by the polynucleotides to be expressed
CC in the host cell; and (d) isolating the antibody comprising the heavy and
CC light chain immunoglobulin amino acid sequences from the host cell. The
CC anti-HIV gp-120 monoclonal antibody is used for providing passive
CC immunotherapy to HIV in a human. They can be administered to high-risk
CC patients to reduce the likelihood and/or severity of HIV-induced disease
CC and to patients who are already HIV-infected. The antibodies are used for
CC neutralising field isolates which provides information about the
CC immunocompetence of an immune response in HIV patients, for detecting HIV
CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
CC producing anti-idiotypic antibodies which can be used for active
CC immunisation and to screen human monoclonal antibodies to identify those
CC with the same binding specificity and to monitor the course of HIV
CC disease therapy by measuring the changes in concentration of HIV present
CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
CC monoclonal antibodies are encoded by a human polynucleotide sequence and
CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
CC reduce the problems of significant host immune response to the antibodies
CC associated with monoclonal antibodies of xenogeneic or chimeric
CC derivation
CC
XX
SQ Sequence 107 AA;
Query Match 87.0%; Score 476; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 9.4e-26;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
Dy 1 ELTQSPSSLASVGVDRVTITCRARQSIISTYLNWYQQRKGAKPKLLIWSASNLQSGVPSRF 60
1 ELTQSPSSLASVGVDRVTITCRARQSIISTYLNWYQQRKGAKPKLLIWSASNLQSGVPSRF 60
Dy 61 SGSGSGTEFTLTISNLQPEDPASYCCOQSYTTLTYTPSGTKLEIKR 106
61 SGSGSGTEFTLTISNLQPEDPASYCCOQSYTTLTYTPSGTKLEIKR 106
Db
RESULT 13
AA95136
ID AAY95136 standard; protein; 107 AA.
AC AAY95136;
XX
XX 30-JUN-2000 (first entry)
DT
DE Anti-gp120 antibody light chain variable region from clone B27.
XX
KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
XX
OS Homo sapiens.
XX
XX AU9948756-A.
XX
XX 17-FEB-2000.
XX
XX 16-SEP-1999; 99AU-00048756.
XX
XX 16-SEP-1999; 99AU-00048756.
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Burton DR, Barbas CF, Lerner RA;
XX
XX WPI; 2000-293393/26.
XX
XX Novel human monoclonal antibodies which immunoreact with and neutralize
XX human immunodeficiency virus useful for treating HIV infections.
XX
XX Example 9; Fig 11; 366pp; English.
XX

CC The present sequence represents a fragment of an anti-human
 CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
 CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
 CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
 CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
 CC in vitro virus infectivity assay by 50% at a concentration of less than
 CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
 CC immunotherapy of HIV induced disease. They are useful as neutralising
 CC field isolates and provide useful information regarding the
 CC immunocompetence of an immune response in HIV infected patients. The
 CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
 CC which can be used to screen human monoclonal antibodies to identify
 CC whether the antibody has the same binding specificity as the antibodies
 CC of the invention. The neutralising antibodies define new epitopes on the
 CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
 CC immunotherapeutic human monoclonal antibodies. A major advantages of the
 CC monoclonal antibodies derives from the fact that they are encoded by a
 CC human polynucleotide sequence. Thus in vivo use of the monoclonal
 CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
 CC reduces the problems of significant host immune response to the passively
 CC administered antibodies which is a problem commonly encountered when
 CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
 CC An additional major advantage of the monoclonal antibodies described
 CC derives from the fact that they immunoreact with a unique determinant
 CC present on mature HIV glycoprotein gp120. This class of antibodies is
 CC particularly effective at neutralising field isolates of HIV

CC Sequence 107 AA;

Query Match 87.0%; Score 476; DB 3; Length 107;
 Best Local Similarity 87.7%; Pred. No. 9.4e-26;
 Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITTCRAROSISTYLNWYQOKPGKAPKLIWSASNLQGVPSRF 60
 Db 1 ELTQSPSSLASVGDRTVITTCRASQISISYLNWYQOKPGKAPKLIYAASLQGVPSRF 60

QY 61 SGGSSGTFEFTLTISNLOFEDPASYYCOQSYTTLYTFSSGTYKLEIKR 106
 Db 61 SGGSSGTFEFTLTISNLOFEDPATYYCOQSYSTPQTFQGTKEIKR 106

RESULT 14

AAG93663
 ID AAG93663 standard; protein; 107 AA.

AC AAG93663;

DT 14-SEP-2001 (first entry)

DE Human anti-Rh(D) antibody clone SH49 protein sequence.

KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KM red blood cell; Rh phenotype; diagnosis; therapeutic.

OS Homo sapiens.

PN US6255455-B1.

PD 03-JUL-2001.

PF 29-JAN-1999; 99US-00240274.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

PA (UTPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

XX WPI: 2001-388931/41.
 DR N-PSDB; AAH68720.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.

PS Claim 1; Col 69; 162pp; English.

CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention

CC Sequence 107 AA;

Query Match 86.8%; Score 475; DB 4; Length 107;
 Best Local Similarity 85.8%; Pred. No. 1.1e-25;
 Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVITTCRAROSISTYLNWYQOKPGKAPKLIWSASNLQGVPSRF 60
 Db 2 ELTQSPSSLASVGDRTVITTCRASQISISYLNWYQOKPGKAPKLIYAASLQGVPSRF 61

QY 61 SGGSSGTFEFTLTISNLOFEDPASYYCOQSYTTLYTFSSGTYKLEIKR 106
 Db 62 SGGSSGTFEFTLTISNLOFEDPATYYCOQSYSTPQTFQGTKEIKR 107

RESULT 15

AAG93664
 ID AAG93664 standard; protein; 107 AA.

AC AAG93664;

DT 14-SEP-2001 (first entry)

DE Human anti-Rh(D) antibody clone SH50 protein sequence.

KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KM red blood cell; Rh phenotype; diagnosis; therapeutic.

OS Homo sapiens.

PN US6255455-B1.

PD 03-JUL-2001.

PF 29-JAN-1999; 99US-00240274.

PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

PA (UTPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

XX WPI: 2001-388931/41.

DR N-PSDB; AAH68721.

PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.

PS Claim 1; Col 69; 162pp; English.

CC The present invention describes an isolated Rh(D) binding protein,

CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AA93558 to AA93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH6815 to AAH68726 represent the nucleotide sequence which encode
 CC AA93558 to AA93669. AA93670 to AA93697 represent anti-Rh (D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention
 CC
 XX
 SQ Sequence 107 AA;

Query Match 86.8%; Score 475; DB 4; Length 107;
 Best Local Similarity 85.8%; Pred. No. 1.1e-25;
 Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ELTQSPSSLSASVGDRTVTTCRAQOSISTYLNWYQOKPKAPKLLIWSASNLQSGVPSRF 60
 Db 2 ELTQSPSSLSASVGDRTVTTCRAQOSISTYLNWYQOKPKAPKLLIYAASLQSGVPSRF 61
 QY 61 SSGSGGTBFTLTITISNLQEPDPAFYCCQSYTTLTYTFSGTKEIKR 106
 Db 62 SSGSGGTBFTLTITISNLQEPDPAFYCCQSYTTLTYTFSGTKEIKR 107

Search completed: July 26, 2005, 09:19:21
 Job time : 80.3394 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:26:32 ; Search time 67.4545 Seconds

(Without alignments)
611.274 Million cell updates/sec

Title: US-10-027-725A-11

Perfect score: 547
Sequence: 1 ELTQSPSSLSASVGRVTIT.....QGSYTLTYRGSGTKLEIKR 106Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCR_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10G_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	547	100.0	106	US-10-027-725A-11	Sequence 11, Appl
2	484	88.5	107	US-10-016-986-104	Sequence 104, Appl
3	483	88.3	107	US-09-848-798-33	Sequence 33, Appl
4	480	87.8	107	US-09-848-798-156	Sequence 156, Appl
5	476	87.0	107	US-10-016-986-105	Sequence 105, Appl
6	475	86.8	107	US-09-848-798-175	Sequence 175, Appl
7	475	86.8	107	US-09-848-798-176	Sequence 176, Appl
8	474	86.7	107	US-09-848-798-179	Sequence 179, Appl
9	473.5	86.6	108	US-09-848-798-32	Sequence 32, Appl
10	473.5	86.6	108	US-09-848-798-43	Sequence 43, Appl
11	473	86.5	107	US-09-848-798-37	Sequence 37, Appl

12	473	86.5	111	14	US-10-203-754A-57	Sequence 57, Appl
13	472.5	86.4	108	10	US-09-848-798-167	Sequence 167, Appl
14	472	86.3	107	10	US-09-848-798-38	Sequence 38, Appl
15	472	86.3	107	10	US-09-848-798-39	Sequence 39, Appl
16	472	86.3	107	10	US-09-848-798-162	Sequence 162, Appl
17	472	86.3	116	17	US-10-783-311-198	Sequence 198, Appl
18	471	86.1	107	10	US-09-848-798-158	Sequence 158, Appl
19	469	85.7	107	10	US-09-848-798-44	Sequence 44, Appl
20	468	85.6	108	17	US-10-726-332-209	Sequence 209, Appl
21	468	85.6	111	14	US-10-203-754A-56	Sequence 56, Appl
22	467	85.4	108	16	US-10-409-814A-4	Sequence 4, Appl
23	467	85.4	108	17	US-10-477-830-90	Sequence 90, Appl
24	467	85.4	240	9	US-09-192-854-2	Sequence 2, Appl
25	467	85.4	240	9	US-09-968-561A-2	Sequence 2, Appl
26	467	85.4	240	10	US-09-968-744A-2	Sequence 2, Appl
27	467	85.4	240	11	US-09-968-561A-2	Sequence 2, Appl
28	467	85.4	240	16	US-10-744-774-1	Sequence 1, Appl
29	466	85.2	107	10	US-09-791-153A-67	Sequence 67, Appl
30	466	85.2	108	17	US-10-726-332-214	Sequence 214, Appl
31	466	85.2	108	17	US-10-805-177-64	Sequence 64, Appl
32	465.5	85.1	107	15	US-10-460-595-9	Sequence 9, Appl
33	465	85.0	107	15	US-10-309-762-89	Sequence 89, Appl
34	465	85.0	108	16	US-10-744-774-15	Sequence 15, Appl
35	465	85.0	108	17	US-10-726-332-28	Sequence 28, Appl
36	464.5	84.9	108	10	US-09-848-798-163	Sequence 163, Appl
37	464	84.8	108	17	US-10-726-332-18	Sequence 18, Appl
38	463	84.6	104	14	US-10-016-986-106	Sequence 106, Appl
39	463	84.6	107	15	US-10-309-762-88	Sequence 88, Appl
40	463	84.6	107	17	US-10-727-155-308	Sequence 308, Appl
41	463	84.6	107	17	US-10-938-353-103	Sequence 103, Appl
42	462	84.5	108	17	US-10-805-177-20	Sequence 20, Appl
43	462	84.5	127	15	US-10-309-762-101	Sequence 101, Appl
44	460.5	84.2	107	15	US-10-363-344-4	Sequence 4, Appl
45	460.5	84.2	288	15	US-10-363-349-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-10-027-725A-11
; Sequence 11, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-11

Query Match 100.0%; Score 547; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 3, 6e-40;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGRVTITCRAROSISTYLYNWOQKPKKLLWSASNLGQVSRF 60
DB 1 ELTQSPSSLSASVGRVTITCRAROSISTYLYNWOQKPKKLLWSASNLGQVSRF 60

QY 61 SGSGSGTEFTLTISNLOFEDPASYYCOQSYTLTYRGSGTKLEIKR 106
DB 61 SGSGSGTEFTLTISNLOFEDPASYYCOQSYTLTYRGSGTKLEIKR 106

RESULT 2

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US-10-016-986-104
; Sequence 104, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbás, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-104

Query Match      88.5%; Score 484; DB 14; Length 107;
Best Local Similarity 88.7%; Pred. No. 1,1e-34;
Matches 94; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRARQSIISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
Db 1 ELTQSPSSLSASVGDVVTITTCRARQSIISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60

QY 61 SSGSGGTFTLTISNLOPEDFASYYCOQSYTTLTYTSGGTKEIKR 106
Db 61 SSGSGGTFTLTISNLOPEDFATYYCOQSYSTPYTFGGTKEIKR 106

Db 61 SSGSGGTFTLTISNLOPEDFATYYCOQSYSTPYTFGGTKEIKR 106

RESULT 3
US-09-848-798-33
; Sequence 33, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR APPLICATION NUMBER: 2001-05-04
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-848-798-33

Query Match      88.3%; Score 483; DB 10; Length 107;
```

```
Best Local Similarity 87.7%; Pred. No. 1.3e-34;
Matches 93; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRARQSIISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
Db 2 ELTQSPSSLSASVGDVVTITTCRARQSIISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 61

QY 61 SSGSGGTFTLTISNLOPEDFASYYCOQSYTTLTYTSGGTKEIKR 106
Db 62 SSGSGGTFTLTISNLOPEDFATYYCOQSYSTLMTTGGTKEIKR 107

Db 62 SSGSGGTFTLTISNLOPEDFATYYCOQSYSTLMTTGGTKEIKR 107

RESULT 4
US-09-848-798-156
; Sequence 156, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR APPLICATION NUMBER: 2001-05-04
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 156
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-848-798-156

Query Match      87.8%; Score 480; DB 10; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.4e-34;
Matches 93; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDVVTITTCRARQSIISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 60
Db 2 ELTQSPSSLSASVGDVVTITTCRARQSIISTYLMWYQKPGKAPKLLIWSASNLQGVPSRF 61

QY 61 SSGSGGTFTLTISNLOPEDFASYYCOQSYTTLTYTSGGTKEIKR 106
Db 62 SSGSGGTFTLTISNLOPEDFATYYCOQSYSTPYTFGGTKEIKR 107

Db 62 SSGSGGTFTLTISNLOPEDFATYYCOQSYSTPYTFGGTKEIKR 107

RESULT 5
US-10-016-986-105
; Sequence 105, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbás, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
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PRIOR APPLICATION NUMBER: US 07/954,148
PRIOR FILING DATE: 1992-09-30
NUMBER OF SEQ ID NOS: 176
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 105
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized
US-10-016-986-105

Query Match 87.0%; Score 476; DB 14; Length 107;
Best Local Similarity 87.7%; Pred. No. 5.5e-34;
Matches 93; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQISITLYLWYQKRGKAPKLLIWSASNLGSPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITCRARQISITLYLWYQKRGKAPKLLIWSASNLGSPSRF 60
QY 61 SGGSGGTEFTLTISNLOFEDPASYCCOOSYTTLYTFSSGTLKEIKR 106
DB 61 SGGSGGTEFTLTISNLOFEDPASYCCOOSYTTLYTFSSGTLKEIKR 106

RESULT 6

US-09-848-798-175
Sequence 175, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 175
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-175

Query Match 86.8%; Score 475; DB 10; Length 107;
Best Local Similarity 85.8%; Pred. No. 6.7e-34;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQISITLYLWYQKRGKAPKLLIWSASNLGSPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITCRARQISITLYLWYQKRGKAPKLLIWSASNLGSPSRF 61
QY 61 SGGSGGTEFTLTISNLOFEDPASYCCOOSYTTLYTFSSGTLKEIKR 106
DB 62 SGGSGGTEFTLTISNLOFEDPASYCCOOSYTTLYTFSSGTLKEIKR 107

RESULT 7

US-09-848-798-176
Sequence 176, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798

CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 176
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH50
US-09-848-798-176

Query Match 86.8%; Score 475; DB 10; Length 107;
Best Local Similarity 85.8%; Pred. No. 6.7e-34;
Matches 91; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQISITLYLWYQKRGKAPKLLIWSASNLGSPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITCRARQISITLYLWYQKRGKAPKLLIWSASNLGSPSRF 61
QY 61 SGGSGGTEFTLTISNLOFEDPASYCCOOSYTTLYTFSSGTLKEIKR 106
DB 62 SGGSGGTEFTLTISNLOFEDPASYCCOOSYTTLYTFSSGTLKEIKR 107

RESULT 8

US-09-848-798-179
Sequence 179, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 179
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-179

Query Match 86.7%; Score 474; DB 10; Length 107;
Best Local Similarity 85.8%; Pred. No. 8.1e-34;
Matches 91; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRARQISITLYLWYQKRGKAPKLLIWSASNLGSPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITCRARQISITLYLWYQKRGKAPKLLIWSASNLGSPSRF 61
QY 61 SGGSGGTEFTLTISNLOFEDPASYCCOOSYTTLYTFSSGTLKEIKR 106
DB 62 SGGSGGTEFTLTISNLOFEDPASYCCOOSYTTLYTFSSGTLKEIKR 107

RESULT 9

US-09-848-798-32
Sequence 32, Application US/09848798
Publication No. US20030040605A1
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

```
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848, 798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
US-09-848-798-32

Query Match      86.6%; Score 473.5; DB 10; Length 108;
Best Local Similarity 87.9%; Pred. No. 9.1e-34;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQOKPGKAPKLLIWAASLSQSGVPSRF 61

QY 61 SSGSGGTFTLITISNLQPEDFASYCCQOSYTT-LYTGSGGTKEIKR 106
Db 62 SSGSGGTDFTLITISLQPEDFATYCCQOSYSTPTTGTGGTKLEIKR 108

RESULT 10
US-09-848-798-43
; Sequence 43, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848, 798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
US-09-848-798-43

Query Match      86.6%; Score 473.5; DB 10; Length 108;
Best Local Similarity 87.9%; Pred. No. 9.1e-34;
Matches 94; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQOKPGKAPKLLIWAASLSQSGVPSRF 61

QY 61 SSGSGGTFTLITISNLQPEDFASYCCQOSYTT-LYTGSGGTKEIKR 106
Db 62 SSGSGGTDFTLITISLQPEDFATYCCQOSYSTPTTGTGGTKLEIKR 108

RESULT 11
US-09-848-798-37
; Sequence 37, Application US/09848798
; Publication No. US20030040605A1
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; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848, 798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I06
US-09-848-798-37

Query Match      86.5%; Score 473; DB 10; Length 107;
Best Local Similarity 86.8%; Pred. No. 1e-33;
Matches 92; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQOKPGKAPKLLIWAASLSQSGVPSRF 61

QY 61 SSGSGGTFTLITISNLQPEDFASYCCQOSYTTLYTGSGGTKEIKR 106
Db 62 SSGSGGTDFTLITISLQPEDFATYCCQOSYSTPTTGTGGTKLEIKR 107

RESULT 12
US-10-203-754A-57
; Sequence 57, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
; APPLICANT: ITAMI, Seima
; APPLICANT: MAKI, Makoto
; APPLICANT: MATSURA, Yoshiharu
; APPLICANT: SHIBUI, Tatsuro
; APPLICANT: YOTSUMOTO, Yoshihisa
; APPLICANT: MIYAMURA, Tatsuo
; TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
; FILE REFERENCE: P22257
; CURRENT APPLICATION NUMBER: US/10/203,754A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/JP01/00967
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 57
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-10-203-754A-57

Query Match      86.5%; Score 473; DB 14; Length 111;
Best Local Similarity 86.7%; Pred. No. 1e-33;
Matches 91; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQOKPGKAPKLLIWSASNLQSGVPSRF 61
Db 4 MTQSPSSLSASVGDRTVITTCRASQISSTYLNWYQOKPGKAPKLLIWAASNLQSGVPSRF 63

QY 62 SSGSGGTFTLITISNLQPEDFASYCCQOSYTTLYTGSGGTKEIKR 106
Db 64 SSGSGGTDFTLITISLQPEDFATYCCQOSYSTPTTGTGGTKLEIKR 108

RESULT 13
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 09:09:56 ; Search time 20.0758 Seconds
(without alignments)
394.147 Million cell updates/sec

Title: US-10-027-725A-10
Perfect score: 543
Sequence: 1 ELTQSPSSLSASVGDRTYIS.....QESLSAGYTFQGTKEIKR 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	475	87.5	107	1	US-08-276-852-104 Sequence 104, App
2	475	87.5	107	1	US-08-899-575-104 Sequence 104, App
3	475	87.5	107	1	US-08-899-575-104 Sequence 104, App
4	475	87.5	107	5	PCT-US95-08743-104 Sequence 104, App
5	474	87.3	107	3	US-09-240-274-179 Sequence 179, App
6	472	86.9	107	3	US-09-240-274-33 Sequence 33, App
7	472	86.9	107	3	US-09-240-274-175 Sequence 175, App
8	472	86.9	107	3	US-09-240-274-176 Sequence 176, App
9	471	86.7	107	3	US-09-240-274-156 Sequence 156, App
10	468	86.2	107	3	US-09-240-274-36 Sequence 36, App
11	467	86.0	107	1	US-08-276-852-105 Sequence 105, App
12	467	86.0	107	1	US-08-899-575-105 Sequence 105, App
13	467	86.0	107	1	US-08-899-575-105 Sequence 105, App
14	467	86.0	107	5	PCT-US95-08743-105 Sequence 105, App
15	464.5	85.5	108	3	US-09-240-274-32 Sequence 32, App
16	464.5	85.5	108	3	US-09-240-274-43 Sequence 43, App
17	464	85.5	107	3	US-09-240-274-37 Sequence 37, App
18	464	85.5	107	4	US-09-192-854-2 Sequence 2, App
19	462	85.1	107	3	US-09-240-274-38 Sequence 38, App
20	462	85.1	107	3	US-09-240-274-39 Sequence 39, App
21	461	84.9	107	3	US-09-240-274-158 Sequence 158, App
22	460.5	84.8	108	3	US-09-240-274-167 Sequence 167, App
23	459.5	84.6	108	3	US-09-240-274-163 Sequence 163, App
24	458	84.3	107	3	US-09-240-274-35 Sequence 35, App
25	458	84.3	107	3	US-09-240-274-173 Sequence 173, App
26	458	84.3	108	2	US-08-379-057-29 Sequence 29, App
27	457	84.2	104	1	US-08-276-852-106 Sequence 106, App

28	457	84.2	104	1	US-08-899-575-106 Sequence 106, App
29	457	84.2	104	1	US-08-899-575-106 Sequence 106, App
30	457	84.2	104	5	PCT-US95-08743-106 Sequence 106, App
31	457	84.2	107	3	US-09-240-274-40 Sequence 40, App
32	457	84.2	214	4	US-09-472-087-71 Sequence 71, App
33	456	84.0	107	3	US-09-240-274-44 Sequence 44, App
34	452	83.2	107	3	US-09-240-274-172 Sequence 172, App
35	452	83.2	107	3	US-09-240-274-174 Sequence 174, App
36	451.5	83.1	108	1	US-08-276-852-109 Sequence 109, App
37	451.5	83.1	108	1	US-08-899-575-109 Sequence 109, App
38	451.5	83.1	108	1	US-08-899-575-109 Sequence 109, App
39	451.5	83.1	108	3	US-09-240-274-41 Sequence 41, App
40	451.5	83.1	108	5	PCT-US95-08743-109 Sequence 109, App
41	451	83.1	107	3	US-09-240-274-168 Sequence 168, App
42	451	83.1	108	3	US-09-025-769B-14 Sequence 14, App
43	451	83.1	108	4	US-09-490-070A-14 Sequence 14, App
44	451	83.1	108	4	US-09-490-153-14 Sequence 14, App
45	451	83.1	108	4	US-09-490-324-14 Sequence 14, App

ALIGNMENTS

RESULT 1
US-08-276-852-104
Sequence 104, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESSES:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESS: Patent Counsel
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-104

Query Match 87.5%; Score 475; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITCRASQSISSYINWYQKPGKAPKLLIYAASSLSQGVPSRF 60

Qy 61 SSGSGYDFTLTISLQEPEDPASYYCOESLSASTYFGQGTVEIKR 106
Db 61 SSGSGYDFTLTISLQEPEDFATYYCOQSYSTPYTFQGTVEIKR 106

RESULT 2
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-575-104

Query Match 87.5%; Score 475; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITCRASQSISSYINWYQKPGKAPKLLIYAASSLSQGVPSRF 60

Qy 61 SSGSGYDFTLTISLQEPEDPASYYCOESLSASTYFGQGTVEIKR 106
Db 61 SSGSGYDFTLTISLQEPEDFATYYCOQSYSTPYTFQGTVEIKR 106

RESULT 3
US-08-899-575-104
; Sequence 104, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-575-104

Query Match 87.5%; Score 475; DB 1; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKPGKAPKLLIYAASSLSQGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITCRASQSISSYINWYQKPGKAPKLLIYAASSLSQGVPSRF 60

Qy 61 SSGSGYDFTLTISLQEPEDPASYYCOESLSASTYFGQGTVEIKR 106
Db 61 SSGSGYDFTLTISLQEPEDFATYYCOQSYSTPYTFQGTVEIKR 106

RESULT 4
PCT-US95-08743-104
; Sequence 104, Application PC/TUS9508743


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; GENERAL INFORMATION:
; APPLICANT: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08743
; FILING DATE: 11-JUL-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08743-104

Query Match 87.5%; Score 475; DB 5; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-39;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASORINTYINWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITCRASQISISYINWYQKRGKAPKLLIYAASSLSQGVPSRF 60

QY 61 SGGSGYDFTLTITSSLOPEDFASYYCOESLSASTFFGQGTVEIKR 106
DB 61 SGGSGYDFTLTITSSLOPEDFATYYCOOSYSTPTFFGQGTVEIKR 106

RESULT 5
US-09-274-179
; Sequence 179, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
; US-09-240-274-179

Query Match 87.3%; Score 474; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.6e-38;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASORINTYINWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITCRASQISITITINWYQKRGKAPKLLIYAASSLSQGVPSRF 61

QY 61 SGGSGYDFTLTITSSLOPEDFASYYCOESLSASTFFGQGTVEIKR 106
DB 62 SGGSGYDFTLTITSSLOPEDFATYYCOOSYSTPTFFGQGTVEIKR 107
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RESULT 6
US-09-240-274-33
; Sequence 33, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
; US-09-240-274-33

Query Match 86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 2.6e-38;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASORINTYINWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITCRASQISISYINWYQKRGKAPKLLIYAASSLSQGVPSRF 61
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QY 61 SGGSGYDFTLTITSSLOPEDFASYYCOESLSASTFFGQGTVEIKR 106
DB 62 SGGSGYDFTLTITSSLOPEDFATYYCOOSYSTPTFFGQGTVEIKR 107

RESULT 7
US-09-240-274-175
; Sequence 175, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
; US-09-240-274-175

Query Match 86.9%; Score 472; DB 3; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.6e-38;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASORINTYINWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITCRASQISISYINWYQKRGKAPKLLIYAASSLSQGVPSRF 61
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FILING DATE: 18-JUL-1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/178,302
 FILING DATE: 30-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/954,148
 FILING DATE: 30-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: SCR1452P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-554-2937
 TELEFAX: 619-554-6312
 INFORMATION FOR SEQ ID NO: 105:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-276-852-105

Query Match 86.0%; Score 467; DB 1; Length 107;
 Best Local Similarity 86.8%; Pred. No. 7,7e-38;
 Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVTCRASQRIINTYINWYQHKRGKAPKLLIYAASSLGSGVPSRF 60
 DB 1 ELTQSPSLASVGDRTVTCRASQRIINTYINWYQHKRGKAPKLLIYAASSLGSGVPSRF 60
 QY 61 SGSGYGTDFLTITSLQFEDFASYYCOESLSASYTFQGTVEIKR 106
 DB 61 SGSGYGTDFLTITSLQFEDFATYYCOQSYSTPQTFQGTVEIKR 106

RESULT 12
 US-08-899-575-105
 Sequence 105, Application US/08899575
 Patent No. 5770440
 GENERAL INFORMATION:
 APPLICANT: Burton, Dennis R
 APPLICANT: Barbias, Carlos F
 APPLICANT: Lerner, Richard A
 TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 NUMBER OF SEQUENCES: 170
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Scripps Research Institute, Office of
 STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/899,575
 FILING DATE: 24-JUL-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/276,852
 FILING DATE: 18-JUL-1994
 APPLICATION NUMBER: US 08/178,302
 FILING DATE: 30-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/954,148
 FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:
 NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: SCR1452P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-554-2937
 TELEFAX: 619-554-6312
 INFORMATION FOR SEQ ID NO: 105:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-899-575-105

Query Match 86.0%; Score 467; DB 1; Length 107;
 Best Local Similarity 86.8%; Pred. No. 7,7e-38;
 Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSLASVGDRTVTCRASQRIINTYINWYQHKRGKAPKLLIYAASSLGSGVPSRF 60
 DB 1 ELTQSPSLASVGDRTVTCRASQRIINTYINWYQHKRGKAPKLLIYAASSLGSGVPSRF 60
 QY 61 SGSGYGTDFLTITSLQFEDFASYYCOESLSASYTFQGTVEIKR 106
 DB 61 SGSGYGTDFLTITSLQFEDFATYYCOQSYSTPQTFQGTVEIKR 106

RESULT 13
 US-08-899-575-105
 Sequence 105, Application US/08899575
 Patent No. 5804440
 GENERAL INFORMATION:
 APPLICANT: Burton, Dennis R
 APPLICANT: Barbias, Carlos F
 APPLICANT: Lerner, Richard A
 TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
 TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
 NUMBER OF SEQUENCES: 170
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Scripps Research Institute, Office of
 STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/899,575
 FILING DATE: 24-JUL-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/276,852
 FILING DATE: 18-JUL-1994
 APPLICATION NUMBER: US 08/178,302
 FILING DATE: 30-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/954,148
 FILING DATE: 30-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Fitting, Thomas
 REGISTRATION NUMBER: 34,163
 REFERENCE/DOCKET NUMBER: SCR1452P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-554-2937
 TELEFAX: 619-554-6312
 INFORMATION FOR SEQ ID NO: 105:

SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-105

Query Match 86.0%; Score 467; DB 1; Length 107;
Best Local Similarity 86.8%; Pred. No. 7.7e-38;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITCRASQRISSYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 60

OY 61 SSGSGYTDFTLTISLSQPEDFASYCQESLSASYTFGGGTVEIKR 106
DB 61 SSGSGYTDFTLTISLSQPEDFATYCCQSYSTPTFGGTVEIKR 106

RESULT 14
PCT-US95-08743-105
Sequence 105, Application PC/TUS9508743
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08743-105

Query Match 86.0%; Score 467; DB 5; Length 107;
Best Local Similarity 86.8%; Pred. No. 7.7e-38;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITCRASQRISSYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 60

OY 61 SSGSGYTDFTLTISLSQPEDFASYCQESLSASYTFGGGTVEIKR 106
DB 61 SSGSGYTDFTLTISLSQPEDFATYCCQSYSTPTFGGTVEIKR 106

RESULT 15
US-09-240-274-32
Sequence 32, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:

APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rn(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain I01
US-09-240-274-32

Query Match 85.5%; Score 464.5; DB 3; Length 108;
Best Local Similarity 86.9%; Pred. No. 1.4e-37;
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVITCRASQRISSYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 61

OY 61 SSGSGYTDFTLTISLSQPEDFASYCQESLSA-SYTFGGGTVEIKR 106
DB 62 SSGSGYTDFTLTISLSQPEDFATYCCQSYSTPTFGGTVEIKR 108

Search completed: July 26, 2005, 09:30:00
Job time : 20.0758 secs

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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:07:26 ; Search time 13.6515 Seconds

(without alignments)
747.095 Million cell updates/sec

Title: US-10-027-725A-10

Sequence: 1 ELTQSPSSLSASVGDRTVTS.....QESLSASYTFGGTKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	464	85.5	127	2	S40367
2	459	84.5	123	2	S40331
3	458	84.3	108	2	B49047
4	456	84.0	108	2	S47182
5	452	83.2	109	2	S31998
6	452	83.2	109	2	S31979
7	448	82.5	109	2	S31980
8	446	82.1	109	2	S44122
9	445	82.0	109	2	S32001
10	441	81.2	108	2	S19674
11	439	80.8	109	2	S31981
12	439	80.8	129	2	S52793
13	438	80.7	107	2	S36264
14	437	80.5	108	2	S31973
15	436	80.3	109	2	S31987
16	436	80.3	122	2	S40370
17	436	80.3	129	1	K1HUK
18	436	80.3	129	2	S40317
19	435	80.1	128	2	S46372
20	434	79.9	120	2	S46370
21	433.5	79.8	125	2	S40315
22	433	79.7	108	1	K1HUK
23	432	79.6	132	2	S40334
24	431	79.4	109	2	S31978
25	430	79.2	108	1	K1HUK
26	430	79.2	132	2	S3646
27	425	78.3	122	2	S40314
28	425	78.3	129	2	S40369
29	424.5	78.2	106	2	PC2397

30	423.5	78.0	124	2	S40336	Ig kappa chain V-J
31	422.5	77.8	107	2	S36275	Ig lambda chain V
32	422	77.7	125	2	S40333	Ig kappa chain V-J
33	422	77.7	131	2	S40352	Ig kappa chain V-J
34	420	77.3	108	1	K1HUK	Ig kappa chain V-I
35	420	77.3	125	2	S40349	Ig kappa chain V-J
36	420	77.3	126	2	S40335	Ig kappa chain V-J
37	419	77.2	125	2	S40350	Ig kappa chain V-h
38	418	77.0	117	2	S46371	Ig kappa chain V-J
39	418	77.0	129	2	S52792	Ig kappa chain V-r
40	417	76.8	117	2	S46376	Ig kappa chain V-r
41	416	76.6	108	1	K1HUK	Ig kappa chain V-I
42	414	76.2	107	2	JL0139	Ig kappa chain V-r
43	414	76.2	107	2	S36262	Ig kappa chain V
44	414	76.2	108	1	K1HUK	Ig lambda chain V
45	413.5	76.2	108	2	S30521	Ig kappa chain V-r

ALIGNMENTS

RESULT 1

S40367

Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40367

Bur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40367

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-127 <KLE>

A:Cross-references: EMBL:X72477

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 85.5%; Score 464; DB 2; Length 127;

Best Local Similarity 84.9%; Pred. No. 2.9e-34;

Matches 90; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVTSGRASORINTYNTQHKRGPALKIITYASSLSQSVPSRF 60

DB 20 QMTQSPSSLSASVGDRTVTCRASQISINMYORKEKAPKLIYASSLSQSVPSRF 79

QY 61 SSGSGVDTFTLTISLQPEDFASYCOESLSASYTFGGTKVEIKR 106

DB 80 SSGSGVDTFTLTISLQPEDFATYYCOQSYNTFWTGGTKVEIKR 125

RESULT 2

S40331

Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40331

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40331

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-123 <KLE>

A:Cross-references: EMBL:X72441; NID:9441350; PIDN:CAA51109.1; PID:9441351

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 459; DB 2; Length 123;

Best Local Similarity 85.7%; Pred. No. 7.9e-34;
Matches 90; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKRGKAPKLLITYAASSLQSGVPSRF 60
Db 19 QMTQSPSSLSASVGDRTVITCRASQSISSYINWYQOKRGKAPKLLITYAASSLQSGVPSRF 78

Qy 61 GSGGYGTDFTLTISLQPEDFASYYCOESLSASYTFGGGTVEIKR 105
Db 79 GSGSGTDFTLTISLQPEDFATYYCQGSYSTPTFGGTVEIKR 123

RESULT 3
Ig kappa chain V region (monoclonal strational autoantibody strAB SA-1A) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: B49047
R/Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A/Title: Human monoclonal strational autoantibodies isolated from thymic B lymphocytes
A/Reference number: A49047; MUID:92387224; PMID:151616
A/Accession: B49047
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-108 <VIC>
A/Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
A/Experimental source: thymic B lymphocytes
A/Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIPI:113209)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 458; DB 2; Length 108;
Best Local Similarity 84.9%; Pred. No. 8.5e-34;
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKRGKAPKLLITYAASSLQSGVPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITCRASQSISSYINWYQOKRGKAPKLLITYAASSLQSGVPSRF 62

Qy 61 GSGGYGTDFTLTISLQPEDFASYYCOESLSASYTFGGGTVEIKR 106
Db 63 GSGSGTDFTLTISLQPEDFATYYCQGSYSTPTFGGTVEIKR 108

RESULT 4
Ig kappa chain - human
S47182
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S47182
R/McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A/Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient
A/Reference number: S47181
A/Accession: S47182
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <MC1>
A/Cross-references: EMBL:X79786; NID:G506422; PIDN:CAA56182.1; PID:G506423
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.0%; Score 456; DB 2; Length 108;
Best Local Similarity 84.9%; Pred. No. 1.3e-33;
Matches 90; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKRGKAPKLLITYAASSLQSGVPSRF 60
Db 3 ELTQSPSSLSASVGDRTVITCRASQSISSYINWYQOKRGKAPKLLITYAASSLQSGVPSRF 62

Qy 61 GSGGYGTDFTLTISLQPEDFASYYCOESLSASYTFGGGTVEIKR 106

Db 63 GSGSGTDFTLTISLQPEDFATYYCQGSYSTPTFGGTVEIKR 108

RESULT 5
Ig kappa chain - human (fragment)
S31978
C/Species: Homo sapiens (man)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S31978
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31978
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <POR>
A/Cross-references: EMBL:Z15075; NID:G38489; PIDN:CAA78790.1; PID:G38490
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 452; DB 2; Length 109;
Best Local Similarity 83.8%; Pred. No. 2.9e-33;
Matches 88; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 2 LTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKRGKAPKLLITYAASSLQSGVPSRF 61
Db 4 MTQSPSSLSASVGDRTVITCRASQSISSYINWYQOKRGKAPKLLITYAASSLQSGVPSRF 63

Qy 62 GSGGYGTDFTLTISLQPEDFASYYCOESLSASYTFGGGTVEIKR 106
Db 64 GSGGTDFTLTISLQPEDFATYYCQGSYSTPTFGGTVEIKR 108

RESULT 6
Ig kappa chain - human (fragment)
S31979
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S31979
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31979
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <POR>
A/Cross-references: EMBL:Z15075; NID:G38489; PIDN:CAA78784.1; PID:G38490
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 452; DB 2; Length 109;
Best Local Similarity 81.9%; Pred. No. 2.9e-33;
Matches 86; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 2 LTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKRGKAPKLLITYAASSLQSGVPSRF 61
Db 4 MTQSPSSLSASVGDRTVITCRASQSISSYINWYQOKRGKAPKLLITYAASSLQSGVPSRF 63

Qy 62 GSGGYGTDFTLTISLQPEDFASYYCOESLSASYTFGGGTVEIKR 106
Db 64 GSGGTDFTLTISLQPEDFATYYCQGSYSTPTFGGTVEIKR 108

RESULT 7
Ig kappa chain - human (fragment)
S31980
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C:Accession: S31980; S32000
 R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
 Submitted to the EMBL Data Library, June 1992
 A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
 A:Reference number: S31977
 A:Accession: S31980
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-109 <FOR>
 A:Cross-references: EMBL:Z15076; NID:g38491; PIDN:CAA78785.1; PID:g38492; EMBL:Z15083; N
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 448; DB 2; Length 109;
 Best Local Similarity 81.0%; Pred. No. 6.6e-33;
 Matches 85; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

Oy 2 LTQSPSSLSASVGDVITISCRASORINTYLMWYOHKPKAKPLIYAASLSQGVPSRFS 61
 Db 4 MTQSPSSLSASVGDVITISCRASORINTYLMWYOHKPKAKPLIYGTSTLSQGVPSRFS 63
 Oy 62 GSGGVTDTFTLTISLQFEDFASYYCOSLSASYTFGGGTKEIKR 106
 Db 64 GSGGVTDTFTLTISLQFEDFATYFCQGSYSSPYTFGGGTKEIKR 108

RESULT 8

S44122
 Ig kappa chain V region - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
 C:Accession: S44122
 R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
 Submitted to the EMBL Data Library, March 1994
 A:Description: Idiolytic vaccination against human B-cell lymphoma: rescue of variable r
 A:Reference number: S44105
 A:Accession: S44122
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-108 <HAW>
 A:Cross-references: EMBL:Z31390; NID:g472976; PIDN:CAA83265.1; PID:g940533
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 446; DB 2; Length 108;
 Best Local Similarity 83.0%; Pred. No. 9.8e-33;
 Matches 88; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Oy 1 ELTQSPSSLSASVGDVITISCRASORINTYLMWYOHKPKAKPLIYAASLSQGVPSR 60
 Db 3 QMTQSPSSLSASVGDVITISCRASORINTYLMWYOHKPKAKPLIYASLSQGVPSR 62
 Oy 61 GSGGVTDTFTLTISLQFEDFASYYCOSLSASYTFGGGTKEIKR 106
 Db 63 GSGGVTDTFTLTISLQFEDFATYFCQGSYSSPYTFGGGTKEIKR 108

RESULT 9

S32001
 Ig kappa chain - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
 C:Accession: S32001
 R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
 Submitted to the EMBL Data Library, June 1992
 A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
 A:Reference number: S31977
 A:Accession: S32001
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-109 <FOR>

A:Cross-references: EMBL:Z15082; NID:g38503; PIDN:CAA78791.1; PID:g38504
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 445; DB 2; Length 109;
 Best Local Similarity 80.0%; Pred. No. 1.2e-32;
 Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Oy 2 LTQSPSSLSASVGDVITISCRASORINTYLMWYOHKPKAKPLIYAASLSQGVPSRFS 61
 Db 4 MTQSPSSLSASVGDVITISCRASORINTYLMWYOHKPKAKPLIYGTSTLSQGVPSRFS 63
 Oy 62 GSGGVTDTFTLTISLQFEDFASYYCOSLSASYTFGGGTKEIKR 106
 Db 64 GSGGVTDTFTLTISLQFEDFATYFCQGSYSSPYTFGGGTKEIKR 108

RESULT 10

S19674
 Ig kappa chain V region (clone alpha-TEL9) - human
 C:Species: Homo sapiens (man)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
 C:Accession: S19674
 R:Mark, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.
 J. Mol. Biol. 222, 581-597, 1991
 A>Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
 A:Reference number: S19663; MUID:92085276; PMID:1748994
 A:Accession: S19674
 A:Molecule type: mRNA
 A:Residues: 1-108 <MAR>
 A:Cross-references: EMBL:X61642; NID:g37860; PIDN:CAA43823.1; PID:g1335386
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.2%; Score 441; DB 2; Length 108;
 Best Local Similarity 82.9%; Pred. No. 2.7e-32;
 Matches 87; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Oy 2 LTQSPSSLSASVGDVITISCRASORINTYLMWYOHKPKAKPLIYAASLSQGVPSRFS 61
 Db 4 LTQSPSSLSASVGDVITISCRASORINTYLMWYOHKPKAKPLIYAASLSQGVPSRFS 63
 Oy 62 GSGGVTDTFTLTISLQFEDFASYYCOSLSASYTFGGGTKEIKR 106
 Db 64 GSGGVTDTFTLTISLQFEDFATYFCQGSYSSPYTFGGGTKEIKR 108

RESULT 11

S31981
 Ig kappa chain - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S31981
 R:Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
 Submitted to the EMBL Data Library, June 1992
 A:Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
 A:Reference number: S31977
 A:Accession: S31981
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-109 <FOR>
 A:Cross-references: EMBL:Z15077; NID:g38493; PIDN:CAA78786.1; PID:g38494
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 439; DB 2; Length 109;
 Best Local Similarity 80.0%; Pred. No. 4.1e-32;
 Matches 84; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Oy 2 LTQSPSSLSASVGDVITISCRASORINTYLMWYOHKPKAKPLIYAASLSQGVPSRFS 61

Db 4 MTQSPSSLSASVGDRTVITCRASQDISRYLNMWQKPKAKPLIYHGAStLSEGVPSRFS 63
Qy 62 GSGGCTDFTLTITSSLOPEDFASYYCQESLSASYTFGGGTVEIKR 106
64 GSGGCTDFTLTITSSLOPEDFATYTCQOSYSTPFTFGGTKLEIKR 108

RESULT 12

552793
Ig kappa chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C/Accession: S52793
R/Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Deret, submitted to the EMBL Data Library, March 1995
A/Description: Light chain V region gene usage restriction and peculiarities in myeloma-
A/Reference number: S52789
A/Accession: S52793
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-129 <ROC>
A/Cross-references: EMBL:X85997, NID:G758600, PIDN:CAA59989.1, PID:G758601
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 439; DB 2; Length 129;
Best Local Similarity 81.9%; Pred. No. 4.8e-32;
Matches 86; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ELTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQHKPKAKPLIYAAStLQSGVPSRF 60
Db 25 QMTQSPSSLSASVGDRTVITCRASQNTISYLNWYQKPKAKPLIYAAStLQSGVPSRF 84
Qy 61 GSGGCTDFTLTITSSLOPEDFASYYCQESLSASYTFGGGTVEIKR 105
Db 85 VGSGGCTDFTLTITSSLOPEDFATYTCQOSYAPLTFGGGTVEIKR 129

RESULT 13

S36264
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C/Accession: S36264
R/Griffith, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMBO J. 12, 725-734, 1993
A/Title: Human anti-self antibodies with high specificity from phage display libraries.
A/Reference number: S36256; MUID:93178448; PMID:7679990
A/Accession: S36264
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-107 <GR1>
A/Cross-references: EMBL:Z18845, NID:G33426, PIDN:CAA79297.1, PID:G939919
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 438; DB 2; Length 107;
Best Local Similarity 83.7%; Pred. No. 4.9e-32;
Matches 87; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 2 LTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQHKPKAKPLIYAAStLQSGVPSRFS 61
Db 4 LTQSPSSLSASVGDRTVITCRASQSTISYLNWYQKPKAKPLIYAAStLQSGVPSRFS 63
Qy 62 GSGGCTDFTLTITSSLOPEDFASYYCQESLSASYTFGGGTVEIKR 105
Db 64 GSGGCTDFTLTITSSLOPEDFATYTCQOSYAPLTFGGGTVEIKR 107

RESULT 14

S31977
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S31977
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31977
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <POR>
A/Cross-references: UNIPROT:Q96SA9, EMBL:Z15073
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.5%; Score 437; DB 2; Length 108;
Best Local Similarity 82.9%; Pred. No. 6.1e-32;
Matches 87; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 2 LTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQHKPKAKPLIYAAStLQSGVPSRFS 61
Db 4 MTQSPSSLSASVGDRTVITCRASQSTISYLNWYQKPKAKPLIYAAStLQSGVPSRFS 63
Qy 62 GSGGCTDFTLTITSSLOPEDFASYYCQESLSASYTFGGGTVEIKR 106
Db 64 GSGGCTDFTLTITSSLOPEDFATYTCQOSYPTVDTFGGTVETIKR 108

RESULT 15

S31983
Ig kappa chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S31983
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B. submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31983
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <POR>
A/Cross-references: EMBL:Z15079, NID:G38497, PIDN:CAA78788.1, PID:G38498
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 436; DB 2; Length 109;
Best Local Similarity 79.0%; Pred. No. 7.6e-32;
Matches 83; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

Qy 2 LTQSPSSLSASVGDRTVITCRASQRIINTYLNWYQHKPKAKPLIYAAStLQSGVPSRFS 61
Db 4 MTQSPSSLSASVGDRTVITCRASQSTISYLNWYQKPKAKPLIYAAStLQSGVPSRFS 63
Qy 62 GSGGCTDFTLTITSSLOPEDFASYYCQESLSASYTFGGGTVEIKR 106
Db 64 GSGGCTDFTLTITSSLOPEDFATYTCQOSYSPYTFGGGTVEIKR 108

Search completed: July 26, 2005, 09:27:50
Job time : 14.6515 secs

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OM protein - protein search, using sw model

Run on: July 26, 2005, 08:52:21 ; Search time 66.6515 Seconds

(without alignments)
814.391 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543

Sequence: 1 ELTQSPSSLSASVGDRTVIS.....QESLSASVTGQGRKVEIKR 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465	85.6	108	2 Q9UL77	Q9UL77 homo sapien
2	449.5	82.8	107	2 Q96SA9	Q96SA9 homo sapien
3	439.5	80.9	107	2 Q9UL81	Q9UL81 homo sapien
4	436	80.8	236	2 Q6GMX0	Q6GMX0 homo sapien
5	436	80.3	129	1 KVI1W_HUMAN	P04431 homo sapien
6	436	80.3	236	2 Q6GMX8	Q6GMX8 homo sapien
7	434	79.9	236	2 Q6GMW1	Q6GMW1 homo sapien
8	433	79.7	108	1 KVI1E_HUMAN	P01597 homo sapien
9	430	79.2	108	1 KVI1H_HUMAN	P01600 homo sapien
10	424	78.1	236	2 Q6PIH7	Q6PIH7 homo sapien
11	422	77.7	108	2 Q9UL79	Q9UL79 homo sapien
12	420	77.3	108	1 KVI1N_HUMAN	P01606 homo sapien
13	420	77.3	108	2 Q9UL70	Q9UL70 homo sapien
14	418	77.0	234	2 Q7Z473	Q7Z473 homo sapien
15	416	76.6	108	1 KVI1F_HUMAN	P01598 homo sapien
16	414	76.2	108	1 KVI1K_HUMAN	P01603 homo sapien
17	413	76.1	108	1 KVI1V_HUMAN	P04430 homo sapien
18	412	75.9	108	1 KVI1O_HUMAN	P01607 homo sapien
19	412	75.9	236	2 Q7Z3V4	Q7Z3V4 homo sapien
20	409	75.3	108	1 KVI1G_HUMAN	P01599 homo sapien
21	408	75.1	108	1 KVI1M_HUMAN	P01605 homo sapien
22	407	75.0	108	1 KVI1B_HUMAN	P01594 homo sapien
23	406	74.8	108	1 KVI1R_HUMAN	P01593 homo sapien
24	404	74.4	108	1 KVI1A_HUMAN	P01610 homo sapien
25	400	73.7	236	2 Q6PIH4	Q6PIH4 homo sapien
26	399.5	73.6	107	1 KVI1D_HUMAN	P01596 homo sapien
27	399	73.5	108	1 KVI1S_HUMAN	P01611 homo sapien
28	398	73.3	108	1 KVI1P_HUMAN	P01608 homo sapien
29	397	73.1	108	1 KVI1L_HUMAN	P01604 homo sapien
30	397	73.1	129	1 KVI1X_HUMAN	P04432 homo sapien
31	397	73.1	236	2 Q6GMX9	Q6GMX9 homo sapien

32	396	72.9	108	1 KVI1Y_HUMAN	P80362 homo sapien
33	396	72.9	236	2 Q6PIH5	Q6PIH5 homo sapien
34	394	72.6	244	2 Q6SZC8	Q6SZC8 homo sapien
35	391	72.0	108	1 KVI1Q_HUMAN	P01609 homo sapien
36	391	72.0	240	2 Q6SZC9	Q6SZC9 homo sapien
37	385.5	71.0	109	1 KVI1T_HUMAN	P01612 homo sapien
38	384	70.7	108	1 KVI1C_HUMAN	P01595 homo sapien
39	376	69.2	108	1 KVI1T_MOUSE	P01653 mus musculus
40	373	68.7	108	1 KVS5_MOUSE	P01652 mus musculus
41	371	68.3	108	2 Q9UL83	Q9UL83 homo sapien
42	371	68.3	116	2 Q96PE6	Q96PE6 homo sapien
43	370.5	68.2	109	1 KVI1B_HUMAN	P01623 homo sapien
44	370	68.1	108	1 KVSQ_MOUSE	P01650 mus musculus
45	368.5	67.9	109	1 KVI1B_HUMAN	P01620 homo sapien

ALIGNMENTS

RESULT 1			
Q9UL77	PRELIMINARY;	PRT;	108 AA.
ID Q9UL77			
AC Q9UL77;			
DT 01-MAY-2000 (TrEMBLrel. 13, Created)			
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=98271139; PubMed=9614934; DOI=10.1006/clin.1998.4531;			
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,			
RA Young D.C.;			
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal			
RT fetus.";			
RL Clin. Immunol. Immunopathol. 87:184-192(1998).			
DR EMBL; AF035037; AAD56273.1; -.			
DR PIR; B49047; B49047.			
DR SRS; S34083; S34083.			
DR HSSP; P01607; IBMW.			
DR InterPro; IPR007110; Ig-like.			
DR InterPro; IPR003596; Ig_v.			
DR SMART; SM00406; IGv; 1.			
DR PROSITE; PS50835; IG LIKE; 1.			
FT NON_TER	1	1	
FT NON_TER	108	108	
SO SEQUENCE	108 AA;	11738 MW;	C06681716C4D16F3 CRC64;
Query Match			
Best Local Similarity	84.9%;	Score 465; DB 2;	Length 108;
Matches	90; Conservative	9; Mismatches	7; Indels 0; Gaps 0;
Qy	1 ELTQSPSSLSASVGDRTVISCRASQRIINTYLNWQHPKGA	PKLLIYAASLSGVSRF	60
Db	3 QMTQSPSSLSASVGDRTVITCRASQSISSYLNWQHPKGA	PKLLIYAASLSGVSRF	62
Qy	61 SGSGSGTDFLTITSSLPEDPASYYCOESLSASYTFQGR	KVEIKR	106
Db	63 SGSGSGTDFLTITSSLPEDPASYYCOQSYSTSWTFGGR	KVEIKR	108
RESULT 2			
ID Q96SA9	PRELIMINARY;	PRT;	107 AA.
AC Q96SA9;			
DT 01-DEC-2001 (TrEMBLrel. 19, Created)			
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain			

DE variable: region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglycosamine/anti-myosin
RT antibody V region genes";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR HSSP; P01607; 1BMW.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;
SQ
Query Match 82.8%; Score 449.5; DB 2; Length 107;
Best Local Similarity 84.9%; Pred. No. 8.7e-40;
Matches 90; Conservative 8; Mismatches 7; Indels 1; Gaps 1;
Qy 1 ELTQSPSSLSASVGDRTVITSCASQRIINTYLNWYQHKRGKAPKLLIYAASLSQGVSPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKRGKAPKLLIYAASLSQGVSPSRF 62
Qy 61 SSGSGYGDFTLTISLQPEDFASYYCOESLSASVTFEGQTKVEIKR 106
Db 63 SSGSGYGDFTLTISLQPEDFATYYCOQSYA-TLTFGGGTKEIKR 107
RESULT 3
Qy 09JUL81 PRELIMINARY; PRT; 107 AA.
ID 09JUL81;
AC 09JUL81;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; P01607; 1BMW.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IGV.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;
SQ

Query Match 80.9%; Score 439.5; DB 2; Length 107;
Best Local Similarity 82.1%; Pred. No. 1e-38;
Matches 87; Conservative 8; Mismatches 10; Indels 1; Gaps 1;
Qy 1 ELTQSPSSLSASVGDRTVITSCASQRIINTYLNWYQHKRGKAPKLLIYAASLSQGVSPSRF 60
Db 3 QMTQSPSSLSASVGDRTVITTCRASQSISSYLNWYQKRGKAPKLLIYAASLSQGVSPSRF 62
Qy 61 SSGSGYGDFTLTISLQPEDFASYYCOESLSASVTFEGQTKVEIKR 106
Db 63 SSGSGYGDFTLTISLQPEDFATYYCOQSYA-TLTFGGGTKEIKR 107
RESULT 4
Qy 06GMX0 PRELIMINARY; PRT; 236 AA.
ID 06GMX0;
AC 06GMX0;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073775; AAH3775.1; -.
DR InterPro; IPR003599; IGV.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_LIKE.
DR InterPro; IPR003006; IGV.
DR InterPro; IPR003596; IGV.
DR Pfam; PF07654; C1-sect; 1.
DR Pfam; PF00047; IGV; 2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IGV_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7B92BF8F CRC64;
Query Match 80.8%; Score 439; DB 2; Length 236;
Best Local Similarity 81.1%; Pred. No. 2.7e-38;
Matches 86; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVITISCRASORINTYLMWYQHKPKAKLLIYAASSLSQGVPSRF 60
DB 25 QMTOSPSLSASVGRVITITCRASQINNNYLMWYQKPKAKLLIYAASSLSQGVPSRF 84
QY 61 SSGSGGTDFTLTISLQFEDFASYYCOESLSASYFGGCTKYEIKR 106
DB 85 SSGSGGTDFTLTISLRPDPATYYCCQSYNPLTFGGGTINVEIKR 130

RESULT 5

K1W HUMAN

ID K1W HUMAN STANDARD; PRT; 129 AA.

AC P04431.
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combriato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006 (1984).
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL, X00965; CAA25477.1; ALT_TERM.
DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; KIHUMK.
DR HSRP; P01607; IBMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 1 229
FT DOMAIN 23 45 Ig kappa chain V-I region Walker.
FT DOMAIN 46 56 Framework-1.
FT DOMAIN 57 71 Complementarity-determining-1.
FT DOMAIN 72 78 Framework-2.
FT DOMAIN 79 110 Complementarity-determining-2.
FT DOMAIN 111 119 Framework-3.
FT DOMAIN 120 129 Complementarity-determining-3.
FT DISULFID 45 110 Framework-4.
FT NON_TER 129 129 By similarity.
SQ SEQUENCE 129 AA; 14069 MW; F941FA07DAFC2F9 CRC64;

Query Match 80.3%; Score 436; DB 1; Length 129;
Best Local Similarity 81.9%; Pred. No. 2.9e-38;
Matches 86; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVITISCRASORINTYLMWYQHKPKAKLLIYAASSLSQGVPSRF 60
DB 25 QMTOSPSLSASVGRVITITCRASQISNNYLMWYQKPKAKLLIYAASSLSQGVPSRF 84
QY 61 SSGSGGTDFTLTISLQFEDFASYYCOESLSASYFGGCTKYEIKR 106
DB 85 SSGSGGTDFTLTISLRPDPATYYCCQSYNPLTFGGGTINVEIKR 130

DB 85 SSGSGGTDFTLTISLRPDPATYYCCQSYNPLTFGGGTINVEIKR 129

RESULT 6

O6GMX8

ID O6GMX8 PRELIMINARY; PRT; 236 AA.

AC O6GMX8.
DT 05-JUN-2004 (TREMBLrel. 27, Created)
DT 05-JUN-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatane P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska J., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RL Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -.
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG_2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8B14B659EFC9 CRC64;

Query Match 80.3%; Score 436; DB 2; Length 236;
Best Local Similarity 80.2%; Pred. No. 5.7e-38;
Matches 85; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 1 ELTOSPSLSASVGRVITISCRASORINTYLMWYQHKPKAKLLIYAASSLSQGVPSRF 60
DB 25 QMTOSPSLSASVGRVITITCRASQISNNYLMWYQKPKAKLLIYAASSLSQGVPSRF 84
QY 61 SSGSGGTDFTLTISLQFEDFASYYCOESLSASYFGGCTKYEIKR 106
DB 85 SSGSGGTDFTLTISLRPDPATYYCCQAHSPFTFGGTVDIKR 130

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RESULT 7
Q6GMW1 PRELIMINARY; PRT; 236 AA.
ID Q6GMW1
AC Q6GMW1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CN NCBI_TaxID=9606;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RC TISSUE=Spleen;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshynski S., Cantinci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hellon E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimmett J., Schmutz J., Myers R.W., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC073791, AAT73791.1; -.
DR InterPro; IPR003599; I9.
DR InterPro; IPR007110; I9-like.
DR InterPro; IPR003597; I9_c1.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; I9; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ
SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Query Match 79.9%; Score 434; DB 2; Length 236;
Best Local Similarity 81.1%; Pred. No. 9.2e-38;
Matches 86; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKGKAPKLLIYAASSLQSGVPSRF 60
DB 25 QMTQSPSSLSASVGDRTVITSCRASQISNDLGWYQOKPKAPKLLIYAASSLQSGVPSRF 84
QY 61 SGSGGTDFTLTISLSLOPEDFASYYCOESLSASTFFGQGTVEIKR 106
DB 85 SGSGGTDFTLTISLSLOPEDFATYTCLODYNPMTFGQGTVEIKR 130

RESULT 8
KYLE_HUMAN STANDARD; PRT; 108 AA.
ID KYLE_HUMAN

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AC P01597;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region DEE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CN NCBI_TaxID=9606;
RX MEDLINE=72053133; PubMed=5124396;
RA Milstein C.P., Deverson E.V.;
RT "The amino acid sequence of a human kappa light chain.";
RL Biochem. J. 123:945-958(1971).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
DR HSSP; P01607; 1BWW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; I9-like.
DR InterPro; IPR003596; I9_v.
DR Pfam; PF00047; I9; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Framework-4.
FT DOMAIN 98 107 Complementarity-determining-3.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11661 MW; BDD6E3500171E51 CRC64;

Query Match 79.7%; Score 433; DB 1; Length 108;
Best Local Similarity 77.4%; Pred. No. 4.9e-38;
Matches 82; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYINWYQHKGKAPKLLIYAASSLQSGVPSRF 60
DB 3 ZMTQSPSSLSASVGDRTVITSCRASQVKNYINWYQOKPKAPKLLIYAASSLQSGVPSRF 62
QY 61 SGSGGTDFTLTISLSLOPEDFASYYCOESLSASTFFGQGTVEIKR 106
DB 63 SGSGGTDFTLTISLSLOPEDFATYTCLODYNPMTFGQGTVEIKR 108

RESULT 9
KYLE_HUMAN STANDARD; PRT; 108 AA.
ID KYLE_HUMAN
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CN NCBI_TaxID=9606;
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANEOUS: This is a Bence-Jones protein.

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DR PIR; A01868; K1HUUH.
DR PDB; 1F6L: X-ray; L=1-108.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR 3D-structure; Bence-Jones protein; direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT 24 34 Complementarity-determining-1.
FT 35 49 Framework-2.
FT 50 56 Complementarity-determining-2.
FT 57 88 Framework-3.
FT 89 97 Framework-4.
FT 98 107 Complementarity-determining-3.
FT 107 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match
Best Local Similarity 79.2%; Score 430; DB 1; Length 108;
Matches 83; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLQSGVPSRF 60
DB 3 QMTQSPSSLSASVGDRTVITTCRASQGISSTYLMWYQOKRGKAPQVLIYAASSLQSGVPSRF 62
QY 61 SGSGVGTFLLTISLQFEDFASYYCOESLSASYTFGGGTVEIKR 106
DB 63 SGSGSGTFLLTISLQFEDFATYYCOQNYITPTSGGTVEIKR 108

RESULT 10
Q6PIH7 PRELIMINARY; PRT; 236 AA.
ID Q6PIH7
AC Q6PIH7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L.H., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marutina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.R.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malik J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
RA Faley J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimoldi J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maita M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
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RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -.
DR HSSP; P01607; IAR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match
Best Local Similarity 78.1%; Score 424; DB 2; Length 236;
Matches 85; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLQSGVPSRF 60
DB 25 QLTQSPSSLSASVGDRTVITTCRASQGISSTYLMWYQOKRGKAPNLLIYAASSLQSGVPSRF 84
QY 61 SGSGVGTFLLTISLQFEDFASYYCOESLSASYTFGGGTVEIKR 106
DB 85 SGSGSGTFLLTISLQFEDFATYYCOQNSPTFGGTVEIKR 130

RESULT 11
Q9UL79 PRELIMINARY; PRT; 108 AA.
ID Q9UL79
AC Q9UL79
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
RA Wu X., Liu B., Van der Werf P.L., Kalls N.N., Betney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus."
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035035; AAD56271.1; -.
DR PIR; S23638; S23638.
DR PIR; S30521; S30521.
DR PIR; S34090; S34090.
DR HSSP; P01607; IBMW.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50835; IGV; 1.
FT NON TER 1 1
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724F84B CRC64;

Query Match
Best Local Similarity 77.7%; Score 422; DB 2; Length 108;
Matches 84; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLQSGVPSRF 61
DB 1 LTQSPSSLSASVGDRTVITTCRASQGISSTYLMWYQOKRGKAPNLLIYAASSLQSGVPSRF 84
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Db 4 MTQSPSLISASTGDRVTISCRMSQGISYLAHWQKPKAKPELLIYAASLTQSGVPSRFS 63
Qy 62 GSGYGTDFTLTITSLQFEDFASVYCOESLSASVYFGQGTKEIKR 106
Db 64 GSGSGTDFTLTITSLQSGSEDPATVYCOQYYSFPPTFGGTKEIKR 108

RESULT 12
ID KVIN HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains."
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenström's
CC macroglobulin.
CC PIR: A01872; K1H10U.
DR HSSP; P01607; 1BMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283DA24105827E CRC64;

Query Match 77.3%; Score 420; DB 1; Length 108;
Best Local Similarity 68.9%; Pred. No. 1.2e-36;
Matches 73; Conservative 22; Mismatches 11; Indels 0; Gaps 0;
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Benney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; 1BMW.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 77.3%; Score 420; DB 2; Length 108;
Best Local Similarity 79.2%; Pred. No. 1.2e-36;
Matches 84; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ELTQSPSLASVGDRTVISCRAQRINTYLNWYQHKRGKAPKLLIYAASLTQSGVPSRF 60
Db 3 QMTQSPSLASVGDRTVITCRASQGISNLYAQKPKKSLIYAASLTQSGVPSRF 62

Qy 61 GSGYGTDFTLTITSLQFEDFASVYCOESLSASVYFGQGTKEIKR 106
Db 63 GSGSGTDFTLTITSLQPEDVATVYCOQYNSAPRTFGGTKEIKR 108

RESULT 14
Q72473 PRELIMINARY; PRT; 234 AA.
AC Q72473;
DT 01-OCT-2003 (TRENBLREL. 25, Created)
DT 01-OCT-2003 (TRENBLREL. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditschenko L., Marutina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedl T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska J., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
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RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -.
DR HSSP; P01834; 1HEZ.
DR InterPro; IPR007110; IG-1ike.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-seel; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match          77.0%; Score 418; DB 2; Length 234;
Best Local Similarity 77.1%; Pred. No. 4,5e-36;
Matches 81; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPKAPKLIYAASSLSQGVPSRF 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 24 MTQSPSSFSASTGDRVITTCRASQSIGSYLAWYQCKPKAPQLLIYAASLTQSGVPSRFS 83
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 GSGGVTDFLTITISLQFEDFASVYCOESLSASVTFGGTKVEIKR 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 84 GSAGTDFLTITISLQFEDFATYVCOQYTYPTWTFGGTKVEIKR 128
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
KVIF_HUMAN
ID _KVIF_HUMAN STANDARD; PRT; 108 AA.
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-1 region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D.; Cunningham B.A.; Kucishauser U.; Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT acid sequence of the light chain.";
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E.; Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein.
DR HSSP; P01607; 1BMW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.

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FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 107 Framework-4.
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2P4D88823 CRC64;

Query Match          76.6%; Score 416; DB 1; Length 108;
Best Local Similarity 77.1%; Pred. No. 3.1e-36;
Matches 81; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKPKAPKLIYAASSLSQGVPSRF 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3 QMTQSPFTLSASVGDRTVITTCRASQINTYLMWYQCKPKAPKLIYAASSLSQGVPSRF 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GSGGVTDFLTITISLQFEDFASVYCOESLSASVTFGGTKVEIKR 105
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 63 IGSGSGTEFTLTITISLQFDDFATYVCOQYNSDKMFGGTKVEIKR 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Job time : 66.6515 secs

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OM protein - protein search, using sw model

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(without alignments)
516.724 Million cell updates/sec

Title: US-10-027-725A-10

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Listing first 45 summaries

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3: geneseqp2000s:*
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5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533	98.2	106	5	ABG30448 Human IGE
2	475	87.5	107	2	AAR54260 Anti-HIV
3	475	87.5	107	2	AAW01283 VL region
4	475	87.5	107	3	AAV98244 Anti-gp12
5	475	87.5	107	3	AAV95135 Anti-gp12
6	474	87.3	107	4	AAV93667 Human ant
7	474	87.3	107	6	ABO27474 Anti-Rh(D
8	472	86.9	107	4	AAV93663 Human ant
9	472	86.9	107	4	AAV93664 Human ant
10	472	86.9	107	4	AAV93590 Human ant
11	472	86.9	107	6	ABO27471 Anti-Rh(D
12	472	86.9	107	6	ABO27397 Anti-Rh(D
13	472	86.9	107	6	ABO27470 Anti-Rh(D
14	471	86.7	107	4	AAV93644 Human ant
15	471	86.7	107	6	ABO27451 Anti-Rh(D
16	468	86.2	107	4	AAV93593 Human ant
17	468	86.2	244	6	ABO27400 Anti-Rh(D
18	468	86.2	244	8	ADH34565 scFv SC02
19	468	86.2	244	8	ADR23318 Human CD7
20	468	86.2	244	8	ADR23330 Human CD7
21	468	86.2	244	8	ADR23332 Human CD7
22	468	86.2	245	8	ADR23320 Human CD7
23	468	86.2	249	8	ADR23322 Human CD7
24	468	86.2	249	8	ADR23326 Human CD7
25	467	86.0	107	2	AAR54261 Anti-HIV

26	467	86.0	107	2	AAW01284
27	467	86.0	107	3	AAV98245
28	467	86.0	107	3	AAV95136
29	467	86.0	114	2	AAW13922
30	465	85.6	111	4	AAV63656
31	465	85.6	111	6	ABJ38615
32	465	85.6	132	2	AAW22842
33	465	85.6	240	6	ABJ38595
34	465	85.6	299	4	AAV63660
35	464.5	85.5	108	4	AAV93589
36	464.5	85.5	108	4	AAV93600
37	464.5	85.5	108	6	ABO27407
38	464.5	85.5	108	6	ABO27396
39	464	85.5	107	4	AAV93594
40	464	85.5	107	6	ABO27401
41	464	85.5	108	6	ABP96009
42	464	85.5	108	8	ADL92386
43	464	85.5	108	8	ADQ14601
44	464	85.5	108	8	ADQ77191
45	464	85.5	108	8	ADQ77181

ALIGNMENTS

RESULT 1	
ABG30448	ID
ABG30448	standard; protein; 106 AA.
XX	AC
XX	ABG30448;
DT	21-OCT-2002 (first entry)
DE	Human IGE Fab clone 94 light chain protein.
KW	Human; fab; anti-allergic; vaccine; grass pollen; phi p 2;
KM	liniothy grass pollen allergen; passive immunotherapy.
XX	XX
OS	Homo sapiens.
XX	XX
FH	Key
FT	Region
FT	Location/Qualifiers
FT	1..21
FT	/note= "FR1 region"
FT	22..32
FT	/note= "CDR1 region"
FT	33..47
FT	/note= "FR2 region"
FT	48..54
FT	/note= "CDR2 protein"
FT	55..86
FT	/note= "FR3 region"
FT	87..95
FT	/note= "CDR2 region"
FT	96..104
FT	/note= "FR4 region"
XX	XX
PN	WO200253595-A1.
XX	XX
PD	11-JUL-2002.
XX	XX
PF	27-DEC-2001; 2001WO-SE002908.
XX	XX
PR	29-DEC-2000; 2000SE-00004892.
PA	(PHARMA) PHARMACIA DIAGNOSTICS AB.
XX	XX
PI	Flicker S, Steinberger P, Kraft D, Valenta R;
XX	XX
DR	WPI: 2002-583604/62.
DR	N-PDB; ABK89640.
PT	Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT	variable region of group 2 allergen specific-human IGE Fabs, useful for

PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
PS Disclosure; Page 39; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgG fabs and methods for their use. The proteins
CC of the invention may have anti-allergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergen. The group
CC antibodies to Pn1 p 2 (a major Timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgG antibodies to Pn1 p 2. The present sequence represents the human IgG
CC fab, clone 94 light chain protein of the invention
XX
SQ Sequence 106 AA;
Query Match 98.2%; Score 533; DB 5; Length 106;
Best Local Similarity 99.1%; Pred. No. 4.6e-33;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLQGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLQGVPSRF 60
QY 61 SSGSGYTDFTLTISLSLOPEDFASYYCOESLSASVTFEGGTVEIKR 106
Db 61 SSGSGYTDFTLTISLSLOPEDFASYYCOESLSASVTFEGGTVEIKR 106
RESULT 2
AAR54260
ID AAR54260 standard; protein; 107 AA.
XX
AC AAR54260;
XX
DT 25-MAR-2003 (revised)
DT 10-NOV-1994 (first entry)
XX
DE Anti-HIV gp120 immunoglobulin light chain variable region b22.
XX
KW Human immunodeficiency virus; HIV1; glycoprotein gp120; epitope;
KW neutralisation; monoclonal antibody; kappa light chain; variable region;
KW framework; complementarity determining region.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..33
FT /label= CDR1
FT Region 34..48
FT /label= FR2
FT Region 49..55
FT /label= CDR2
FT Region 56..87
FT /label= FR3
FT Region 88..95
FT /label= CDR3
FT Region 96..107
FT /label= FR4
XX
XX MO9407922-A1.
XX
XX 14-APR-1994.
XX

PF 30-SEP-1993; 93WO-US009328.
XX
PR 30-SEP-1992; 92US-00954148.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Burton DR, Barbas CF, Lerner RA;
XX
DR WPI; 1994-135516/16.
XX
PT New human monoclonal antibodies neutralising HIV - react with gp120 or
PT gp1 and nucleic acid encoding them, useful for in vivo or in vitro
PT diagnosis and for passive immuno-therapy.
XX
XX Claim 5; Page 189; 248pp; English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR amplification
CC using primers specific for heavy and light chain variable regions. The
CC amplification products were inserted into a dicistronic vector to produce
CC a library of fragments. E.coli XLI Blue cells were transformed with the
CC library. Filamentous phage were produced which expressed the MAb regions
CC on their surface. Panning with gp120 and gp41 resulted in the recovery of
CC immunoreactive clones. The light chain VK region sequence AAR54260
CC neutralises HIV1 gp120. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 107 AA;
Query Match 87.5%; Score 475; DB 2; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.1e-28;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITSCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLQGVPSRF 60
Db 1 ELTQSPSSLSASVGDRTVITSCRASQSISSYLMWYQHKRGKAPKLLIYAASSLQGVPSRF 60
QY 61 SSGSGYTDFTLTISLSLOPEDFASYYCOESLSASVTFEGGTVEIKR 106
Db 61 SSGSGYTDFTLTISLSLOPEDFASYYCOESYSTPTTFEGGTVEIKR 106
RESULT 3
AAW01283
ID AAW01283 standard; protein; 107 AA.
XX
AC AAW01283;
XX
DT 29-JAN-1997 (first entry)
DT
XX
DE VL region of HIV neutralising MAb, clone b22 and B35.
XX
KW Heavy chain; light chain; variable region; VH; monoclonal antibody; MAb;
KW HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
KW virus infectivity assay; precursor gp160; immunocompetence; human;
KW anti-HIV antibody; detection; HIV infection.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT Region 1..21
FT /label= FR1
FT Region 22..32
FT /label= CDR1
FT Region 33..47
FT /label= FR2
FT Region 48..54
FT /label= CDR2
FT Region 55..86
FT /label= FR3
FT Region 87..95
FT /label= CDR3
FT Region 96..107
FT /label= FR4
XX

PN MO9602273-A1.
 XX 01-FEB-1996.
 XX 11-JUL-1995; 95WO-US008743.
 XX 18-JUL-1994; 94US-00276852.
 XX (SCRI) SCRIPPS RES INST.
 XX Burton DR, Barbas CF, Lerner RA;
 XX WPI, 1996-179601/18.
 PT Monoclonal antibody binding to VL/V2 loop of HIV gp120 - used in passive
 PT immunotherapy and detection of HIV infection.
 PS Example; Fig 11; 366pp; English.
 XX The sequences given in AAM01261-92 represent the light chain variable
 CC regions (VL) of a series of monoclonal antibodies (MAb's) which are
 CC immunoreactive with HIV glycoprotein gp120 and are capable of
 CC neutralising HIV. This sequence represents the sequence of the JK2 gene
 CC clones, b22 and B35. A MAb containing this VL sequence has the capacity
 CC to reduce HIV infectivity titre in an in vivo virus infectivity assay by
 CC 50 % at a concentration of less than 700 ng of antibody/ml, and binds
 CC mature gp120 preferentially over the precursor gp160. The MAb may be used
 CC for determining immunocompetence of a human anti-HIV antibody and in the
 CC detection of HIV infection
 CC
 SQ Sequence 107 AA;
 QY Query Match 87.5%; Score 475; DB 2; Length 107;
 QY Best Local Similarity 87.7%; Pred. No. 1.1e-28;
 Db Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
 QY 1 ELTGSPSSLSASVGDRTVITSCRASORINTYLMWYQHKPKAKPLKLIYAASSLSQGVPSRF 60
 Db 1 ELTGSPSSLSASVGDRTVITSCRASOSISSYLMWYQHKPKAKPLKLIYAASSLSQGVPSRF 60
 QY 61 SSGSGYDTFTLTISLQEPDFASYYCOESLSASVTFGGGTKEIKR 106
 Db 61 SSGSGYDTFTLTISLQEPDFATYYCQOSYSTPTTFGGGTKEIKR 106
 RESULT 4
 ID AAY98244 standard; protein; 107 AA.
 AC AAY98244;
 DT 04-JUL-2000 (first entry)
 DE Anti-gp120 antibody light chain variable region from clone b22.
 XX
 KW Antibody; anti-HIV monoclonal antibody; glycoprotein-120;
 KW human immunodeficiency virus type 1; HIV-1; infectivity titre;
 KW passive immunotherapy; reduce severity; HIV-induced disease;
 KW immunocompetence; active immunisation.
 OS Homo sapiens.
 PN AU9948754-A.
 XX 17-FEB-2000.
 XX 16-SEP-1999; 99AU-00048754.
 XX 16-SEP-1999; 99AU-00048754.
 XX (SCRI) SCRIPPS RES INST.
 XX Burton DR, Barbas CF, Lerner RA;

XX WPI, 2000-246867/22.
 DR Human neutralizing monoclonal antibodies to human immunodeficiency virus
 PT (HIV) used for providing passive immunotherapy to HIV are specific for
 PT glycoprotein-120.
 XX Example 9; Fig 11; 374pp; English.
 XX This sequence represents a fragment of the antibodies of the invention.
 CC The invention relates to the production of an anti-HIV (human
 CC immunodeficiency virus) glycoprotein (gp)-120 monoclonal antibody capable
 CC of reducing an HIV infectivity titre in an in vitro virus infectivity
 CC assay by 50% at a concentration of less than 70 ng/ml. The method for the
 CC production of the antibody comprises: (a) providing a first
 CC polynucleotide encoding a heavy chain immunoglobulin amino acid sequence
 CC (which does not comprise the sequence represented by AAY98206) and a
 CC second polynucleotide encoding a light chain immunoglobulin amino acid
 CC sequence; (b) inserting the first and second polynucleotide sequences
 CC into a host cell; (c) maintaining the host cell in conditions which allow
 CC the amino acid sequences encoded by the polynucleotides to be expressed
 CC in the host cell; and (d) isolating the antibody comprising the heavy and
 CC light chain immunoglobulin amino acid sequences from the host cell. The
 CC anti-HIV gp-120 monoclonal antibody is used for providing passive
 CC immunotherapy to HIV in a human. They can be administered to high-risk
 CC patients to reduce the likelihood and/or severity of HIV-induced disease
 CC and to patients who are already HIV-infected. The antibodies are used for
 CC neutralising field isolates which provides information about the
 CC immunocompetence of an immune response in HIV patients, for detecting HIV
 CC in a biological fluid or tissue sample e.g. by radioimmunoassay, for
 CC producing anti-idiotypic antibodies which can be used for active
 CC immunisation and to screen human monoclonal antibodies to identify those
 CC with the same binding specificity and to monitor the course of HIV
 CC disease therapy by measuring the changes in concentration of HIV present
 CC in the body or in body fluids by immunoassay. The anti-HIV gp-120
 CC monoclonal antibodies are encoded by a human polynucleotide sequence and
 CC when used in vivo for diagnosis and immunotherapy of HIV-induced disease
 CC reduce the problems of significant host immune response to the antibodies
 CC associated with monoclonal antibodies of xenogeneic or chimeric
 CC derivation
 CC
 SQ Sequence 107 AA;
 QY Query Match 87.5%; Score 475; DB 3; Length 107;
 QY Best Local Similarity 87.7%; Pred. No. 1.1e-28;
 Db Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
 QY 1 ELTGSPSSLSASVGDRTVITSCRASORINTYLMWYQHKPKAKPLKLIYAASSLSQGVPSRF 60
 Db 1 ELTGSPSSLSASVGDRTVITSCRASOSISSYLMWYQHKPKAKPLKLIYAASSLSQGVPSRF 60
 QY 61 SSGSGYDTFTLTISLQEPDFASYYCOESLSASVTFGGGTKEIKR 106
 Db 61 SSGSGYDTFTLTISLQEPDFATYYCQOSYSTPTTFGGGTKEIKR 106
 RESULT 5
 ID AAY95135 standard; protein; 107 AA.
 AC AAY95135;
 DT 30-JUN-2000 (first entry)
 DE Anti-gp120 antibody light chain variable region from clone b22.
 XX
 KW Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
 KW reduce HIV infection; diagnosis; immunotherapy; HIV induced disease;
 KW glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.
 OS Homo sapiens.
 PN AU9948756-A.

```

XX 17-FEB-2000.
PD
XX
XX 16-SEP-1999; 99AU-00048756.
PE
XX 16-SEP-1999; 99AU-00048756.
PR
XX (SCRI ) SCRIpps RES INST.
PA
XX Burton DR, Barbas CF, Lerner RA;
PI
XX WPI; 2000-293393/26.
XX
XX Novel human monoclonal antibodies which immunoreact with and neutralize
PT human immunodeficiency virus useful for treating HIV infections.
PS
XX Example 9; Fig 11; 366pp; English.
XX
XX The present sequence represents a fragment of an anti-human
CC immunodeficiency virus type 1 (HIV-1) antibody. The invention relates to
CC a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
CC gp160 and neutralizes HIV and which reduces HIV infectivity titre in an
CC in vitro virus infectivity assay by 50%, at a concentration of less than
CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
CC immunotherapy of HIV induced disease. They are useful as neutralising
CC field isolates and provide useful information regarding the
CC immunocompetence of an immune response in HIV infected patients. The
CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
CC which can be used to screen human monoclonal antibodies to identify
CC whether the antibody has the same binding specificity as the antibodies
CC of the invention. The neutralising antibodies define new epitopes on the
CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
CC immunotherapeutic human monoclonal antibodies. A major advantages of the
CC monoclonal antibodies derives from the fact that they are encoded by a
CC human polynucleotide sequence. Thus in vivo use of the monoclonal
CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
CC reduces the problems of significant host immune response to the passively
CC administered antibodies which is a problem commonly encountered when
CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
CC An additional major advantage of the monoclonal antibodies described
CC derives from the fact that they immunoreact with a unique determinant
CC present on mature HIV glycoprotein gp120. This class of antibodies is
CC particularly effective at neutralising field isolates of HIV
CC
XX Sequence 107 AA;
SQ
Query March 87.5%; Score 475; DB 3; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.1e-28;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITICRASQRIINTYLNWYQHKRGKAPKLLIYAASSLQSGVPSRF 60
DB 1 ELTQSPSSLSASVGDRTVITICRASQSISSYLNWYQKRGKAPKLLIYAASSLQSGVPSRF 60
QY 61 SSGSGYGTDFLTITISLQFEDFASYYCOESLSASTTFGCGTKVEIKR 106
DB 61 SSGSGGTDFLTITISLQPEDFATYYCOOSYSTPTFFCGTKLEIKR 106
RESULT 6
AAG93667
ID AAG93667 standard; protein; 107 AA.
XX
XX AAG93667;
XX
XX 14-SEP-2001 (first entry)
XX
XX Human anti-Rh(D) antibody clone SH54 protein sequence.
DE
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX

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OS Homo sapiens.
XX
XX US6255455-B1.
XX
XX 03-JUL-2001.
XX
XX 29-JAN-1999; 99US-00240274.
XX
XX 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
PA
XX
XX Siegel DJ;
PI
XX WPI; 2001-388931/41.
XX
XX N-PSDB; AAH68724.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX Claim 1; Col 70; 162pp; English.
PS
XX
XX The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
XX Sequence 107 AA;
SQ
Query March 87.3%; Score 474; DB 4; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-28;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 ELTQSPSSLSASVGDRTVITICRASQRIINTYLNWYQHKRGKAPKLLIYAASSLQSGVPSRF 60
DB 2 ELTQSPSSMSASVGDRTVITICRASQSIGTYLNWYQKRGKAPKLLIYAASSLQSGVPSRF 61
QY 61 SSGSGYGTDFLTITISLQFEDFASYYCOESLSASTTFGCGTKVEIKR 106
DB 62 SSGSGGTDFLTITISLQPEDFATYYCOOSYSTPTFFCGTKVEIKR 107
RESULT 7
ABO27474
ID ABO27474 standard; protein; 107 AA.
XX
XX ABO27474;
XX
XX 12-SEP-2003 (first entry)
XX
XX Anti-Rh(D) light chain SH54.
DE
XX Human; RH(D) binding protein; blood typing; blood product; antibody;
KW magnetically activated cell sorting.
XX
XX Homo sapiens.
OS
XX US2003040605-A1.
XX
XX 27-FEB-2003.
PD
XX 04-MAY-2001; 2001US-00848798.
XX

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PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-0088404S.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX (TYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2001-312273/48.
DR N-PSDB; ACD45388.
XX
XX New human Rh(D) -binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
XX
PS Claim 4; Page 53; 187pp; English.
XX
CC The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents the amino acid sequence of a human anti-Rh(D) chain
XX
SQ Sequence 107 AA;

Query Match 87.3%; Score 474; DB 6; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.3e-28;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVTCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLQSGVPSRF 60
Db 2 ELTQSPSSMSASVGDRTVTCRASQISGTYLMWYQKRGKAPKLLIYAASSLQSGVPSRF 61
QY 61 SSGSGYTDFTLTISLQPEDPASYCQESLSASTYFGGTVEIKR 106
Db 62 SSGSGYTDFTLTISLQPEDPASYCQESYSTPWTFGGTVEIKR 107

RESULT 8
AAG93663
ID AAG93663 standard; protein; 107 AA.
XX
AC AAG93663;
XX
DT 14-SEP-2001 (first entry)
XX
DE Human anti-Rh(D) antibody clone SH49 protein sequence.
XX
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
OS Homo sapiens.
XX
PN US6255455-B1.
XX
PD 03-JUL-2001.
XX
PE 29-JAN-1999; 99US-00240274.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-0088404S.
PR 10-APR-1998; 98US-0081380P.
XX (TYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2001-388931/41.
DR N-PSDB; AAH68720.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.

XX
PS Claim 1; Col 69; 162pp; English.
XX
CC The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 4; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.9e-28;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLASVGDRTVTCRASQRIINTYLMWYQHKRGKAPKLLIYAASSLQSGVPSRF 60
Db 2 ELTQSPSSLSASVGDRTVTCRASQISSYLMWYQKRGKAPKLLIYAASSLQSGVPSRF 61
QY 61 SSGSGYTDFTLTISLQPEDPASYCQESLSASTYFGGTVEIKR 106
Db 62 SSGSGYTDFTLTISLQPEDPASYCQESYSTPWTFGGTVEIKR 107

RESULT 9
AAG93664
ID AAG93664 standard; protein; 107 AA.
XX
AC AAG93664;
XX
DT 14-SEP-2001 (first entry)
XX
DE Human anti-Rh(D) antibody clone SH50 protein sequence.
XX
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
OS Homo sapiens.
XX
PN US6255455-B1.
XX
PD 03-JUL-2001.
XX
PE 29-JAN-1999; 99US-00240274.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-0088404S.
PR 10-APR-1998; 98US-0081380P.
XX (TYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2001-388931/41.
DR N-PSDB; AAH68721.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
PS Claim 1; Col 69; 162pp; English.
XX
CC The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies

are used in diagnostics that require human antibodies instead of animal antibodies, such as determine the Rh phenotype of human red blood cells. AAH6815 to AAH68726 represent the nucleotide sequence which encode AAH6815 to AAH68726. AAH6815 to AAH68726 represent anti-Rh(D) heavy chain CDR3 amino acid sequences which are given in the exemplification of the present invention

Sequence 107 AA;

Query Match 86.9%; Score 472; DB 4; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.9e-28;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVCDRTVITSCRASQRIINTYINWYQHKPKAKPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVCDRTVITSCRASQRIINTYINWYQHKPKAKPKLLIYAASSLSQGVPSRF 61
QY 61 SSGSGVGTDFLTITSSLOPEDFASYYCOESLSASTYFGGKTVEIKR 106
DB 62 SSGSGVGTDFLTITSSLOPEDFATYYCOQSYSTPMTFGGKTVEIKR 107

RESULT 10

AAH63590 standard; protein; 107 AA.

AC AAG93590;

DT 14-SEP-2001 (first entry)

XX Human anti-Rh(D) chain 102 protein sequence.

XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;

KM red blood cell; Rh phenotype; diagnosis; therapeutic.

OS Homo sapiens.

XX US625455-B1.

PD 03-JUL-2001.

PF 29-JAN-1999; 99US-00240274.

FR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

PA (UYPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

DR WPI; 2001-388931/41.

DR N-PSDB; AAH68647.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in

PT diagnostics requiring a human instead of an animal antibody and in

PT therapeutic medicine.

PS Claim 1; Col 43; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,

CC preferably a human antibody, (I) having an amino acid sequence comprising

CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has

CC immunostimulant activity, and can be used as an immune system stimulant.

CC (I) can be used in diagnostic and therapeutic medicine. The antibodies

CC are used in diagnostics that require human antibodies instead of animal

CC antibodies, such as determine the Rh phenotype of human red blood cells.

CC AAH6815 to AAH68726 represent the nucleotide sequence which encode

CC AAH6815 to AAH68726. AAH6815 to AAH68726 represent anti-Rh(D) heavy

CC chain CDR3 amino acid sequences which are given in the exemplification of

CC the present invention

XX Sequence 107 AA;

Query Match 86.9%; Score 472; DB 4; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.9e-28;
Matches 92; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVCDRTVITSCRASQRIINTYINWYQHKPKAKPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVCDRTVITSCRASQRIINTYINWYQHKPKAKPKLLIYAASSLSQGVPSRF 61
QY 61 SSGSGVGTDFLTITSSLOPEDFASYYCOESLSASTYFGGKTVEIKR 106
DB 62 SSGSGVGTDFLTITSSLOPEDFATYYCOQSYSTPMTFGGKTVEIKR 107

RESULT 11

ABO27471 standard; protein; 107 AA.

AC ABO27471;

DT 12-SEP-2003 (first entry)

XX Anti-Rh(D) light chain SH50.

XX Human; RH(D) binding protein; blood typing; blood product; antibody;

KM magnetically activated cell sorting.

OS Homo sapiens.

PN US2003040605-A1.

PD 27-FEB-2003.

PF 04-MAY-2001; 2001US-00848798.

FR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

PR 29-JAN-1999; 99US-00240274.

PA (UYPE-) UNIV PENNSYLVANIA.

PI Siegel DL;

DR WPI; 2003-512273/48.

DR N-PSDB; ACD45385.

XX New human Rh(D)-binding protein useful for various diagnostic and

PT therapeutic applications, including typing of blood or blood products.

PS Claim 4; Page 52; 187pp; English.

XX The invention relates to an isolated Rh(D) binding protein. The protein

CC can be used for magnetically activated cell sorting. The protein is

CC useful in various diagnostic and therapeutic applications in humans,

CC including typing of blood or blood products. The present sequence

CC represents the amino acid sequence of a human anti-Rh(D) chain

XX Sequence 107 AA;

Query Match 86.9%; Score 472; DB 6; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.9e-28;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVCDRTVITSCRASQRIINTYINWYQHKPKAKPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVCDRTVITSCRASQRIINTYINWYQHKPKAKPKLLIYAASSLSQGVPSRF 61
QY 61 SSGSGVGTDFLTITSSLOPEDFASYYCOESLSASTYFGGKTVEIKR 106
DB 62 SSGSGVGTDFLTITSSLOPEDFATYYCOQSYSTPMTFGGKTVEIKR 107

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RESULT 12
ABO27397
ID ABO27397 standard; protein, 107 AA.
XX
AC ABO27397;
XX
DT 12-SEP-2003 (first entry)
XX
DE Anti-Rh(D) chain 102.
XX
KM Human, RH(D) binding protein; blood typing; blood product; antibody;
XX magnetically activated cell sorting.
XX
OS Homo sapiens.
XX
PN US2003040605-A1.
XX
PD 27-FEB-2003.
XX
PF 04-MAY-2001; 2001US-00848798.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX
XX (TYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2003-512273/48.
DR N-PSDB; ACD45311.
XX
PT New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
XX
XX
PS Claim 4; Page 26; 187pp; English.
XX
CC The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents the amino acid sequence of a human anti-Rh(D) chain
XX
SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 6; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.9e-28;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVTCRASQRIINTYINWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVTCRASQRIINTYINWYQHKRGKAPKLLIYAASSLSQGVPSRF 61
QY 61 SGGSGYGDFTLTISLQPEDFASYYCOESLSASYTFQGTVEIKR 106
DB 62 SGGSGYGDFTLTISLQPEDFATYYCOQSYSTLMTFQGTVEIKR 107

RESULT 13
ABO27470
ID ABO27470 standard; protein, 107 AA.
XX
AC ABO27470;
XX
DT 12-SEP-2003 (first entry)
XX
DE Anti-Rh(D) light chain SH49.
XX
KM Human, RH(D) binding protein; blood typing; blood product; antibody;
KM magnetically activated cell sorting.
XX
OS Homo sapiens.

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XX
PN US2003040605-A1.
XX
PD 27-FEB-2003.
XX
PF 04-MAY-2001; 2001US-00848798.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX
XX (TYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2003-512273/48.
DR N-PSDB; ACD45384.
XX
PT New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
XX
XX
PS Claim 4; Page 52; 187pp; English.
XX
CC The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents the amino acid sequence of a human anti-Rh(D) chain
XX
SQ Sequence 107 AA;

Query Match 86.9%; Score 472; DB 6; Length 107;
Best Local Similarity 86.8%; Pred. No. 1.9e-28;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVTCRASQRIINTYINWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTQSPSSLSASVGDRTVTCRASQRIINTYINWYQHKRGKAPKLLIYAASSLSQGVPSRF 61
QY 61 SGGSGYGDFTLTISLQPEDFASYYCOESLSASYTFQGTVEIKR 106
DB 62 SGGSGYGDFTLTISLQPEDFATYYCOQSYSTLMTFQGTVEIKR 107

RESULT 14
AAG93644
ID AAG93644 standard; protein, 107 AA.
XX
AC AAG93644;
XX
DT 14-SEP-2001 (first entry)
XX
DE Human anti-Rh(D) antibody clone SH13 protein sequence.
XX
KM Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KM red blood cell; Rh phenotype; diagnosis; therapeutic.
XX
OS Homo sapiens.
XX
PN US6255455-B1.
XX
PD 03-JUL-2001.
XX
PF 29-JAN-1999; 99US-00240274.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
XX
XX (TYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;

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XX WPI; 2001-388931/41.
DR N-PSDB; AAH68701.
XX
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
PS Claim 1; Col 68; 162pp; English.
XX
CC The present invention describes an isolated Rh(D) binding protein.
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AA69358 to AA69369. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68815 to AAH68726 represent the nucleotide sequence which encode
CC AA69358 to AA69369. AA693670 to AA693697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 107 AA;

Query Match 86.7%; Score 471; DB 4; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.3e-28;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTSPSSLASVGDRTYISCRASORINTYLNWYOHKPKAKPKLLIYAASSLSQGVPSRF 60
Db 2 ELTSPSSLASVGDRTYITCRASQSSISYLNWYQKPKAKPKLLIYAASSLSRSGVPSRF 61
Qy 61 SSGSGYTDFTLTITISLQFEDPASYYCOESLSASYTFQGTKEIKR 106
Db 62 SSGSGGTDFTLTITISLQPEDFATYYCQOSYSTPTFTFGGTKEIKR 107

RESULT 15

ABO27451
ID ABO27451 standard; protein; 107 AA.

XX AC ABO27451;

XX DT 12-SEP-2003 (first entry)

XX DE Anti-Rh(D) light chain SH13.

XX Human: RH(D) binding protein; blood typing; blood product; antibody;

XX magnetically activated cell sorting.

XX OS Homo sapiens.

XX PN US2003040605-A1.

XX PD 27-FEB-2003.

XX PF 04-MAY-2001; 2001US-00848798.

XX PR 11-OCT-1996; 96US-0028550P.

XX PR 27-JUN-1997; 97US-0088404S.

XX PR 10-APR-1998; 98US-0081380P.

XX PR 29-JAN-1999; 99US-00240274.

XX PA (UYPE-) UNIV PENNSYLVANIA.

XX PI Siegel DL;

XX WPI; 2003-512273/48.

XX DR N-PSDB; ACD45365.

XX New human Rh(D) -binding protein useful for various diagnostic and

PT therapeutic applications, including typing of blood or blood products.

PS Claim 4; Page 50; 187pp; English.

XX

CC The invention relates to an isolated Rh(D) binding protein. The protein

CC can be used for magnetically activated cell sorting. The protein is

CC useful in various diagnostic and therapeutic applications in humans,

CC including typing of blood or blood products. The present sequence

CC represents the amino acid sequence of a human anti-Rh(D) chain

XX

SQ Sequence 107 AA;

Query Match 86.7%; Score 471; DB 6; Length 107;
Best Local Similarity 86.8%; Pred. No. 2.3e-28;
Matches 92; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ELTSPSSLASVGDRTYISCRASORINTYLNWYOHKPKAKPKLLIYAASSLSQGVPSRF 60
Db 2 ELTSPSSLASVGDRTYITCRASQSSISYLNWYQKPKAKPKLLIYAASSLSRSGVPSRF 61
Qy 61 SSGSGYTDFTLTITISLQFEDPASYYCOESLSASYTFQGTKEIKR 106
Db 62 SSGSGGTDFTLTITISLQPEDFATYYCQOSYSTPTFTFGGTKEIKR 107

Search completed: July 26, 2005, 09:19:20
Job time : 80.3394 secs

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OM protein - protein search, using SW model

Run on: July 26, 2005, 09:26:32 ; Search time 67.4545 Seconds

(without alignments)
611.274 Million cell updates/sec

Title: US-10-027-725A-10

Perfect score: 543
Sequence: 1 ELTQSPSSLSASVGDRTVIS.....QESLSASTYFGGKTVEIKR 106

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	543	100.0	106	14	US-10-027-725A-10
2	475	87.5	107	14	US-10-016-986-104
3	474	87.3	107	10	US-09-848-798-119
4	472	86.9	107	10	US-09-848-798-131
5	472	86.9	107	10	US-09-848-798-175
6	472	86.9	107	10	US-09-848-798-176
7	471	86.7	107	10	US-09-848-798-156
8	468	86.2	107	10	US-09-848-798-36
9	468	86.2	107	17	US-10-783-311-198
10	467	86.0	107	14	US-10-016-986-105
11	465	85.6	111	14	US-10-203-754A-57

12	464.5	85.5	108	10	US-09-848-798-32	Sequence 32, Appl
13	464.5	85.5	108	10	US-09-848-798-43	Sequence 43, Appl
14	464	85.5	107	10	US-09-848-798-37	Sequence 37, Appl
15	464	85.5	107	16	US-10-409-814A-4	Sequence 4, Appl1
16	464	85.5	240	9	US-09-192-854-2	Sequence 2, Appl1
17	464	85.5	240	9	US-09-968-561A-2	Sequence 2, Appl1
18	464	85.5	240	10	US-09-968-744A-2	Sequence 2, Appl1
19	464	85.5	240	11	US-09-968-561A-2	Sequence 2, Appl1
20	464	85.5	240	16	US-10-744-774-1	Sequence 1, Appl1
21	463	85.3	107	10	US-09-791-153A-67	Sequence 67, Appl
22	463	85.3	108	17	US-10-726-332-214	Sequence 214, Appl
23	463	85.3	108	17	US-10-805-177-64	Sequence 64, Appl
24	462	85.1	106	14	US-10-027-725A-12	Sequence 12, Appl
25	462	85.1	107	10	US-09-848-798-39	Sequence 39, Appl
26	462	85.1	107	10	US-09-848-798-39	Sequence 39, Appl
27	462	85.1	108	16	US-10-744-774-15	Sequence 15, Appl
28	462	85.1	108	17	US-10-805-177-20	Sequence 20, Appl
29	461	84.9	107	10	US-09-848-798-158	Sequence 158, Appl
30	461	84.9	108	17	US-10-726-332-18	Sequence 18, Appl
31	460.5	84.8	108	10	US-09-848-798-167	Sequence 167, Appl
32	460	84.7	106	14	US-10-027-725A-11	Sequence 11, Appl
33	460	84.7	106	16	US-10-466-242-38	Sequence 38, Appl
34	460	84.7	106	16	US-10-466-242-56	Sequence 56, Appl
35	460	84.7	108	17	US-10-726-332-28	Sequence 28, Appl
36	459.5	84.6	108	10	US-09-848-798-163	Sequence 163, Appl
37	459	84.5	108	17	US-10-726-332-209	Sequence 209, Appl
38	459	84.5	111	18	US-10-916-840-100	Sequence 100, Appl
39	458	84.3	107	10	US-09-848-798-35	Sequence 35, Appl
40	458	84.3	107	10	US-09-848-798-173	Sequence 173, Appl
41	458	84.3	108	17	US-10-477-830-90	Sequence 90, Appl
42	458	84.3	111	14	US-10-203-754A-56	Sequence 56, Appl
43	457	84.2	104	14	US-10-016-986-106	Sequence 106, Appl
44	457	84.2	107	10	US-09-848-798-10	Sequence 40, Appl
45	457	84.2	214	14	US-10-153-382-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-027-725A-10
; Sequence 10, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGF-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-10

Query Match 100.0%; Score 543; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.4e-42;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELTQSPSSLSASVGDRTVISCRASGRINTYINWYQKFKGKAPKLLIYAASSIQGVPRF 60
DB 1 ELTQSPSSLSASVGDRTVISCRASGRINTYINWYQKFKGKAPKLLIYAASSIQGVPRF 60
QY 61 SSSGVTDTFTLTSISLQFEDFASYYCQSSLSASTYFGGKTVEIKR 106
DB 61 SSSGVTDTFTLTSISLQFEDFASYYCQSSLSASTYFGGKTVEIKR 106

RESULT 2

```
US-10-016-986-104
; Sequence 104, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Letner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-104

Query Match      87.5%; Score 475; DB 14; Length 107;
Best Local Similarity 87.7%; Pred. No. 5.8e-36;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy      1 ELTSPSSLSASVGDRTVITISCRASQRIINTYINWYQHKPKAKPLIYAASSLSQGVPSRF 60
Db      1 ELTQSPSSLSASVGDRTVITICRASQSISSYINWYQKRGKAPKLIYAASSLSQGVPSRF 60

Qy      61 SSGSGVDFTLTISLSLPEDPASYYCOESLSASYTFQGTKEIKR 106
Db      61 SSGSGVDFTLTISLSLPEDPATYYCOQSYSTPPTFGGTKEIKR 106

RESULT 3
US-09-848-798-179
; Sequence 179, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-179

Query Match      87.3%; Score 474; DB 10; Length 107;
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Best Local Similarity 87.7%; Pred. No. 7.2e-36;
Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy      1 ELTQSPSSLSASVGDRTVITISCRASQRIINTYINWYQHKPKAKPLIYAASSLSQGVPSRF 60
Db      2 ELTQSPSSMSASVGDRTVITICRASQSIIGTYINWYQKRGKAPKLIYAASSLSQGVPSRF 61

Qy      61 SSGSGVDFTLTISLSLPEDPASYYCOESLSASYTFQGTKEIKR 106
Db      62 SSGSGVDFTLTISLSLPEDPATYYCOQSYSTPPTFGGTKEIKR 107

RESULT 4
US-09-848-798-33
; Sequence 33, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-848-798-33

Query Match      86.9%; Score 472; DB 10; Length 107;
Best Local Similarity 87.7%; Pred. No. 1.1e-35;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy      1 ELTQSPSSLSASVGDRTVITISCRASQRIINTYINWYQHKPKAKPLIYAASSLSQGVPSRF 60
Db      2 ELTQSPSSLSASVGDRTVITICRASQSISSYINWYQKRGKAPKLIYAASSLSQGVPSRF 61

Qy      61 SSGSGVDFTLTISLSLPEDPASYYCOESLSASYTFQGTKEIKR 106
Db      62 SSGSGVDFTLTISLSLPEDPATYYCOQSYSTPPTFGGTKEIKR 107

RESULT 5
US-09-848-798-175
; Sequence 175, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 175
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
```

```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 116

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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Light Chain amino acid sequence
US-10-783-311-198

Query Match 86.2%; Score 468; DB 17; Length 116;
Best Local Similarity 85.8%; Pred. No. 2.8e-35;
Matches 91; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 ELTSPSSLSASVGDRTVITSCRASORINTYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
DB 4 QMTSPSSLSASVGDRTVITCRASQSISSYLNWYQKRGKAPKLLIYAASSLSQGVPSRF 63

QY 61 SSGSGTDFTLTISLQPEDFASYYCOESLSASYTFGGGTKEIKR 106
DB 64 SSGSGTDFTLTISLQPEDFATYYCQGSYSTRWTFGGGTKEIKR 109

RESULT 10
US-10-016-986-105
Sequence 105, Application US/10016986
Publication No. US20030187247A1

GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
FILE REFERENCE: 313.2CON1
CURRENT APPLICATION NUMBER: US/10/016,986
PRIORITY FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 09/149,898
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: US 08/899,575
PRIOR FILING DATE: 1997-07-24
PRIOR APPLICATION NUMBER: US 08/276,852
PRIOR FILING DATE: 1994-07-18
PRIOR APPLICATION NUMBER: US 08/178,302
PRIOR FILING DATE: 1994-01-06
PRIOR APPLICATION NUMBER: PCT/US93/09328
PRIOR FILING DATE: 1993-09-30
PRIOR APPLICATION NUMBER: US 07/954,148
PRIOR FILING DATE: 1992-09-30
NUMBER OF SEQ ID NOS: 176
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 105

LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized
US-10-016-986-105

Query Match 86.0%; Score 467; DB 14; Length 107;
Best Local Similarity 86.8%; Pred. No. 3.1e-35;
Matches 92; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 ELTSPSSLSASVGDRTVITSCRASORINTYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
DB 1 ELTSPSSLSASVGDRTVITCRASQSISSYLNWYQKRGKAPKLLIYAASSLSQGVPSRF 60

QY 61 SSGSGTDFTLTISLQPEDFASYYCOESLSASYTFGGGTKEIKR 106
DB 61 SSGSGTDFTLTISLQPEDFATYYCQGSYSTRWTFGGGTKEIKR 106

RESULT 11
US-10-203-754A-57
Sequence 57, Application US/10203754A
Publication No. US2003015732A1
GENERAL INFORMATION:
APPLICANT: ITAMI, Seima

APPLICANT: SEKI, Makoto
APPLICANT: MATSURA, Yoshiharu
APPLICANT: SHIBUI, Tatsuro
APPLICANT: YOSHIMOTO, Yoshinisa
APPLICANT: MIYAMURA, Tatsuo
TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
FILE REFERENCE: P22257
CURRENT APPLICATION NUMBER: US/10/203,754A
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: PCT/JP01/00967
PRIOR FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn version 3.1
SEQ ID NO 57
LENGTH: 111
TYPE: PRT
ORGANISM: Homo sapiens
US-10-203-754A-57

Query Match 85.6%; Score 465; DB 14; Length 111;
Best Local Similarity 84.8%; Pred. No. 5e-35;
Matches 89; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 2 LTQSPSSLSASVGDRTVITSCRASORINTYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 61
DB 4 MTQSPSSLSASVGDRTVITCRASQSISSYLNWYQKRGKAPKLLIYAASSLSQGVPSRF 63

QY 62 SSGSGTDFTLTISLQPEDFASYYCOESLSASYTFGGGTKEIKR 106
DB 64 SSGSGTDFTLTISLQPEDFATYYCQGSYSTRWTFGGGTKEIKR 108

RESULT 12
US-09-848-798-32
Sequence 32, Application US/09848798
Publication No. US20030040605A1

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/848,798
PRIORITY FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32

LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain I01
US-09-848-798-32

Query Match 85.5%; Score 464.5; DB 10; Length 108;
Best Local Similarity 86.9%; Pred. No. 5.4e-35;
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 ELTSPSSLSASVGDRTVITSCRASORINTYLNWYQHKRGKAPKLLIYAASSLSQGVPSRF 60
DB 2 ELTSPSSLSASVGDRTVITCRASQSISSYLNWYQKRGKAPKLLIYAASSLSQGVPSRF 61

QY 61 SSGSGTDFTLTISLQPEDFASYYCOESLSA-SYTFGGGTKEIKR 106
DB 62 SSGSGTDFTLTISLQPEDFATYYCQGSYSTRWTFGGGTKEIKR 108

RESULT 13
US-09-848-798-43
Sequence 43, Application US/09848798

	Query Match	Similarity	85.5%	Score	464	DB	10	Length	107
	Best Local	Similarity	85.8%	Score	No. 5	95-35			
	Matches	91	Conservative	7	Mismatches	8	Indels	0	Gaps
QY	1	ETTSPSSLSASVGRVITSCRASORINLYMWYOHKPKAKKLITYASSIQSGPSPF	:	:	:	:	:	:	60
Db	2	ETIOPSSLSASVGRVITTCRASOSISSYLMWYOHKPKAKKLITYASSIQSGVPSRF	:	:	:	:	:	:	61
QY	61	SGSGYGDFTLTITSSIQEDFPASYYCOESLSASYFGGCTKVEIKR	:	:	:	:	:	:	106
Db	62	SSSGGCTDFTLTITSSIQEDFPATYYCOQSGSYSPITFGQTRLEIKR	:	:	:	:	:	:	107

Search completed: July 26, 2005, 10:05:20
Job time : 68.6212 secs

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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:09:56 ; Search time 21.5909 Seconds
(without alignments)
394.147 Million cell updates/sec

Title: US-10-027-725A-9
Perfect score: 614
Sequence: 1 LKSPGHWKSQLSLTCTV.....RSDGYTLDMWGQTLVTSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	521	84.9	473	US-09-049-672A-4	Sequence 4, Appli
2	508	82.7	172	US-09-472-087-7	Sequence 7, Appli
3	508	82.7	172	US-09-472-087-86	Sequence 86, Appli
4	502.5	81.8	119	US-09-025-769B-39	Sequence 39, Appli
5	502.5	81.8	119	US-09-025-769B-65	Sequence 65, Appli
6	502.5	81.8	119	US-09-490-070A-39	Sequence 39, Appli
7	502.5	81.8	119	US-09-490-070A-65	Sequence 65, Appli
8	502.5	81.8	119	US-09-490-153-39	Sequence 39, Appli
9	502.5	81.8	119	US-09-490-153-65	Sequence 65, Appli
10	502.5	81.8	119	US-09-490-324-39	Sequence 39, Appli
11	502.5	81.8	119	US-09-490-324-65	Sequence 65, Appli
12	496	80.8	122	US-08-360-125-11	Sequence 11, Appli
13	496	80.8	122	US-08-450-578-11	Sequence 11, Appli
14	496	80.8	122	US-09-017-628-11	Sequence 11, Appli
15	496	80.8	122	US-09-014-880-11	Sequence 11, Appli
16	496	80.8	122	US-08-450-363-11	Sequence 11, Appli
17	496	80.8	122	US-09-467-903-11	Sequence 11, Appli
18	492.5	80.2	117	US-09-720-493-2	Sequence 2, Appli
19	492	80.1	487	US-09-800-729-145	Sequence 145, App
20	491	80.0	118	US-09-025-769B-25	Sequence 25, Appli
21	491	80.0	118	US-09-490-070A-25	Sequence 25, Appli
22	491	80.0	118	US-09-490-153-25	Sequence 25, Appli
23	491	80.0	118	US-09-490-324-25	Sequence 25, Appli
24	491	80.0	120	US-09-424-840B-20	Sequence 20, Appli
25	487.5	79.4	119	US-08-360-125-5	Sequence 5, Appli
26	487.5	79.4	119	US-08-450-578-5	Sequence 5, Appli
27	487.5	79.4	119	US-09-017-628-5	Sequence 5, Appli

28	487.5	79.4	119	2	US-09-014-880-5	Sequence 5, Appli
29	487.5	79.4	119	4	US-08-450-363-5	Sequence 5, Appli
30	487.5	79.4	119	4	US-09-467-903-5	Sequence 5, Appli
31	472	76.9	244	3	US-08-918-148-79	Sequence 79, Appli
32	472	76.9	244	4	US-09-138-091A-77	Sequence 77, Appli
33	467	76.1	118	3	US-08-545-809A-116	Sequence 116, App
34	466.5	76.0	142	2	US-08-480-774A-2	Sequence 2, Appli
35	460.5	75.0	119	2	US-08-652-816A-10	Sequence 10, Appli
36	460.5	75.0	155	4	US-09-471-276-888	Sequence 888, App
37	460	74.9	278	3	US-09-260-527-3	Sequence 3, Appli
38	457	74.4	118	3	US-08-545-809A-142	Sequence 142, App
39	457	74.4	118	4	US-09-343-698-6	Sequence 6, Appli
40	457	74.4	118	4	US-08-325-955-6	Sequence 6, Appli
41	455.5	74.2	117	4	US-09-232-290-47	Sequence 47, App
42	455	74.1	139	4	US-09-471-276-837	Sequence 837, App
43	450.5	73.4	219	3	US-09-460-384-37	Sequence 37, Appli
44	450	73.3	832	3	US-08-630-820-7	Sequence 7, Appli
45	450	73.3	832	4	US-09-273-453-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-049-672A-4
Sequence 4, Application US/09049672A
Patent No. 6135941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HERewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Carrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANCYTUT01

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; CLONE: 1513264
US-09-049-672A-4
Query Match      84.9%; Score 521; DB 3; Length 473;
Best Local Similarity 83.2%; Pred. No. 2.6e-44;
Matches 99; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

Oy 2  EGGGLVPSQTLSTCTVSGSGSIRSGYWSMIRPQKGLWIGYIHSGNTYNSLK 61
Db 25  EGGGLVPSQTLSTCTVSGSGSIRSGYWSMIRPQKGLWIGYIHSGNTYNSLK 84

Oy 62  KSRVTISVDTSKNPSLRSLSSVTADTAADTAAYVCARSDG--YTLDMNGGGLTVTVSS 114
Db 85  KSRVTISVDTSKNPSLRSLSSVTADTAADTAAYVCARSDGGLRGAGNGMDVWGQGLTVTVSS 143

RESULT 2
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-7

Query Match      82.7%; Score 508; DB 4; Length 172;
Best Local Similarity 85.1%; Pred. No. 1.6e-43;
Matches 97; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

Oy 3  SGPGLVPSQTLSTCTVSGSGSIRSGYWSMIRPQKGLWIGYIHSGNTYNSLK 62
Db 1  SGPGLVPSQTLSTCTVSGSGSIRSGYWSMIRPQKGLWIGYIHSGNTYNSLK 60

Oy 63  SRVTMSVDTSKNPSLRSLSSVTADTAADTAAYVCARSDG--YTLDMNGGGLTVTVSS 114
Db 61  SRVTISVDTSKNPSLRSLSSVTADTAADTAAYVCARSDGVDYGDVWGQGLTVTVSS 114

RESULT 3
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
```

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; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-86

Query Match      82.7%; Score 508; DB 4; Length 172;
Best Local Similarity 85.1%; Pred. No. 1.6e-43;
Matches 97; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

Oy 3  SGPGLVPSQTLSTCTVSGSGSIRSGYWSMIRPQKGLWIGYIHSGNTYNSLK 62
Db 1  SGPGLVPSQTLSTCTVSGSGSIRSGYWSMIRPQKGLWIGYIHSGNTYNSLK 60

Oy 63  SRVTMSVDTSKNPSLRSLSSVTADTAADTAAYVCARSDG--YTLDMNGGGLTVTVSS 114
Db 61  SRVTISVDTSKNPSLRSLSSVTADTAADTAAYVCARSDGVDYGDVWGQGLTVTVSS 114

RESULT 4
US-09-025-769B-39
; Sequence 39, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vlc
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-39

Query Match      81.8%; Score 502.5; DB 3; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.7e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

Oy 2  EGGGLVPSQTLSTCTVSGSGSIRSGYWSMIRPQKGLWIGYIHSGNTYNSLK 61
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Db      6  ESGGLVPSRSTLSLCTVSGSIS--YWSWIRQPGKGLWIGIYSGSTNYPNL 63
Oy      62  KSRVTMSVDTSKNHSRLSSVTADTAIVYCAR--SDG-YTLDNWGGGTLVTYSS 114
        64  KSRVTISVDTSKNPSLKLSSVTADTAIVYCARWGSDGFYAMDYWGGLVTYSS 119

```

RESULT 5

```

US-09-025-769B-65
; Sequence 65, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-65

Query Match      81.8%; Score 502.5; DB 3; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.7e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

Oy      2  ESGGLVPSQTLSTLCTVSGSISRSRGYWSWIRQPGKGLWIGIYHSGNTIYNPSL 61
        6  ESGGLVPSRSTLSLCTVSGSIS--YWSWIRQPGKGLWIGIYSGSTNYPNL 63
Db      62  KSRVTMSVDTSKNHSRLSSVTADTAIVYCAR--SDG-YTLDNWGGGTLVTYSS 114
        64  KSRVTISVDTSKNPSLKLSSVTADTAIVYCARWGSDGFYAMDYWGGLVTYSS 119

RESULT 6
US-09-490-070A-39
; Sequence 39, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim

```

```

; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
; US-09-490-070A-39

```

```

Query Match      81.8%; Score 502.5; DB 4; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.7e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

Oy      2  ESGGLVPSQTLSTLCTVSGSISRSRGYWSWIRQPGKGLWIGIYHSGNTIYNPSL 61
        6  ESGGLVPSRSTLSLCTVSGSIS--YWSWIRQPGKGLWIGIYSGSTNYPNL 63
Db      62  KSRVTMSVDTSKNHSRLSSVTADTAIVYCAR--SDG-YTLDNWGGGTLVTYSS 114
        64  KSRVTISVDTSKNPSLKLSSVTADTAIVYCARWGSDGFYAMDYWGGLVTYSS 119

RESULT 7
US-09-490-070A-65
; Sequence 65, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Achim
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300

```

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-070A-65

Query Match 81.8%; Score 502.5; DB 4; Length 119;
Best Local Similarity 85.3%; Pred. No. 3,7e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

Qy 2 ESGGGLVPSQTLTCTVSGSGSIRSGGYWWSWIRPPGKLEWIGYIYHSGNTYNPSTL 61
Db 6 ESGGGLVPSSTLTCTVSGSGSIS--YWSWIRPPGKLEWIGYIYHSGNTYNPSTL 63

Qy 62 KSRVTMSVDTSKNHFSRLSSVTADTAIVYCAR--SDG-YTLDMWGGTIVTVSS 114
Db 64 KSRVTISVDTSKNQPSLKLSSVTADTAIVYICARWGSGGFYAMDYWGQGLIVTVSS 119

RESULT 8
US-09-490-153-39
Sequence 39, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-153-39

Query Match 81.8%; Score 502.5; DB 4; Length 119;
Best Local Similarity 85.3%; Pred. No. 3,7e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

Qy 2 ESGGGLVPSQTLTCTVSGSGSIRSGGYWWSWIRPPGKLEWIGYIYHSGNTYNPSTL 61
Db 6 ESGGGLVPSSTLTCTVSGSGSIS--YWSWIRPPGKLEWIGYIYHSGNTYNPSTL 63

Qy 62 KSRVTMSVDTSKNHFSRLSSVTADTAIVYCAR--SDG-YTLDMWGGTIVTVSS 114
Db 64 KSRVTISVDTSKNQPSLKLSSVTADTAIVYICARWGSGGFYAMDYWGQGLIVTVSS 119

RESULT 9
US-09-490-153-65
Sequence 65, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000

TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-153-65

Query Match 81.8%; Score 502.5; DB 4; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.7e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

Qy 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWMIROPKGLIEMIGIYHSGNTYNSL 61
Db 6 ESGPGLVPSSTLSTCTVSGSIS--YWSWIRPQKGLIEMIGIYHSGNTYNSL 63

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYCAR--SDG-YTLDNWGQGLVTVSS 114
Db 64 KSRVTISVDTSKNPSLKLSSVTADTAIVYCARWGSDGFYAMDYWGQGLVTVSS 119

RESULT 10
US-09-490-324-39
Sequence 39, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-324-39

Query Match 81.8%; Score 502.5; DB 4; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.7e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

Qy 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWMIROPKGLIEMIGIYHSGNTYNSL 61
Db 6 ESGPGLVPSSTLSTCTVSGSIS--YWSWIRPQKGLIEMIGIYHSGNTYNSL 63

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYCAR--SDG-YTLDNWGQGLVTVSS 114
Db 64 KSRVTISVDTSKNPSLKLSSVTADTAIVYCARWGSDGFYAMDYWGQGLVTVSS 119

RESULT 11
US-09-490-324-65
Sequence 65, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-324-65

Query Match 81.8%; Score 502.5; DB 4; Length 119;
Best Local Similarity 85.3%; Pred. No. 3.7e-43;
Matches 99; Conservative 6; Mismatches 6; Indels 5; Gaps 3;

Qy 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWMIROPKGLIEMIGIYHSGNTYNSL 61
Db 6 ESGPGLVPSSTLSTCTVSGSIS--YWSWIRPQKGLIEMIGIYHSGNTYNSL 63

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVYCAR--SDG-YTLDNWGQGLVTVSS 114
Db 64 KSRVTISVDTSKNPSLKLSSVTADTAIVYCARWGSDGFYAMDYWGQGLVTVSS 119

RESULT 12
US-08-360-125-11
Sequence 11, Application US/08360125
Patent No. 5767246
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246ihiko ITO
APPLICANT: Kazuhito NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
SPECIFICALLY BINDING TO SURFACE ANTIGEN OF CANCER
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Menderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:

NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-11
Query Match 80.8%; Score 496; DB 1; Length 122;
Best Local Similarity 81.2%; Pred. No. 1,7e-42;
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;
Qy 2 ESGPGLVPSQTSLSLTCTVSGSGSIRSGYYSWIRPPGKLEWIGYIYHSGNTYNPSTL 61
Db 6 ESGPGLVPSSETLSLTCTVSGSGSISSSYTWGWIROPKGLWIGISYISGSIYNPSTL 65
Qy 62 KSRVTMSVDTSKHFSLRLSSVTADTAVYYCARSD---GYTLDMNGGTLTVSS 114
Db 66 KSRVTISVDTSKQFSLKLSVTAADTAVYYCARSGYGYGMDVWGQGTITVSS 122
RESULT 13
US-08-450-578-11
Sequence 11, Application US/08450578
Patent No. 5837845
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845ihiko ITO
APPLICANT: Kazuhito NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
SPECIFICALLY BINDING TO SURFACE ANTIGEN OF CANCER
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Menderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850

TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEetical:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-11

Query Match 80.8%; Score 496; DB 2; Length 122;
Best Local Similarity 81.2%; Pred. No. 1.7e-42;
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

QY 2 ESGPGLVPSQTLSTCTVSGGSIKSGIYWSWIRQPPGKLEWIGIYHSGNTYINPSL 61
DB 6 ESGPGLVPSQTLSTCTVSGGSIKSGIYWSWIRQPPGKLEWIGIYHSGNTYINPSL 65

QY 62 KSRVTMSVDTSKNFSLRLSSVTADTAIVYCCARSD---GYTLDNMGQGLTVTVSS 114
DB 66 KSRVTISVDTSKNFSLRLSSVTADTAIVYCCARSD---GYTLDNMGQGLTVTVSS 122

RESULT 14
US-09-017-628-11
Sequence 11, Application US/09017628
Patent No. 5990287
GENERAL INFORMATION:
APPLICANT: HOSOKAWA, Saiko
APPLICANT: TAGAWA, Toshiaki
APPLICANT: HIRAKAWA, Yoko
APPLICANT: ITO, No. 5990287Jiniko
APPLICANT: NAGAIKE, Kazuhito
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE

FILE REFERENCE: 177/527361KH
CURRENT APPLICATION NUMBER: US/09/017, 628
CURRENT FILING DATE: 1998-02-02
EARLIER APPLICATION NUMBER: 08/360,125
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 122
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-11

Query Match 80.8%; Score 496; DB 2; Length 122;
Best Local Similarity 81.2%; Pred. No. 1.7e-42;
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

QY 2 ESGPGLVPSQTLSTCTVSGGSIKSGIYWSWIRQPPGKLEWIGIYHSGNTYINPSL 61
DB 6 ESGPGLVPSQTLSTCTVSGGSIKSGIYWSWIRQPPGKLEWIGIYHSGNTYINPSL 65

QY 62 KSRVTMSVDTSKNFSLRLSSVTADTAIVYCCARSD---GYTLDNMGQGLTVTVSS 114
DB 66 KSRVTISVDTSKNFSLRLSSVTADTAIVYCCARSD---GYTLDNMGQGLTVTVSS 122

RESULT 15
US-09-014-880-11
Sequence 11, Application US/09014880
Patent No. 5990297
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014, 880
FILING DATE: January 26, 1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450, 578
FILING DATE: May 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360, 125
FILING DATE: December 20, 1994
APPLICATION DATA:
APPLICATION NUMBER: 07/905, 534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids

```

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; CELL TYPE: Hybridoma producing human antibody 1-3-1
US-09-014-880-11

```

```

Query Match      80.8%; Score 496; DB 2; Length 122;
Best Local Similarity 81.2%; Pred. No. 1.7e-42;
Matches 95; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

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QY      2  ESGGGLVYKPSOTLSLTCTVSGGSIRSGGYWWSWIRQPPGKLEWIGYIYHSGNTYINPSL 61
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      6  ESGGGLVYKPSOTLSLTCTVSGGSISSSSYWGWIRQPPGKLEWIGSIYSGSTYINPSL 65

QY      62  KSRVTMSVDTSKNHSRLSSVTADPTAVYYCARSD---GYTLDNMGQGLTVVSS 114
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      66  KSRVTISVDISKQPSLKLSSVTADPTAVYYCARSGSYGYYGMDVMGQGLTVVSS 122

```

Search completed: July 26, 2005, 09:30:00
 Job time : 22.5909 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:07:26 ; Search time 14.618 Seconds
(without alignments)
747.095 Million cell updates/sec

Title: US-10-027-725a-9

Perfect score: 614
Sequence: 1 LESGPGILVKSQTLSTCTV.....RSDGYTLDMNGQGLTVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	501.5	81.7	135 2 S78051	Ig heavy chain pre
2	497.5	81.0	147 2 S13519	Ig heavy chain v r
3	492.5	80.2	140 2 I37782	Ig variable region
4	490	79.8	130 2 S30534	Ig heavy chain v r
5	488.5	79.6	116 2 S37456	Ig mu chain - huma
6	487.5	79.4	130 2 S31690	Ig heavy chain v r
7	480.5	78.3	121 2 S44113	Ig heavy chain v r
8	479.5	78.1	155 2 S31511	Ig heavy chain - h
9	477.5	77.8	146 2 S09710	Ig heavy chain v r
10	477.5	77.8	155 2 S31512	Ig heavy chain - h
11	473.5	77.1	146 2 S09711	Ig heavy chain v r
12	472.5	77.0	127 2 S19668	Ig heavy chain v r
13	472.5	77.0	128 2 S31514	Ig heavy chain - h
14	472	76.9	137 2 S31676	Ig heavy chain v r
15	469	76.4	99 2 S26803	Ig heavy chain v r
16	467.5	76.1	123 2 S30530	Ig heavy chain v r
17	467	76.1	99 2 S26801	Ig heavy chain v r
18	467	76.1	122 2 S69912	Ig V-D-J region (N
19	465	75.7	133 2 S31586	Ig heavy chain v r
20	464	75.6	99 2 S26802	Ig heavy chain v r
21	461	75.1	105 2 S78055	Ig heavy chain pre
22	460.5	75.0	149 2 PH1673	Ig heavy chain v r
23	459	74.8	110 2 S44110	Ig heavy chain V-D
24	458	74.6	139 2 A41287	Ig heavy chain pre
25	457	74.4	118 2 A26340	Ig heavy chain pre
26	454	73.9	97 2 PLO118	Ig heavy chain v r
27	454	73.9	99 2 S26899	Ig heavy chain v r
28	452	73.6	135 2 S31604	Ig heavy chain v r
29	451	73.5	118 2 S20780	Ig heavy chain v r

30	451	73.5	129 2 S44114	Ig heavy chain v r
31	448	73.0	99 2 S12418	Ig heavy chain v r
32	447.5	72.9	139 2 S31696	Ig heavy chain v r
33	445.5	72.6	137 2 S31585	Ig heavy chain v r
34	445.5	72.6	140 2 A49045	Ig heavy chain v r
35	445	72.5	120 2 P70370	Ig mu chain precu
36	444	72.3	126 2 S47010	Ig heavy chain V4.
37	443	72.1	99 2 S26800	Ig heavy chain v r
38	442	72.0	99 2 S12412	Ig heavy chain v r
39	442	72.0	105 2 S44125	Ig lambda chain V
40	442	72.0	118 2 S24443	Ig heavy chain v r
41	442	72.0	140 2 S78052	Ig heavy chain pre
42	441.5	71.9	98 2 S12421	Ig heavy chain v r
43	441.5	71.9	132 2 A38911	Ig heavy chain v r
44	441.5	71.9	140 2 A24770	hypothetical hybr
45	441	71.8	97 2 S26906	Ig heavy chain v r

ALIGNMENTS

RESULT 1
Ig heavy chain precursor V-D-J region (clone mAB 61VH) - human (fragment)
S78051
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78051, S23716
R:Harindranath, N.
Submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78051
A:Molecule type: mRNA
A:Residues: 1-135 <HAR>
A:Cross-references: EMBL:X54437, NID:937814, PIDD:CA38306.1, PID:9930117
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burrastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A>Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A:Reference number: S23716, MUID:92031262, PMID:11718404
A:Accession: S23716
A:Molecule type: mRNA
A:Residues: 13-111 <HAM>
A:Cross-references: EMBL:X54437
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-13/Domain: signal sequence (fragment) #status predicted <SIG>
F:14-135/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:27-111/Domain: immunoglobulin homology <IMM>
Query Match 81.7% Score 501.5; DB 2; Length 135;
Best local similarity 82.2% Pred. No. 3.1e-38;
Matches 97; Conservative 6; Mismatches 10; Indels 5; Gaps 2;
OY 2 ESFGPLVPSQTLSTCTVSGSIRSGGYWMTROPKGLWIGVYHSNGTYNPSL 61
DB 18 ESFGPLVPSQTLSTCTVSGSIRSGGYWMTROPKGLWIGVYHSNGTYNPSL 77
OY 62 KSRVTMSYDTSKNTFSLRLSSVTAAADTAVYCAR--SDGYTLDM--WGQGLTVTVSS 114
DB 78 KSRVTMSYDTSKNTFSLRLSSVTAAADTAVYCAR--SDGYTLDM--WGQGLTVTVSS 135
RESULT 2
S13519
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S13519
R:Morlat, P.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A>Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A:Reference number: S13519, MUID:91187691, PMID:2011536
A:Accession: S13519

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <MOR>
A;Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 81.0%; Score 497.5; DB 2; Length 147;
Best Local Similarity 82.8%; Pred. No. 7.8e-38;
Matches 96; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

Qy 2 ESGGGLVKSQTLSTCTVSGSGSIRSGGYWMSWIRPGKLEWIGIYHSGNTYNPSTL 61
Db 32 ESGGGLVKSQTLSTCTVSGSGSISSGSYWMSWIRPGKLEWIGIYHSGNTYNPSTL 91

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADPAVYVCARSDG--GYTLDMNGGGLTVTVSS 114
Db 92 KSRVTISVDTSKNQPSLKLSSVTADPAVYVCARPLMFGELFDYWGGLTVTVSS 147

RESULT 3

Ig variable region (VDJ) (clone T23-9) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C;Accession: J37782; S25476
R;Demason, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A;Title: Somatic diversification in the heavy chain variable region genes expressed by B
A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: J37782
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <RES>

A;Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;46-128/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 492.5; DB 2; Length 140;
Best Local Similarity 82.2%; Pred. No. 2.1e-37;
Matches 97; Conservative 6; Mismatches 8; Indels 7; Gaps 2;

Qy 2 ESGGGLVKSQTLSTCTVSGSGSIRSGGYWMSWIRPGKLEWIGIYHSGNTYNPSTL 61
Db 25 ESGGGLVKSQTLSTCTVSGSGSIS--YWSWIRPGKLEWIGIYHSGNTYNPSTL 82

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADPAVYVCARSDG--GYTLDMNGGGLTVTVSS 114
Db 83 KSRVTISVDTSKNQPSLKLSSVTADPAVYVCARHNSSSWYGRYFDYWGGLTVTVSS 140

RESULT 4

Ig heavy chain V region - human

C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30534
R;Mariette, X.
submitted to the EMBL Data Library, October 1992

A;Reference number: S30520
A;Accession: S30534
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <MAR>
A;Cross-references: EMBL:Z18320
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 79.8%; Score 490; DB 2; Length 130;
Best Local Similarity 78.4%; Pred. No. 3.2e-37;
Matches 98; Conservative 4; Mismatches 11; Indels 12; Gaps 2;

Qy 2 ESGGGLVKSQTLSTCTVSGSGSIRSGGYWMSWIRPGKLEWIGIYHSGNTYNPSTL 61
Db 6 ESGGGLVKSQTLSTCTVSGSGSISSGSYWMSWIRPGKLEWIGIYHSGNTYNPSTL 65

Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADPAVYVCARSDG-----YT-----LDNMGGGLTV 109
Db 66 KSRVTISVDTSKNQPSLKLSSVTADPAVYVCARDKGFWGYYTRNSRAFPDIWGGLTV 125

RESULT 5

Ig mu chain - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37456
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993

A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from I
A;Reference number: S37453
A;Accession: S37456
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <MC1>
A;Cross-references: EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;6-90/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 488.5; DB 2; Length 116;
Best Local Similarity 81.2%; Pred. No. 3.9e-37;
Matches 95; Conservative 7; Mismatches 6; Indels 9; Gaps 2;

Qy 6 GLVKSQTLSTCTVSGSGSIRSGGYWMSWIRPGKLEWIGIYHSGNTYNPSTLKS RV 65
Db 1 GLVKSQTLSTCTVSGSGSISSGGYWMSWIRPGKLEWIGIYHSGNTYNPSTLKS RV 60

Qy 66 TMSVDTSKNHFSLRLSSVTADPAVYVCARSDGT-----LDNMGGGLTVTVSS 114
Db 61 TISVDTSKNQPSLKLSSVTADPAVYVCARG-GYSGYGYYYMDVWGGLTVTVSS 116

RESULT 6

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31690
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31690
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <CHI>
A;Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78566.1; PID:g30985
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 487.5; DB 2; Length 130;
Best Local Similarity 78.7%; Pred. No. 5.4e-37;
Matches 96; Conservative 5; Mismatches 10; Indels 11; Gaps 2;

Qy 2 ESGGGLVKSQTLSTCTVSGSGSIRSGGYWMSWIRPGKLEWIGIYHSGNTYNPSTL 61
Db 11 ESGGGLVKSQTLSTCTVSGSGSIS--YWSWIRPGKLEWIGIYHSGNTYNPSTL 68

QY	62	KSRVMSVDTSKMHSESLRSSVTAADTAVYYCARSDG-----	YTLDMNQGLTVY	112
		:		
Db	69	KSRVTSVDTSKMQSLKSSVTAADTAVYYCARSGSVLLMFEGELL	YPTPWQGLTVY	128
QY	113	SS	114	
Db	129	SS	130	

RESULT 7
S4413
IG heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S44113
R:Hawkins, R.E.; Zhu, D.; Owecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A:Description: Idiotype vaccination against human B-cell lymphoma: rescue of variable
A:Reference number: S44105
A:Accession: S44113
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-121 <HAM>
A:Cross-references: EMBL:Z31389; NID:g472967; PIDD:CAA3264.1; PIDD:g940524
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterodimer; immunoglobulin
;15-99/Domain: immunoglobulin homology <IMM>

Query Match	78.3%;	Score 480.5;	DB 2;	Length 11;
Best Local Similarity	80.2%;	Pred. No. 2.2e-36;		
Matches	93;	Mismatches 14;	Indels 3;	Gaps 2

Qy 2 ESAGGLVKEPSGTTLLCTVSGGSLIRSGGYWSWIRQPGGLGEMIGYIYHSAGTYNPSL 61

Db 6 ESAGGLVKEPSGTTLLCTVSGGSLIRSGGYWSWIRQPGGLGEMIGYIYHSAGTYNPSL 65

Qy 62 KSRRTMSVDTSKHFSLRLSSVTPADPAIVYCAR-SNGY--TLDNMGCGTLLTVSS 114

Db 66 KSRRTLSVDTSKDFSLRLSSVTPADPAIVYCARSLSGGYSDPMSQGLTLTVSS 121

```

RESULT 8
S31511
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C/Accession: S31511
R/Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A/Reference number: S31509
A/Accession: S31511
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-155 <GHA>
A/Cross-references: EMBL:X69866; NID:g33094; PIDD:CAA4500.1; PID:g33095
C/Superfamily: immunoglobulin V region, immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:47-129/Domain: immunoglobulin homology <IMM>

```

Query Match	Similarity	Score	479.5%	DB 2:	length	155;
Best Local	Similarity	77.5%	Pred. No.	3.4e-36;		
Matches	93;	Conservative	8;	Mismatches	10;	Indels 9; Gaps 2
Qy	2	ESGPGLVKRSQTLSTLCYVSGSIRSPGCGYWMIRPPKGLGEMTGYTHSGNTYNNPRL				61
Db	38	ESGPGLVKRSQTLSTLCYVSGSIRSPGCGYWMIRPPKGLGEMTGYTHSGNTYNNPRL				95
Qy	62	KSRVTMSVDTSKQHPSRLSLSTYAADTAVYYCARSDG-----YTLDMWGQGLTVVSS				114
Db	96	KSRVTISVDTSKQFSLKAVSYTAADTAVYYCARGGGISRWYDYEMDMWGQGLTVVSS				155

```

RESULT 9
S09710
Ig heavy chain V region - human
C.Species: Homo sapiens (man)
C.Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C.Accession: S09710
R.Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A.Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of
A.Reference number: S09710; MUID:90262535; PMID:2111699
A.Accession: S09710
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-146 <HUG>
A.Cross-references: GB:X52110; NID:g311447; PIDN:CA3634.1; PID:g311448
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
E:34-118/Domain: immunoglobulin homology <IMM>

```

Query Match	77.8%;	Score 477.5;	DB 2;	Length 146;
Best Local Similarity	74.0%;	Pred. No. 4.9e-36;		
Matches 91;	Conservative 11;	Mismatches 10;	Indels 11;	Gaps 2;

QY 2 ESQGLVLPSPQTLSTLCYVSGSIRSGGYWNSIRPPGKGLMEIGIYHSQNTVYNPST 61
 Db 25 ESGPGLVPSRTELSTLCVSGSVSGGHWVRQPPGKGLMEIGIYFSQSTVYNPST 84
 QY 62 KSRVMSVDTSKNHSKLRLSSVTADTAYVYCARSGY-----TLDMNGGGLVLT 111
 Db 85 KSRVIVSDTLKNNSLKLSSVTADTAYVYCLR-PGYGDTSVRKYVANNMLMGQGITV 143

QY	112	VSS	114
Db	144	VSS	146

RESULT 10
S31512
IG heavy chain - human
C.Species: Homo sapiens (man)
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C.Accession: S31512
R.Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A.Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto-
A.Reference number: S31509
A.Accession: S31512
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-155 <CHA>
A.Cross-references: EMBL:X69860; NID:G33082; PIDD:CAA49494.1; PID:G33083
C.Superfamily: Immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F.4-7-129/Domain: immunoglobulin homology <IMM>

Query Match	77.8%	Score 477.5	DB 2	length 155
Best Local Similarity	76.7%	Pred. No. 5,2e-36		
Matches	92	Conservative	9	Mismatches 10, Indels 9, Gaps 2

QY	2	ESGPELVNPSQTLSTCTCWSGGSITFSGGYWVSWINQPGKGLFWYGYTHSANTYVNSL	61
	:::.....	
DB	38	ESGPELVNPSSTLSTCTCWSGGSIS--YVSWINQPGKGLFWYGYTHSANTYVNSL	95
	:::.....	
QY	62	KSRVTVSVDTSKNHFSLRLSSVTADTAIVVYCARSDG-----YTLNMGGLTVTVSS	114
	:::.....	
DB	96	KSRVTVSVDTSKNQSFLKVVSSVTADTAIVVYCARSGGSISWVYVYGMGVWGGGTVTVSS	155
	:::.....	

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RESULT 11
S09711
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
```

C/Accession: S09711
R/Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coatswell, J.
Biochem. J. 268, 135-140, 1990
A/Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of
A/Reference number: S09710; MUID:90262535; PMID:2111699
A/Accession: S09711
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-146 <HUG>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 473.5; DB 2; Length 146;
Best Local Similarity 73.8%; Pred. No. 1.1e-35;
Matches 90; Conservative 10; Mismatches 13; Indels 9; Gaps 1;

Qy 2 ESGGGLVPSQTSLTCTVSGGSIRSGGYWMTROPKGLKLEWIGYIHSGNTYNPSTL 61
Db 25 ESGGGLVPSQTSLTCTVSGGSIRSGGYWMTROPKGLKLEWIGYIHSGNTYNPSTL 84
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAADTAAYVYCAR-----SDGYTLDMWGQTLVTV 112
Db 85 KSRVTISVDTSENGFSLRLTSVTPADTAAYVYCARIGVNFPGFDPWGQTLVTV 144
Qy 113 SS 114
Db 145 SS 146

RESULT 12

S19668
Ig heavy chain V region (VH4D9H6) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 20-Jun-2000
C/Accession: S19668; S24445
R/Markes, U.D.; Hoogenboom, H.R.; Bonmert, T.P.; McGafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A/Reference number: S19663; MUID:92085276; PMID:1748994
A/Accession: S19668
A/Molecule type: mRNA
A/Residues: 1-127 <MAR>
A/Cross-references: EMBL:X61648
R/Jones, P.T.
submitted to the EMBL Data Library, October 1991
A/Reference number: S24442
A/Accession: S24445
A/Molecule type: mRNA
A/Residues: 1-118, 'E', '120-121', 'T', '123-126', 'P' <JON>
A/Cross-references: EMBL:X61648; NID:937722; PIDN:CAA43829.1; PID:g1335380
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 127;
Best Local Similarity 74.6%; Pred. No. 1.2e-35;
Matches 91; Conservative 9; Mismatches 13; Indels 9; Gaps 1;

Qy 2 ESGGGLVPSQTSLTCTVSGGSIRSGGYWMTROPKGLKLEWIGYIHSGNTYNPSTL 61
Db 6 QSGGGLVPSQTSLTCTVSGGSIRSGGYWMTROPKGLKLEWIGYIHSGNTYNPSTL 65
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAADTAAYVYCARSDG-----YTLDNWGQTLVTV 112
Db 66 KSRVTMSVDTSKNHFSLRLSSVTADTAADTAAYVYCARSDG-----YTLDNWGQTLVTV 125
Qy 113 SS 114
Db 126 SS 127

RESULT 13

S31514
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C/Accession: S31514
R/Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autoe
A/Reference number: S31509
A/Accession: S31514
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-128 <CHA>
A/Cross-references: EMBL:X59862; NID:933086; PIDN:CAA49496.1; PID:g33087
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;22-106/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 128;
Best Local Similarity 78.4%; Pred. No. 1.2e-35;
Matches 91; Conservative 8; Mismatches 14; Indels 3; Gaps 1;

Qy 2 ESGGGLVPSQTSLTCTVSGGSIRSGGYWMTROPKGLKLEWIGYIHSGNTYNPSTL 61
Db 13 ESGGGLVPSQTSLTCTVSGGSIRSGGYWMTROPKGLKLEWIGYIHSGNTYNPSTL 72
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAADTAAYVYCAR---SDGYTLDMWGQTLVTV 114
Db 73 KSRVTISVDTSENGFSLRLTSVTPADTAAYVYCARIGVNFPGFDPWGQTLVTV 128

RESULT 14

S31676
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31676
R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31855
A/Accession: S31676
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-137 <COI>
A/Cross-references: EMBL:Z14182; NID:931031; PIDN:CAA78551.1; PID:g31032
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 472; DB 2; Length 137;
Best Local Similarity 82.6%; Pred. No. 1.4e-35;
Matches 95; Conservative 4; Mismatches 12; Indels 4; Gaps 2;

Qy 2 ESGGGLVPSQTSLTCTVSGGSIRSGGYWMTROPKGLKLEWIGYIHSGNTYNPSTL 61
Db 25 ESGGGLVPSQTSLTCTVSGGSIRSGGYWMTROPKGLKLEWIGYIHSGNTYNPSTL 82
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAADTAAYVYCARSDG---YTLDNWGQTLVTV 114
Db 83 KSRVTMSVDTSKNHFSLRLSSVTADTAADTAAYVYCARSDG---YTLDNWGQTLVTV 137

RESULT 15

S26803
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C/Accession: S26803
R/Weng, N.; Snyder, J.G.; Yu-Lee, L.; Marcus, D.M.
Eur. J. Immunol. 22, 1075-1082, 1992
A/Title: Polymorphism of human immunoglobulin V(H)4 germ-line genes.
A/Reference number: S26800; MUID:92201299; PMID:1348029

A;Accession: S26803
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-99 <MEN>
 C;Cross-references: EMBL:Z14238; NID:937710; PIDN:CAA78607.1; PID:g1335374
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 469; DB 2; Length 99;
 Best Local Similarity 92.6%; Pred. No. 1.9e-35;
 Matches 87; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy	2	ESGPGLVKPSQTLSTCTVSGSGSIRSGGYWMIROPGKLEWIGYIYHSGNTYINPSL	61
Db	6	ESGPGLVKPSQTLSTCTVSGSGSIRSGGYWMIROPGKLEWIGYIYHSGNTYINPSL	65
Qy	62	KSRVTMSVDTSKNHPSLRLSSVTADTAIVYYCAR	95
Db	66	KSRVTISVDTSKNQFSLKLSSTVADTAIVYYCAR	99

Search completed: July 26, 2005, 09:27:49
 Job time : 15.6818 secs

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Thu Jul 28 05:42:34 2005

GenCore version 5.1.5 cd.
Copyright (c) 1993 - 2005 CO
Time 71.6818 Seconds
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using sw m04.391 Million cell updates/sec

OM protein - protein search, July 26, 2005, 08:57
.....RSDGYTLDMWGQGLTVVSS 114

Run on: us-10-027-xt 0.5

Title: Perfect score: 1 LEF
Sequence: 614 512079187 residues
Scoring table: 2000000000
Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	504.5	82.2	476	2	O6GMX1
2	480	78.2	465	2	O6GMX6
3	480	78.2	478	2	O7Z379
4	470.5	76.6	119	2	O9UL73
5	469.5	76.5	492	2	O7Z374
6	469	76.4	477	2	O6GMX7
7	468	76.2	150	2	O95973
8	460	74.9	496	2	O96KX8
9	460	74.9	620	2	O96KX0
10	452	73.6	576	2	O6P418
11	441	71.8	139	2	O86SX2
12	439.5	71.6	129	1	HV2F_HUMAN
13	431	70.2	130	2	O81ZD7
14	429.5	70.0	595	2	O8WUX4
15	428.5	70.0	597	2	O6GMX5
16	429.5	70.0	597	2	O9BU10
17	429.5	70.0	625	2	O96A66
18	425.5	69.3	597	2	O9BQB8
19	424.5	69.1	478	2	O6NTH3
20	420	68.4	146	1	HV21_HUMAN
21	412	67.1	473	2	O8TC63
22	393.5	64.1	117	1	HV26_HUMAN
23	392.5	63.9	479	2	O99M22
24	389	63.4	116	2	O7Z3Y6
25	387	63.0	136	2	O6LBO5
26	377.5	61.5	476	2	O6MX7
27	372.5	60.7	137	1	HV4E_MOUSE
28	370.5	60.3	122	2	O6S2I1
29	364	59.3	122	2	O9UL75
30	357.5	58.2	113	1	HV47_MOUSE
31	349.5	56.9	144	1	HV43_MOUSE

32	348.5	56.8	116	1	HV61_MOUSE	P18532	mus musculus
33	347	56.5	117	1	HV62_MOUSE	P18533	mus musculus
34	344.5	56.1	121	2	O9UL96	O9UL96	homo sapien
35	343	55.9	118	2	O81IUS	O81IUS	mus musculus
36	342.5	55.8	116	1	HV60_MOUSE	P18531	mus musculus
37	340	55.4	121	2	O99NG4	O99NG4	mus musculus
38	336	54.7	482	2	O91X92	O91X92	mus musculus
39	330	53.7	135	1	HV02_XENTIA	P20957	xenopus lae
40	314.5	51.2	118	2	O9UL74	O9UL74	homo sapien
41	313	51.0	120	1	HV2B_HUMAN	P01815	homo sapien
42	303.5	49.4	240	2	O65ZC9	O65ZC9	homo sapien
43	302.5	49.3	119	1	HV2C_HUMAN	P01816	homo sapien
44	301.5	49.1	466	2	O6IN78	O6IN78	homo sapien
45	299	48.7	473	2	O6MZV7	O6MZV7	homo sapien

ALIGNMENTS

RESULT 1
O6GMX1 PRELIMINARY; PRT; 476 AA.
AC O6GMX1, 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ustin T.B., Yoshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smaluk D.E., Scherch A., Schein J.E.,
Jones S.J., Warr M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
EMBL: BC073773; AAH73773.1; -
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG.
DR InterPro: IPR003597; IG.
DR InterPro: IPR003006; IG.
DR InterPro: IPR003596; IG.
DR Pfam: PF07654; Cl-sect; 3.
DR Pfam: PF00047; IG; 4.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IG; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS00835; IG LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
DR

Query Match 82.2%; Score 504.5; DB 2; Length 476;
Best Local Similarity 76.6%; Pred. No. 1e-43;
Matches 95; Conservative 12; Mismatches 4; Indels 13; Gaps 2

QY 2 ESGPLVMPSPQSLTCTVSGGSIRSGGYWMIROPQPKGLGWLVIYHSGNTYNNPSL 61
DB 25 ESGPLVMPSPQSLTCTVSGGSIRSGGYWMIROPQPKGLGWLVIYHSGNTYNNPSL 84
QY 62 KSRVTMSYDTSKNHPSRLSSVTADTAVYCYARS-----DGYTLDMWGQSTLV 110
DB 85 KSRVTISLDTSGNGQSLKKNSTVADTAVYFCARAGWGSFRWALDGFRI--WGQSTWV 142
QY 111 TVSS 114
DB 143 TVSS 146

RESULT 2
Q6GMX6 PRELIMINARY; PRT; 465 AA.
Q6GMX6
AC Q6GMX6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
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SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Heien F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Mullay S.,
Tha S.S., Iaconello N.A., Peters G.J., Abramson R.D., Mullay S.,
Tha S.S., McKernan K.J., Malek J.A., Gunaratne P.H.,
Tha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RT D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RL Pheilon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RN [2] Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RP SEQUENCE=Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA TISSUE=Primary B-Cells;
RC MEDLINE=12477932; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Heien F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Mullay S.,
Tha S.S., Iaconello N.A., Peters G.J., Abramson R.D., Mullay S.,
Tha S.S., McKernan K.J., Malek J.A., Gunaratne P.H.,
Tha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RT D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RL Pheilon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RN [2] Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RP SEQUENCE=Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA TISSUE=Primary B-Cells;
RC MEDLINE=12477932; PubMed=12477932; DOI=10.1073/pnas.242603899;
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RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Heien F.,
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Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Mullay S.,
Tha S.S., Iaconello N.A., Peters G.J., Abramson R.D., Mullay S.,
Tha S.S., McKernan K.J., Malek J.A., Gunaratne P.H.,
Tha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RT D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RP SEQUENCE=Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
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RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Heien F.,
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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Tha S.S., McKernan K.J., Malek J.A., Gunaratne P.H.,
Tha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RT D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RP SEQUENCE=Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA TISSUE=Primary B-Cells;
RC MEDLINE=12477932; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Heien F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Mullay S.,
Tha S.S., Iaconello N.A., Peters G.J., Abramson R.D., Mullay S.,
Tha S.S., McKernan K.J., Malek J.A., Gunaratne P.H.,
Tha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RT D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RL Pheilon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RN [2] Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RP SEQUENCE=Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA TISSUE=Primary B-Cells;
RC MEDLINE=12477932; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Heien F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Mullay S.,
Tha S.S., Iaconello N.A., Peters G.J., Abramson R.D., Mullay S.,
Tha S.S., McKernan K.J., Malek J.A., Gunaratne P.H.,
Tha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RT D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RL Pheilon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RN [2] Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RP SEQUENCE=Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA TISSUE=Primary B-Cells;
RC MEDLINE=12477932; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Heien F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Mullay S.,
Tha S.S., Iaconello N.A., Peters G.J., Abramson R.D., Mullay S.,
Tha S.S., McKernan K.J., Malek J.A., Gunaratne P.H.,
Tha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RT D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RL Pheilon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RN [2] Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RP SEQUENCE=Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA TISSUE=Primary B-Cells;
RC MEDLINE=12477932; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Heien F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Mullay S.,
Tha S.S., Iaconello N.A., Peters G.J., Abramson R.D., Mullay S.,
Tha S.S., McKernan K.J., Malek J.A., Gunaratne P.H.,
Tha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RT D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RL Pheilon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RN [2] Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RP SEQUENCE=Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA TISSUE=Primary B-Cells;
RC MEDLINE=12477932; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Heien F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Mullay S.,
Tha S.S., Iaconello N.A., Peters G.J., Abramson R.D., Mullay S.,
Tha S.S., McKernan K.J., Malek J.A., Gunaratne P.H.,
Tha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Query Match	Best Local Similarity	Matches	Score	DB 2;	Length	465;
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.	84.1%;	3;	Mismatches	13;	Indels	2;
KW Hypothetical protein.						Gaps
SO SEQUENCE 465 AA; 51083 MM; B3A9B7D0FDB1386E CRC64;						
QY 2 ESGGGLVKKPSGQTLSTCTVSGGSIIRSGGYWSWIRPPGKLEWIGIYHSGNTYNSL 61						
DB 25 ESGGGLVKKPSGQTLSTCTVSGGSI--SGYWSWIRPPAGKLEWIGIYHSGNTYNSL 82						
QY 62 KSRVTMSVDTSKHNFSRLSSVTADPAVYVCARSDGVTLDNMGGTLTVSS 114						
DB 83 KSRVTMSVDTSKHNFSRLSSVTADPAVYVCARSDGVTLDNMGGTLTVSS 135						
RESULT 3						
Q72379	PRELIMINARY;	PRT;	478 AA.			
ID Q72379						
AC Q72379						
DT 01-OCT-2003 (TREMBlrel. 25, Created)						
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)						
DT 01-MAR-2004 (TREMBlrel. 25, Last annotation update)						
DE Hypothetical protein DKFP686K04218 (Fragment).						
GN Name=DKFP686K04218;						
OS Homo sapiens (Human).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.						
OX NCBI_TaxId=9606;						
RN [1]						
RP SEQUENCE FROM N.A.						
RC TISSUE=Human rectum tumor;						
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,						
RA Podo G., Han M., Wiemann S.;						
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.						
DR EMBL; BX538066; CAD97996.1; -						
DR HSSP; P01820; IG7J.						
DR InterPro; IPR007110; Ig-like.						
DR InterPro; IPR003597; Ig C1.						
DR InterPro; IPR003006; Ig MHC.						
DR InterPro; IPR003596; Ig V.						
DR Pfam; PF07654; C1-sect; 2.						
DR SMART; SM00406; IGV; 1.						
DR PROSITE; PS50835; IG_LIKE; 4.						
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.						
KW Hypothetical protein.						
FT NON TER 1						
SO SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;						
Query Match	78.2%;	Score	480;	DB 2;	Length	478;
Best Local Similarity	77.4%;	Pred. No.	3.5e-41;			
Matches	89;	Conservative	14;	Mismatches	10;	Indels
						Gaps
QY 2 ESGGGLVKKPSGQTLSTCTVSGGSIIRSGGYWSWIRPPGKLEWIGIYHSGNTYNSL 61						
DB 24 ESGGGLVKKPSGQTLSTCTVSGGSIIRSGGYWSWIRPPGKLEWIGIYHSGNTYNSL 83						
QY 62 KSRVTMSVDTSKHNFSRLSSVTADPAVYVCARSDGVTLDNMGGTLTVSS 114						
DB 84 ESRLLSISIDTSKHNFSRLSSVTADPAVYVCARSDGVTLDNMGGTLTVSS 138						
RESULT 4						
Q9UL73	PRELIMINARY;	PRT;	119 AA.			
ID Q9UL73						
AC Q9UL73						
DT 01-MAY-2000 (TREMBlrel. 13, Created)						
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)						
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)						
DE Myosin-reactive immunoglobulin heavy chain variable region						
DE (Fragment).						
OS Homo sapiens (Human).						

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN NCB1_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9827139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Betney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035041; AAD56277.1; -.
 DR PIR; PH0876; PH0876.
 DR PIR; S12416; S12416.
 DR HSSP; P01820; 1G7J.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON TER 1 1
 FT NON TER 119 119
 SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EAOBE CRC64;

Query Match 76.6%; Score 470.5; DB 2; Length 119;
 Best Local Similarity 79.3%; Pred. No. 7.4e-41;
 Matches 92; Conservative 8; Mismatches 11; Indels 5; Gaps 2;

Oy 2 ESGPGLVPSQTLSTCTVSGSGSIRSGGYMSWIROPKGLGEMIGIYHSGNTYNNPSL 61
 Db 6 ESGPGLVPSQTLSTCTVSGSGSIRSGGYMSWIROPKGLGEMIGIYHSGNTYNNPSL 63
 Oy 62 KSRVTSVDTSKNHFSLRLSSVTADTVAYYCAR---SDGYTLDMWGQGLTVTVSS 114
 Db 64 KSRVTSVDTSKNHFSLRLSSVTADTVAYYCARLSNMGPPYFDWGGGLTVTVSS 119

RESULT 5
 Q72374 PRELIMINARY; PRT; 492 AA.
 AC Q72374;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein DKFZp686C02218 (Fragment).
 GN Name=DKFZp686C02218;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCB1_TaxID=9606;
 RN NCB1_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RA Bloeker H., Boeher M., Mewes H.W., Weil B., Amd C., Oeanger A.,
 RA Rob G., Han M., Wieman S.,
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX538077; CAD98001.1; -.
 DR HSSP; P01820; 1G7J.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003596; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; CL-sec; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 FT NON TER 1 1
 FT NON TER 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
 SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;

Query Match 76.5%; Score 469.5; DB 2; Length 492;
 Best Local Similarity 76.9%; Pred. No. 4.4e-40;
 Matches 90; Conservative 10; Mismatches 12; Indels 5; Gaps 2;

Oy 2 ESGPGLVPSQTLSTCTVSGSGSIRSGGYMSWIROPKGLGEMIGIYHSGNTYNNPSL 61
 Db 37 ESGPGLVPSQTLSTCTVSGSGSIRSGGYMSWIROPKGLGEMIGIYHSGNTYNNPSL 96
 Oy 62 KSRVTSVDTSKNHFSLRLSSVTADTVAYYCAR---SDGYTLDMWGQGLTVTVSS 114
 Db 97 KSRVTSVDTSKNHFSLRLSSVTADTVAYYCARHVEGPGW-FDWMGGGLTVTVSS 152

RESULT 6
 Q6GKX7 PRELIMINARY; PRT; 477 AA.
 AC Q6GKX7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCB1_TaxID=9606;
 RN NCB1_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derje J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stadler M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Topolycki S., Carninci P., Prange C.,
 RA Rana S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.U., McKernan K.U., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.B., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN NCB1_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073765; AAH73765.1; -.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003596; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; CL-sec; 2.
 DR Pfam; PF00047; IG; 3.
 DR SMART; SM00409; IGV; 4.
 DR SMART; SM00407; IGV; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 FT NON TER 1 1
 FT NON TER 477 AA; 51631 MW; 9FB59C09C50CF85 CRC64;
 SQ SEQUENCE 477 AA; 51631 MW; 9FB59C09C50CF85 CRC64;

Query Match 76.4%; Score 469; DB 2; Length 477;
 Best Local Similarity 80.0%; Pred. No. 4.8e-40;
 Matches 92; Conservative 6; Mismatches 13; Indels 4; Gaps 2;

Oy 2 ESGPGLVPSQTLSTCTVSGSGSIRSGGYMSWIROPKGLGEMIGIYHSGNTYNNPSL 61
 Db 25 ESGPGLVPSQTLSTCTVSGSGSIRSGGYMSWIROPKGLGEMIGIYHSGNTYNNPSL 82

Oy		62	KSRVTLSVDTSKNPFSILRLNSTADTAVVYCARSDG--YYLDMNGGGTLTVSS	114
Dd		83	KSRVTLSLDPTSKNPFLRNLNSTADTAVVICAHSSNDPAFDYGCGTLTVSS	137
RESULT 7				
ID	095973	PRELIMINARY;	PRT; 150 AA.	
AC	095973:			
DT	01-MAY-1999	(TREMBLrel. 10, Created)		
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	VH4 heavy chain variable region precursor (Fragment).			
GN	Name=IGM;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCB1_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;			
RL	Submitted (OCT-1998) to the EMBL/genbank/DDBJ databases.			
DR	EMBL; AF103795; AAC79084.1; -			
DR	PIR; S31673; S31673.			
DR	PIR; S78056; S78056.			
DR	HSPB; P01820; I67J.			
DR	InferPro; IPRO07110; IG-like.			
DR	InferPro; IPRO03596; IG_v.			
DR	SMART; SMART0406; IGV. 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KW	Signal.			
FT	CCHAIN	1 19	Potential.	
FT	NON TER	20 >150	VH4 heavy chain variable region.	
SO	SEQUENCE	150 AA; 16315 MW; 85664E04938AA7C9 CRC64;		
 Query Match Best Local Similarity 76.2%; Score 468; DB 2; Length 150; Matches 89; Conservative 78.8%; Pred. No. 1.7e+40; 8; Mismatches 16; Indels 0; Gaps 0				
Oy		2	ESGPGLVPQSOTSLSTICTVSQGSIRSGGYWSWRIPPGKGLEMTGIYHSNTTYNSPL	61
Dd		25	ESGPLVRPSBTLLSICTVSGGISISTYWMVMIQPEPKGLEMGISLNHSGSYDYNPSL	84
Oy		62	KSRVTMSVDTCKNHFRSLRSYSTADTAVVYCARGDGITLDWGCGTLTVSS	114
Dd		85	KSRVTISVDTSKNPFLRNLNSTADTAVVICARLGMAFPDFGHGTIVTVSS	137
RESULT 8				
ID	096KK8	PRELIMINARY;	PRT; 496 AA.	
AC	096KK8:			
DT	01-DEC-2001	(TREMBLrel. 19, Created)		
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	MGC27165 protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K., Aleschki S.F., Zeeberg B., Bluetow K.H., Schaeffer C.F., Bhut N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heise F., Diatchenko L., Marustina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares W.B., Bonaldi M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usslin T.B., Yoshiyuki S., Carninci P., Prange C,			

RA Rana S.S, Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosnak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A..
RC TISSUE=Lung;
RA Strausberg R.,
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC016369; AAH16369.1; -.
DR HSSP; P01876; IOM0.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

```

Query Match 94.9% Score 460; DB 2; Length 496;
Best Local Similarity 75.0%; Pred. No. 4,3e-39;
Matches 90; Conservative 8; Mismatches 14; Indels 8; Gaps 2

Oy 2 ESGPGLVPSQTLSTCTVSGGSIIRSGGYWMIROPGKGLWIIGYIHSNGTYNPSL 61
Db 25 ESGPGLVKSSTLSLTCTVSGGSISSSYWGMIRPGKGLWIIANTYYSGITYPNPSL 84
Oy 62 KSRVLTMSVDTSKNHSLSLSSVTAADTVVYCARSDGT-----LDNWGGCTLVTVSS 114
Db 85 KSRVLTMSVDTSKNHSLSLSSVTAADTVVYFCAR-HGYSRSGRTAIDWGGCTLVTVSS 143

RESULT 9
O96EYO PRELIMINARY; PRT: 620 AA.
AC O96EYO
AC O96EYO
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE IGHM protein.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altshul S.F., Zdebberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussidi T.B., Toshiyuki S., Carnacci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011857; AAH11857.2; -.
DR PIR; S15590; S15590.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR003599; 1G.
DR InterPro; IPR007110; 1G-like.
DR InterPro; IPR003597; 1G-cl.
DR InterPro; IPR003006; 1G_MHC.
DR Pfam; PF07654; C1-set; 4.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; 1G; 2.
DR SMART; SM00407; 1Gcl; 4.
DR SMART; SM00406; 1Gv; 1.
DR PROSITE; PS50835; 1G_MHC; 5.
DR PROSITE; PS00290; 1G_MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;

Query Match 74.9%; Score 460; DB 2; Length 620;
Best Local Similarity 80.5%; Pred. No. 5.5e-39;
Matches 95; Conservative 4; Mismatches 11; Indels 8; Gaps 3;

Qy 2 ESGGLVPSQTLSTCTVSGSGSIRSGGYWMIROPKGLKLEWIGYIHSGNTYNSPL 61
Db 32 ESGGLVPSQTLSTCTVSGSGSIS--YMSWIRQPKGLKLEWIGYIHSGNTYNSPL 89
Qy 62 KSRVTVSVDSKQNFSLRLSSVTADTAIVYVCARSDGYTLDN-----WGQGTIVTVSS 114
Db 90 KSRVTVSVDSKQNFSLRLSSVTADTAIVYCA--SQPELPFLVGLFYWGQGTIVTVSS 146

RESULT 10
Q6P418 PRELIMINARY; PRT; 576 AA.
ID Q6P418;
AC Q6P418;
DT 05-JUN-2004 (TREMBLrel. 27, Created)
DT 05-JUN-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUN-2004 (TREMBLrel. 27, Last annotation update)
DE IGHG protein.
GN Name=IGHG;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo W.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalhus D.E., Scherch A., Schein J.E.,

RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -.
DR HSSP; P01820; 1A7N.
DR InterPro; IPR003599; 1G.
DR InterPro; IPR007110; 1G-like.
DR InterPro; IPR003597; 1G-cl.
DR InterPro; IPR003006; 1G_MHC.
DR InterPro; IPR003596; 1G v.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; 1G; 1.
DR SMART; SM00409; 1G; 1.
DR SMART; SM00407; 1Gcl; 3.
DR SMART; SM00406; 1Gv; 1.
DR PROSITE; PS50835; 1G_MHC; 4.
DR PROSITE; PS00290; 1G_MHC; UNKNOWN 2.
SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;

Query Match 73.6%; Score 452; DB 2; Length 576;
Best Local Similarity 77.6%; Pred. No. 3.4e-38;
Matches 90; Conservative 6; Mismatches 16; Indels 4; Gaps 2;

Qy 2 ESGGLVPSQTLSTCTVSGSGSIRSGGYWMIROPKGLKLEWIGYIHSGNTYNSPL 61
Db 32 ESGGLVPSQTLSTCTVSGSGSIS--YMSWIRQPKGLKLEWIGYIHSGNTYNSPL 90
Qy 62 KSRVTVSVDSKQNFSLRLSSVTADTAIVYVCARSDG---YTLDMWGQGTIVTVSS 114
Db 91 KSRVTVSVDSKQNFSLRLSSVTADTAIVYCA--SQPELPFLVGLFYWGQGTIVTVSS 146

RESULT 11
Q6SXX2 PRELIMINARY; PRT; 139 AA.
ID Q6SXX2;
AC Q6SXX2;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CSDD1004YMI19 of B cells (Ramos cell line) of
DE Homo sapiens (human) (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Li W.B., Gruber C., Jeesee J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=B cells;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX248300; CAD62627.1; -.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; 1G-like.
DR InterPro; IPR003597; 1G-cl.
DR InterPro; IPR003006; 1G_MHC.
DR Pfam; PF07654; C1-set; 1.
DR PROSITE; PS50835; 1G_MHC; 1.
FT NON TER 1
SQ SEQUENCE 139 AA; 15573 MW; 7D1E202410B4F8C CRC64;

Query Match 71.8%; Score 441; DB 2; Length 139;
Best Local Similarity 89.4%; Pred. No. 9.9e-38;
Matches 84; Conservative 5; Mismatches 3; Indels 2; Gaps 1;

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Qy 2 ESGPGLVPSQSLTCTVSGSGSIRSGYWSMIRPPGKGLWIGIYHSGNTYNSL 61
Dy 38 ESGPGLVPSQSLTCTVSGSGSIS--YYWSMIRPPGKGLWIGIYHSGNTYNSL 95
Qy 62 KSRVTMSVDTSKNFSRLSSVTADPAVYVCAR 95
Dy 96 KSRVTISVDTSRNQSLRLSSVTADPAVYVCAR 129

RESULT 12
HV2F HUMAN
ID HV2F HUMAN STANDARD; PRT; 129 AA.
AC P01824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG heavy chain V-II region WH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82222235; PubMed=6806818;
RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
RT "Complete amino acid sequence of the delta heavy chain of human
RT Immunoglobulin D.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
CC -1- MSCELANEOUS: This chain was isolated from an Igd myeloma
CC protein.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02099; D2HWA.
DR HSSP; P01820; 1G7J.
DR GlycositeDB; P01824; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 113
FT NON TER 129
SQ SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 71.6%; Score 439.5; DB 1; Length 129;
Best Local Similarity 66.7%; Pred. No. 1.3e-37;
Matches 84; Conservative 12; Mismatches 15; Indels 15; Gaps 2;

Qy 2 ESGPGLVPSQSLTCTVSGSGSIRSGYWSMIRPPGKGLWIGIYHSGNTYNSL 61
Dy 6 ESGPGLVPSQSLTCTVSGSGSIRSGYWSMIRPPGKGLWIGIYHSGNTYNSL 65
Qy 62 KSRVTMSVDTSKNFSRLSSVTADPAVYVCAR-----SDGYTLDNWGQGT 108
Dy 66 KSRVTISVDTSRNQSLRLSSVTADPAVYVCAR-----SDGYTLDNWGQGT 123
Qy 109 LVTYSS 114
Dy 124 TVHVS 129

RESULT 13
Q81ZD7 PRELIMINARY; PRT; 130 AA.
AC Q81ZD7;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Anti-chyotoglobulin heavy chain variable region (Fragment).
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Y.-T., Chung J., Park J.-Y.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY145445; AAN64329.1; -.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Igv.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 130
SQ SEQUENCE 130 AA; 13901 MW; 036131FC6EC1551E CRC64;

Query Match 70.2%; Score 431; DB 2; Length 130;
Best Local Similarity 71.2%; Pred. No. 1e-36;
Matches 89; Conservative 8; Mismatches 16; Indels 12; Gaps 4;

Qy 2 ESGPGLVPSQSLTCTVSGSGSIRSGYWSMIRPPGKGLWIGIYHSGNT-----Y 56
Dy 6 QSGPGLVPSQSLTCTVSGSGSISSSSYTWGMRPPGKGLWIGIYHSGNTSPY 65
Qy 57 YNPSLKSRTVMSVDTSKNFSRLSSVTADPAVYVCAR---SDG--YT-LDNWGQGT 109
Dy 66 YAPSLKSRVTISVDTSKNFSRLSSVTADPAVYVCASPTHCSGGCGYAFQWGGQFL 125
Qy 110 VTVSS 114
Dy 126 TVVSS 130

RESULT 14
Q8WUX4 PRELIMINARY; PRT; 595 AA.
AC Q8WUX4;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lottuano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smalins D.B., Schermer A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
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RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.2; -.
DR PIR; G34964; G34964.
DR HSSP; P01861; 1ADQ.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 595 AA; 65290 MW; 0D4B5076545714B CRC64;

Query Match 70.0%; Score 429.5; DB 2; Length 595;
Best Local Similarity 72.5%; Pred. No. 7.6e-36;
Matches 87; Conservative 7; Mismatches 15; Indels 11; Gaps 3;

QY 4 GPGIVKPSQTLSTLCYVSGSIRSGYVSWIRPPGKGLWIGIYHSGNTYVNPISLS 63
DB 34 GAGLLKSEITSLTCGYVGSF--SGYVSWIRPPGKGLWIGIYHSGNTYVNPISLS 91
QY 64 RVTVSVDTSKNHFSLRLSSVTAADTAVYYCAR-----SDG-YTLDMNGQGLTVYSS 114
DB 92 RVTVSVDTSKKQLSLKLSVNAADTAVYYCARVITRASPGTDGRYGMVWGQGLTVYSS 151

RESULT 15
Q6GMX5 PRELIMINARY; PRT; 597 AA.
ID Q6GMX5
AC Q6GMX5;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carinci P., Prange C.,
RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073767; AAH73767.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-LIKE.
DR InterPro; IPR003597; IG-cl.

DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 4.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;

Query Match 70.0%; Score 429.5; DB 2; Length 597;
Best Local Similarity 72.5%; Pred. No. 7.6e-36;
Matches 87; Conservative 7; Mismatches 15; Indels 11; Gaps 3;

QY 4 GPGIVKPSQTLSTLCYVSGSIRSGYVSWIRPPGKGLWIGIYHSGNTYVNPISLS 63
DB 27 GAGLLKSEITSLTCGYVGSF--SGYVSWIRPPGKGLWIGIYHSGNTYVNPISLS 84
QY 64 RVTVSVDTSKNHFSLRLSSVTAADTAVYYCAR-----SDG-YTLDMNGQGLTVYSS 114
DB 85 RVTVSVDTSKKQLSLKLSVNAADTAVYYCARVITRASPGTDGRYGMVWGQGLTVYSS 144

Search completed: July 26, 2005, 09:26:19
Job time : 72.6818 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 08:50:20 ; Search time 85.3273 Seconds
(without alignments)
516.724 Million cell updates/sec

Title: US-10-027-725a-9
Perfect score: 614
Sequence: 1 LESGPGLVKRSQTLSTLCV.....RSDGYTLDMNQGLTVTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq.16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	605	98.5	114	5	ABG30447
2	600	97.7	114	5	ABG30446
3	556	90.6	114	5	ABG30445
4	524.5	85.4	121	7	ADP03982
5	524	85.3	118	7	ADP03988
6	523.5	85.3	123	7	ADP03870
7	521	84.9	120	7	ADP03974
8	521	84.9	120	7	ADP03873
9	521	84.9	122	7	ADP03977
10	521	84.9	473	4	AA836206
11	520	84.7	221	7	ADP03981
12	519.5	84.6	121	7	ADP03871
13	519.5	84.6	125	7	ADP03970
14	517.5	84.3	119	7	ADP03970
15	516.5	84.1	123	2	AAW78433
16	516.5	84.1	123	5	AAW78433
17	516.5	84.1	123	7	ADP03872
18	516.5	84.1	123	7	ADP03872
19	516	84.0	124	7	ADP03935
20	515.5	84.0	117	7	ADP03978
21	515.5	84.0	117	7	ADP03978
22	515.5	84.0	117	7	ADP03978
23	514	83.7	120	7	ADP03969
24	514	83.7	120	7	ADP03969
25	514	83.7	121	7	ADJ80377

26	513.5	83.6	120	4	AAB62775	AAB62775 Human HIV
27	513	83.6	116	7	ADP03957	ADP03957 Murine-ex
28	512.5	83.5	125	7	ADP03868	ADP03868 Murine-ex
29	512.5	83.5	125	7	ADP03876	ADP03876 Murine-ex
30	512	83.4	123	4	AAB62745	AAB62745 Human HIV
31	511.5	83.3	119	7	ADP03961	ADP03961 Murine-ex
32	511	83.2	110	7	ADP03934	ADP03934 Murine-ex
33	510.5	83.1	122	4	AAB62765	AAB62765 Human HIV
34	510.5	83.1	123	7	ADP03869	ADP03869 Murine-ex
35	510.5	83.1	127	7	ADP03874	ADP03874 Murine-ex
36	510	83.1	246	3	AA15126	AA15126 Anti-muri
37	508.5	82.8	125	7	ADP03983	ADP03983 Murine-ex
38	508	82.7	128	8	ADP22124	ADP22124 Human ant
39	508	82.7	128	8	ADP22104	ADP22104 Human ant
40	508	82.7	128	8	ADP22096	ADP22096 Human ant
41	508	82.7	172	3	AA193713	AA193713 The heavy
42	508	82.7	172	6	AAE35892	AAE35892 Human 2.1
43	507.5	82.7	117	7	ADP03976	ADP03976 Anti-huma
44	507.5	82.7	117	7	ADP05380	ADP05380 Anti-MUC1
45	507.5	82.7	117	7	ADP09818	ADP09818 Human ant

ALIGNMENTS

RESULT 1	ABG30447	standard; protein; 114 AA.
ID	ABG30447	
XX	ABG30447	
AC	ABG30447	
XX	ABG30447	
DT	21-OCT-2002	(first entry)
XX	Human IGE Fab clone 100 heavy chain protein.	
DE	Human, fab; anti-allergic; vaccine; grass pollen; Phi p 2;	
XX	Human, fab; anti-allergic; vaccine; grass pollen; Phi p 2;	
KW	linocthy grass pollen allergen; passive immunotherapy.	
KM	linocthy grass pollen allergen; passive immunotherapy.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX		
XX		
FT	Key	Location/Qualifiers
FT	Region	1..26
FT	Region	/note= "FRI region"
FT	Region	27..33
FT	Region	/note= "CDR1 region"
FT	Region	34..47
FT	Region	/note= "FR2 region"
FT	Region	48..63
FT	Region	/note= "CDR2 protein"
FT	Region	64..95
FT	Region	/note= "FR3 region"
FT	Region	96..103
FT	Region	/note= "CDR2 region"
FT	Region	104..114
FT	Region	/note= "FR4 region"
XX	WO200253595-A1.	
XX	11-JUL-2002.	
XX	27-DEC-2001; 2001WO-SE002908.	
XX	29-DEC-2000; 2000SF-00004892.	
XX	(PHAA) PHARMACIA DIAGNOSTICS AB.	
XX	Flicker S, Steinberger P, Kraft D, Valenta R;	
XX	WPI; 2002-583604/62.	
XX	N-PSDB; AAK89639.	
XX	Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising	
XX	variable region of group 2 allergen specific-human Igr Fabs, useful for	

PT diagnosing or passive immunotherapy of type I allergy, for environmental
XX allergen detection.
XX
PS Disclosure; Page 38; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergenic patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific Fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The Fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific Fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergenic patients
CC IgE antibodies to Phi p 2. The present sequence represents the human IgG
CC Fab, clone 100 heavy chain protein of the invention
XX
SQ Sequence 114 AA;
XX
Query Match 98.5%; Score 605; DB 5; Length 114;
Best Local Similarity 99.1%; Pred. No. 3.4e-44;
Matches 113; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 LESGPGLVKPSQTLSTLCTVSGGSIKSGGYWMSWIRQPPGKLEWIGYIYHSGNTYVNS 60
1 LESGPGLVKPSQTLSTLCTVSGGSIKSGGYWMSWIRQPPGKLEWIGYIYHSGNTYVNS 60
XX
Db 1 LESGPGLVKPSQTLSTLCTVSGGSIKSGGYWMSWIRQPPGKLEWIGYIYHSGNTYVNS 60
XX
QY 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAAYYCARSDGYTLDMWGQGLTVTVSS 114
61 LKSRVTMSVDTSKNHFSLRLSVTAADTAAYYCARSDGYTLDMWGQGLTVTVSS 114
XX
Db 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAAYYCARSDGYTLDMWGQGLTVTVSS 114
XX
RESULT 2
ID ABG30446 standard; protein; 114 AA.
XX
AC ABG30446;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human IgE Fab clone 60 heavy chain protein.
XX
DE Human IgE Fab clone 60 heavy chain protein.
XX
KM Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;
KM timothy grass pollen allergen; passive immunotherapy.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FH Region 1..26
FT /note= "FR1 region"
FT 27..33
FT /note= "CDR1 region"
FT 34..47
FT /note= "FR2 region"
FT 48..63
FT /note= "CDR2 protein"
FT 64..95
FT /note= "FR3 region"
FT 96..103
FT /note= "CDR2 region"
FT 104..114
FT /note= "FR4 region"
XX
XX WO200253595-A1.
XX
XX 11-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-SE002908.
XX

PR 29-DEC-2000; 2000SE-00004892.
XX
XX (PHAA) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
XX WPI; 2002-583604/62.
DR N-PSDB; ABK89638.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
XX variable region of group 2 allergen specific-human IgE Fabs, useful for
XX diagnosing or passive immunotherapy of type I allergy, for environmental
XX allergen detection.
XX
PS Disclosure; Page 37; 45pp; English.
XX
XX
XX This invention relates to the DNA and protein sequences of group 2
XX allergen-specific human IgE Fabs and methods for their use. The proteins
XX of the invention may have antiallergic activities and may be used as a
XX vaccine or an inhibitor of binding of grass pollen allergenic patient's IgE
XX antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
XX 2 allergen-specific Fabs of the invention may be useful for environmental
XX allergen detection and for standardisation of allergen extracts. The Fabs
XX - or a vaccine against a type I allergy is useful for passive
XX immunotherapy of type I allergy, it is also useful for diagnosing a type
XX I allergy. The allergen-specific Fabs of the invention are useful for
XX inter alia, diagnosis, therapy and prevention of type I allergy. They are
XX also useful for identification of group 2 allergen-containing pollen and
XX may be used for blocking the binding of grass pollen allergenic patients
XX IgE antibodies to Phi p 2. The present sequence represents the human IgG
XX Fab, clone 60 heavy chain protein of the invention
XX
SQ Sequence 114 AA;
XX
Query Match 97.7%; Score 600; DB 5; Length 114;
Best Local Similarity 96.5%; Pred. No. 9.1e-44;
Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 LESGPGLVKPSQTLSTLCTVSGGSIKSGGYWMSWIRQPPGKLEWIGYIYHSGNTYVNS 60
1 LESGPGLVKPSQTLSTLCTVSGGSIKSGGYWMSWIRQPPGKLEWIGYIYHSGNTYVNS 60
XX
Db 1 LESGPGLVKPSQTLSTLCTVSGGSIKSGGYWMSWIRQPPGKLEWIGYIYHSGNTYVNS 60
XX
QY 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAAYYCARSDGYTLDMWGQGLTVTVSS 114
61 LKSRVTMSVDTSKNHFSLRLSVTAADTAAYYCARSDGYTLDMWGQGLTVTVSS 114
XX
Db 61 LKSRVTMSVDTSKNHFSLRLSVTAADTAAYYCARSDGYTLDMWGQGLTVTVSS 114
XX
RESULT 3
ID ABG30445 standard; protein; 114 AA.
XX
AC ABG30445;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human IgE Fab clone 94 heavy chain protein.
XX
DE Human IgE Fab clone 94 heavy chain protein.
XX
KM Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;
KM timothy grass pollen allergen; passive immunotherapy.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FH Region 1..26
FT /note= "FR1 region"
FT 27..33
FT /note= "CDR1 region"
FT 34..47
FT /note= "FR2 region"
FT 48..63
FT /note= "CDR2 protein"
FT 64..95
FT /note= "FR3 region"
XX
XX

```

FT Region 96.103
FT /note= "CDR2 region"
FT Region 104.114
FT /note= "FR4 region"
XX WO200253595-A1.
XX
XX PD 11-JUL-2002.
XX
XX PF 27-DEC-2001; 2001WO-SE002908.
XX
XX PR 29-DEC-2000; 2000SE-00004892.
XX
XX PA (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX
XX PI Flicker S, Steiberger P, Kraft D, Valenta R;
XX
XX DR WPI; 2002-583604/62.
XX
XX DR N-PSDB; ABK89637.
XX
XX PT Group 2 allergen-specific immunoglobulin (Ig) E Fabs or IgG comprising
XX PT variable region of group 2 allergen specific-human IgE Fabs, useful for
XX PT diagnosing or passive immunotherapy of type I allergy, for environmental
XX PT allergen detection.
XX
XX PS Disclosure; Page 36; 45pp; English.
XX
XX CC This invention relates to the DNA and protein sequences of group 2
XX CC allergen-specific human IgE Fabs and methods for their use. The proteins
XX CC of the invention may have anti-allergic activities and may be used as a
XX CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE
XX CC antibodies to Phl p 2 (a major timothy grass pollen allergen). The group
XX CC 2 allergen-specific Fabs of the invention may be useful for environmental
XX CC allergen detection and for standardisation of allergen extracts. The Fabs
XX CC - or a vaccine against a type I allergy is useful for passive
XX CC immunotherapy of type I allergy, it is also useful for diagnosing a type
XX CC I allergy. The allergen-specific Fabs of the invention are useful for
XX CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
XX CC also useful for identification of group 2 allergen-containing pollen and
XX CC may be used for blocking the binding of grass pollen allergic patients
XX CC IgE antibodies to Phl p 2. The present sequence represents the human IgG
XX CC Fab, clone 94 heavy chain protein of the invention
XX
XX SQ Sequence 114 AA;
XX
XX Query Match 90.6%; Score 556; DB 5; Length 114;
XX Best Local Similarity 90.4%; Pred. No. 5.3e-40;
XX Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 1 LESGGLVKKPSQTLSTCTVSGSIRSGGYWMTROPKGLKLEWIGYIYHSGNTYNNPS 60
XX DB 1 LESGGLVKKPAQTSLSCVSGSIRSGGYWMTROPKGLKLEWIGYIYHSGNTYNNPS 60
XX
XX QY 61 LKSRVTMSVDTSKNHPSLRSLSSVTADPAVYVCARSDGYTLDMWCGTLVTYSS 114
XX DB 61 LKSRVTMSVDTSKNHPSLRSLSSVTADPAVYVCARSDGYTLDMWCGTLVTYSS 114
XX
XX RESULT 4
XX ADP03982
XX ID ADP03982 standard; protein; 121 AA.
XX
XX AC ADP03982;
XX
XX DT 29-JUN-2004 (first entry)
XX
XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 152.
XX
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX KW cytosolic; colorectal neoplasm; renal cell carcinoma;
XX KW cervical intraepithelial squamous neoplasia;
XX KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX KW gene therapy; murine; mouse; human; heavy chain variable domain.

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XX XX Unidentified.
XX OS
XX WO2003048328-A2.
XX
XX PD 12-JUN-2003.
XX
XX PF 02-DEC-2002; 2002WO-US038550.
XX
XX PR 03-DEC-2001; 2001US-0337275P.
XX
XX PA (ABGE-) ABGENIX INC.
XX
XX PI Gudas J, Foltz I, Handa M, Gallo M;
XX
XX DR WPI; 2003-523295/49.
XX
XX PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Example 2; SEQ ID NO 152; 89pp; English.
XX
XX CC The invention relates to a novel isolated monoclonal antibody (mAb)
XX CC comprising a heavy chain polypeptide and light chain polypeptide having a
XX CC sequence chosen from one of 53 fully defined amino acid sequences given
XX CC in the specification, where the antibody specifically binds carbonic
XX CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX CC demonstrates cytostatic activity and may be useful for treating a tumour,
XX CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX CC tumour or breast cancer, possibly via gene therapy. The current sequence
XX CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX CC (heavy chain variable domain) protein of the invention. The protein was
XX CC generated via the introduction of the human CA IX protein into a
XX CC transgenic mouse strain.
XX
XX SQ Sequence 121 AA;
XX
XX Query Match 85.4%; Score 524.5; DB 7; Length 121;
XX Best Local Similarity 86.2%; Pred. No. 2.8e-37;
XX Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;
XX
XX QY 2 ESGPGLVKKPSQTLSTCTVSGSIRSGGYWMTROPKGLKLEWIGYIYHSGNTYNNPSL 61
XX DB 6 ESGPGLVKKPSQTLSTCTVSGSIRSGGYWMTROPKGLKLEWIGYIYHSGNTYNNPSL 65
XX
XX QY 62 KSRVTMSVDTSKNHPSLRSLSSVTADPAVYVCARSD--GYTLDMWCGTLVTYSS 114
XX DB 66 KSRVTMSVDTSKNHPSLRSLSSVTADPAVYVCAYYDILTYAFDLMWCGTIVTYSS 121
XX
XX RESULT 5
XX ADP03968
XX ID ADP03968 standard; protein; 118 AA.
XX
XX AC ADP03968;
XX
XX DT 29-JUN-2004 (first entry)
XX
XX DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.
XX
XX KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX KW cytosolic; colorectal neoplasm; renal cell carcinoma;
XX KW cervical intraepithelial squamous neoplasia;
XX KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX KW gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX OS Unidentified.
XX
XX XX WO2003048328-A2.
XX
XX PD 12-JUN-2003.

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PF	02-DEC-2002; 2002WO-US038550.	
XX		
XX	03-DEC-2001; 2001US-0337275P.	
XX		
PA	(ABGE-) ABGENIX INC.	
XX		
PI	Gudas J, Foltz I, Handa M, Gallo M,	
XX		
XX	WPI; 2003-523295/49.	
DR		
XX		
PT	New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,	
PT	colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical	
XX	intraepithelial squamous and glandular neoplasia or esophageal tumors.	
PT		
PS	Example 2; SEQ ID NO 138; 89pp; English.	
XX		
CC	The invention relates to a novel isolated monoclonal antibody (mAb)	
CC	comprising a heavy chain polypeptide and light chain polypeptide having a	
CC	sequence chosen from one of 53 fully defined amino acid sequences given	
CC	in the specification, where the antibody specifically binds carbonic	
CC	anhydrase IX (CA IX) tumour antigen. The antibody of the invention	
CC	demonstrates cytostatic activity and may be useful for treating a tumour,	
CC	such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,	
CC	cervical intraepithelial squamous and glandular neoplasia, oesophageal	
CC	tumour or breast cancer, possibly via gene therapy. The current sequence	
CC	is that of a murine-expressed anti-human CA IX monoclonal antibody VH	
CC	(heavy chain variable domain) protein of the invention. The protein was	
CC	generated via the introduction of the human CA IX protein into a	
XX	transgenic mouse strain.	
XX		
SQ	Sequence 118 AA;	
	Query Match 85.3%; Score 524; DB 7; Length 118;	
	Best Local Similarity 88.5%; Pred. No. 3e-37;	
	Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0	
QY	2 ESGPGLVPSQTLSLTCTVSGSGIRSGYMSWIRQPEKGLWIGYTHSGNTYNSPL 61	
DB	6 ESGPGLVPSQTLSLTCTVSGSGISGGYMSWIRQPEKGLWIGYTHSGNTYNSPL 65	
QY	62 KSRVTMSVDTSKNHSRLSSVTADTVAVYCARSDGYTLNDWGQGTLYTVSS 114	
DB	66 KSRVTISVDTSKNPSLKLSSVTADTVAVYCARRYGSGSDYWGQGTLYTVSS 118	
	RESULT 6	
	ADP03870	
ID	ADP03870 standard; protein; 123 AA.	
XX		
AC	ADP03870;	
XX		
DT	29-JUN-2004 (first entry)	
XX		
DB	Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10.	
XX		
KW	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;	
KW	cytostatic; colorectal neoplasm; renal cell carcinoma;	
KW	cervical intraepithelial squamous neoplasia;	
KW	cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;	
KW	gene therapy; murine; mouse; human; heavy chain variable domain.	
XX		
OS	Unidentified.	
XX		
PN	WO2003048328-A2.	
XX		
PD	12-JUN-2003.	
XX		
PF	02-DEC-2002; 2002WO-US038550.	
XX		
FR	03-DEC-2001; 2001US-0337275P.	
XX		
PA	(ABGE-) ABGENIX INC.	

XX	Gudas J,	Foltz I,	Handa M,	Gallo M;
PI				
DR	WPI; 2003-523295/49.			
XX				
PT	New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,			
PT	colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical			
PT	intraepithelial squamous and glandular neoplasia or esophageal tumors.			
XX				
PS	Claim 1; SEQ ID NO 10; 89pp; English.			
XX				
CC	The invention relates to a novel isolated monoclonal antibody (mab)			
CC	comprising a heavy chain polypeptide and light chain polypeptide having a			
CC	sequence chosen from one of 53 fully defined amino acid sequences given			
CC	in the specification, where the antibody specifically binds carbonic			
CC	anhydrase IX (CA IX) tumour antigen. The antibody of the invention			
CC	demonstrates cytostatic activity and may be useful for treating a tumour,			
CC	such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,			
CC	cervical intraepithelial squamous and glandular neoplasia, oesophageal			
CC	tumour or breast cancer, possibly via gene therapy. The current sequence			
CC	is that of a murine-expressed anti-human CA IX monoclonal antibody VH			
CC	(heavy chain variable domain) protein of the invention. The protein was			
CC	generated via the introduction of the human CA IX protein into a			
CC	transgenic mouse strain.			
XX				
SQ	Sequence 123 AA;			
Query Match	85.3%; Score 523.5; DB 7; Length 123;			
Best Local Similarity	85.6%; Pred. No. 3.4e-37;			
Matches 101; Conservative	5; Mismatches 7; Indels 5; Gaps 1;			
OY	2 ESGFGLVSPGSLTLCVSGSIRSGGYWSWIRPGKGLEMIGIYHSGNTYYNSL 61			
Db	6 ESGGVLVPSSQTLSLTCTVSGGSISGGYWSMWRHPKGKLEWIGIYYSGSITYNPSL 65			
OY	62 KSRVTMSVDTSKNHPSRLSSVTLADNAVYYCARS-----DGYTLDMWGQGLTVTVSS 114			
Db	66 KSRVTISVDTSKNQFSKLTSSTVAADNAVYYCARAKRYGSGSYLDYWGQGLTVTVSS 123			
RESULT 7				
ID	ADP03974 standard; protein, 120 AA.			
AC	ADP03974;			
XX				
DT	29-JUN-2004 (first entry)			
XX				
DE	Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.			
XX				
KM	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;			
KM	cytostatic; colorectal neoplasm; renal cell carcinoma;			
KM	cervical intraepithelial squamous neoplasia;			
KM	cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;			
KM	gene therapy; murine; mouse; human; heavy chain variable domain.			
XX				
OS	Unidentified.			
XX				
PN	WO2003048328-A2.			
PD	12-JUN-2003.			
XX				
Pf	02-DEC-2002; 2002WO-USO38550.			
PR	03-DEC-2001; 2001US-0337275P.			
XX				
PA	(ABGE-) ABGENIX INC.			
XX				
PI	Gudas J, Foltz I, Handa M, Gallo M;			
XX				
DR	WPI; 2003-523295/49.			
PT	New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,			

PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS Example 2; SEQ ID NO 144; 89pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody (mab)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 120 AA;
XX
Query Match 84.9%; Score 521; DB 7; Length 120;
Best Local Similarity 87.1%; Pred. No. 5.5e-37;
Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;
QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWIRQPGKLEWIGYTHSGNTYYNPSL 61
DB 6 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWIRQPGKLEWIGYTHSGNTYYNPSL 65
QY 62 KSRVTMSVDTSKNHPSRLSSVTADTAIVYVCARSDGYT--LDNMGGGTLVTWSS 114
DB 66 KSRVTISVDTSKNQPSLKLSSVTADTAIVYCAR-DGYNVYFPDLMGRGTLVTWSS 120
Db
QY 62 KSRVTMSVDTSKNHPSRLSSVTADTAIVYVCARSDGYT--LDNMGGGTLVTWSS 114
DB 66 KSRVTISVDTSKNQPSLKLSSVTADTAIVYCAR-DGYNVYFPDLMGRGTLVTWSS 120
Db
RESULT 8
ADP03873
ID ADP03873 standard; protein; 120 AA.
XX
AC ADP03873;
XX
DT 29-JUN-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.
XX
KM monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM cytosolic; colorectal neoplasm; renal cell carcinoma;
KM cervical intraepithelial squamous neoplasia;
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM gene therapy; murine; mouse; human; heavy chain variable domain.
XX
OS Unidentified.
XX
PN WO2003048328-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038550.
XX
PR 03-DEC-2001; 2001US-0337275P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Foltz I, Handa M, Gallo M;
XX
DR WPI; 2003-523295/49.
XX
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS Claim 1; SEQ ID NO 13; 89pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody (mab)

CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 120 AA;
XX
Query Match 84.9%; Score 521; DB 7; Length 120;
Best Local Similarity 87.1%; Pred. No. 5.5e-37;
Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;
QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWIRQPGKLEWIGYTHSGNTYYNPSL 61
DB 6 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWIRQPGKLEWIGYTHSGNTYYNPSL 65
QY 62 KSRVTMSVDTSKNHPSRLSSVTADTAIVYVCARSDGYT--LDNMGGGTLVTWSS 114
DB 66 KSRVTISVDTSKNQPSLKLSSVTADTAIVYCAR-DGYNVYFPDLMGRGTLVTWSS 120
Db
RESULT 9
ADP03977
ID ADP03977 standard; protein; 122 AA.
XX
AC ADP03977;
XX
DT 29-JUN-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.
XX
KM monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM cytosolic; colorectal neoplasm; renal cell carcinoma;
KM cervical intraepithelial squamous neoplasia;
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM gene therapy; murine; mouse; human; heavy chain variable domain.
XX
OS Unidentified.
XX
PN WO2003048328-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038550.
XX
PR 03-DEC-2001; 2001US-0337275P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Foltz I, Handa M, Gallo M;
XX
DR WPI; 2003-523295/49.
XX
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS Example 2; SEQ ID NO 147; 89pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody (mab)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,

CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 122 AA;

Query Match 84.9%; Score 521; DB 7; Length 122;
Best Local Similarity 85.5%; Pred. No. 5.6e-37;
Matches 100; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 2 ESGGGLVKKPSQTLSTLTCTVSGSGSTRSGGYWWSWIRPPGKLEWIGYIHSGNTYNPSTL 61
DB 6 ESGGGLVKKPSQTLSTLTCTVSGSGSTRSGGYWWSWIRPPGKLEWIGYIHSGNTYNPSTL 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCAR-----SDGYTLDMNGGGLTVTVSS 114
DB 66 KSRVTISVDTSKNHFSLRLSSVTADTAVYYCARVDYDILTGYGMDVWGQGITTVVSS 122

RESULT 10
AAB36206
ID AAB36206 standard; protein; 473 AA.
XX
AC AAB36206;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human immune system associated protein HISAP-4.
XX
KM Human; immune system associated protein; HISAP-4; immune disorder;
KM infection; autoimmune disease; cancer.
XX
OS Homo sapiens.
XX
PN US6135941-A.
XX
PD 24-OCT-2000.
XX
PF 27-MAR-1998; 98US-00049672.
XX
PR 27-MAR-1998; 98US-00049672.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
PI Hillman JL, Au-Young J;
XX
DR WPI; 2001-030926/04.
DR N-PSDB; AAC66522.
XX
PT New human immune system associated proteins (HISAP) and polynucleotides
PT encoding the HISAP, useful for diagnosing, treating or preventing immune
PT or cell proliferative disorders or infections.
XX
PS Claim 1; Col 53-56; 54pp; English.
XX
CC The present invention provides the coding and protein sequences for a
CC number of human immune system associated proteins (HISAPs). These can be
CC used in the diagnosis and treatment of various autoimmune disorders,
CC infections and cell proliferation diseases. The diseases include AIDS,
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, arteriosclerosis, cirrhosis and cancer
XX
SQ Sequence 473 AA;

Query Match 84.9%; Score 521; DB 4; Length 473;
Best Local Similarity 83.2%; Pred. No. 2.3e-36;
Matches 99; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

QY 2 ESGGGLVKKPSQTLSTLTCTVSGSGSTRSGGYWWSWIRPPGKLEWIGYIHSGNTYNPSTL 61
DB 25 ESGGGLVKKPSQTLSTLTCTVSGSGSTRSGGYWWSWIRPPGKLEWIGYIHSGNTYNPSTL 84
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSD-----GYTLDMNGGGLTVTVSS 114
DB 85 KSRVTISVDTSKNHFSLRLSSVTADTAVYYCARDDVGLRGNGYGMVWGQGITTVVSS 143

RESULT 11
ADJ32126
ID ADJ32126 standard; protein; 221 AA.
XX
AC ADJ32126;
XX
DT 22-APR-2004 (first entry)
XX
DE Human interferon-gamma antibody heavy chain amino acid sequence SeqID80.
XX
KM antibody; antigen binding domain; interferon-gamma; INF-gamma;
KM antagonist antibody; antiinflammatory; immunosuppressive;
KM autoimmune disease; inflammatory condition; human; heavy chain.
XX
OS Homo sapiens.
XX
PN US2003099647-A1.
XX
PD 29-MAY-2003.
XX
PF 05-OCT-2001; 2001US-00972656.
XX
PR 05-OCT-2001; 2001US-00972656.
XX
PA (DESH/) DESHPANDE R V.
PA (TSAI/) TSAI M.
XX
PI Deshpande RV, Tsai M;
XX
DR WPI; 2003-696068/66.
DR N-PSDB; ADJ32125.
XX
PT New antibody or antigen binding domain, or its fragment, variant or
PT derivative, which binds to an interferon-gamma protein, useful for
PT preparing a composition for preventing or treating inflammatory or
PT autoimmune disorders.
XX
PS Claim 10; SEQ ID NO 80; 113pp; English.
XX
CC This invention relates to a novel antibody or antigen binding domain, or
CC its fragment, variant or derivative, which binds to an interferon-gamma
CC (INF-gamma) protein, and is an antagonist antibody. The invention may be
CC useful for the development of compounds with an antiinflammatory or
CC immunosuppressive activity through action as interferon-gamma agonists. A
CC composition containing the antibody is useful for preventing or treating
CC an autoimmune disease and an inflammatory condition. The present sequence
CC is that of an antibody heavy chain of a human IFN-gamma antibody which
CC may be part of the invention.
XX
SQ Sequence 221 AA;

Query Match 84.7%; Score 520; DB 7; Length 221;
Best Local Similarity 86.7%; Pred. No. 1.3e-36;
Matches 98; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 2 ESGGGLVKKPSQTLSTLTCTVSGSGSTRSGGYWWSWIRPPGKLEWIGYIHSGNTYNPSTL 61
DB 6 ESGGGLVKKPSQTLSTLTCTVSGSGSTRSGGYWWSWIRPPGKLEWIGYIHSGNTYNPSTL 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDGYTLDMNGGGLTVTVSS 114
DB 66 KSRVTISVDTSKNHFSLRLSSVTADTAVYYCARGDGVPYWGQGITTVVSS 118

RESULT 12
ADP03981 ID ADP03981 standard; protein, 121 AA.
XX
AC ADP03981;
XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 151.
XX
KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW cytosolic; colorectal neoplasm; renal cell carcinoma;
KW cervical intraepithelial squamous neoplasia;
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KW gene therapy; murine; mouse; human; heavy chain variable domain.
XX
OS Unidentified.
XX
PN MO2003048328-A2.
XX
PD 12-JUN-2003.
XX
PP 02-DEC-2002; 2002WO-US038550.
XX
PR 03-DEC-2001; 2001US-0337275P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Foltz I, Handa M, Gallo M;
XX
DR WPI; 2003-523295/49.
XX
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS Example 2; SEQ ID NO 151; 89pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 121 AA;
XX
Query Match 84.6%; Score 519.5; DB 7; Length 121;
Best Local Similarity 86.2%; Pred. No. 7.4e-37;
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;
XX
QY 2 ESGPGLVPSQTLSTLTCTVSGSIRSGGYWSWIRQPGKGLWIGYIYHSGNTYNNPSL 61
DB 6 ESGPGLVPSQTLSTLTCTVSGSIRSGGYWSWIRQPGKGLWIGYIYHSGNTYNNPSL 65
XX
QY 62 KSRVTMSYDTSKNHFSRLSSVTADTAIVYYCARSG---DGYTLDNWGGGTLVTYSS 114
DB 66 KSRVTISYDTSKNQPSLKLSSVTADTAIVYYCARVLWFGMDVWGQGITVTYSS 121
XX
RESULT 13
ADP03871 ID ADP03871 standard; protein, 125 AA.
XX
AC ADP03871;

XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 11.
XX
KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW cytosolic; colorectal neoplasm; renal cell carcinoma;
KW cervical intraepithelial squamous neoplasia;
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KW gene therapy; murine; mouse; human; heavy chain variable domain.
XX
OS Unidentified.
XX
PN MO2003048328-A2.
XX
PD 12-JUN-2003.
XX
PP 02-DEC-2002; 2002WO-US038550.
XX
PR 03-DEC-2001; 2001US-0337275P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Foltz I, Handa M, Gallo M;
XX
DR WPI; 2003-523295/49.
XX
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS Claim 1; SEQ ID NO 11; 89pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 125 AA;
XX
Query Match 84.6%; Score 519.5; DB 7; Length 125;
Best Local Similarity 83.3%; Pred. No. 7.7e-37;
Matches 100; Conservative 6; Mismatches 7; Indels 7; Gaps 2;
XX
QY 2 ESGPGLVPSQTLSTLTCTVSGSIRSGGYWSWIRQPGKGLWIGYIYHSGNTYNNPSL 61
DB 6 ESGPGLVPSQTLSTLTCTVSGSIRSGGYWSWIRQPGKGLWIGYIYHSGNTYNNPSL 65
XX
QY 62 KSRVTMSYDTSKNHFSRLSSVTADTAIVYYCARSG---DGYTLDNWGGGTLVTYSS 114
DB 66 KSRVTISYDTSKNQPSLKLSSVTADTAIVYYCARVYDFLTGYDPDAFDIMQGITVTYSS 125
XX
RESULT 14
ADP03970 ID ADP03970 standard; protein, 119 AA.
XX
AC ADP03970;
XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 140.
XX
KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;

KM cytosstatic; colorectal neoplasm; renal cell carcinoma;
KM cervical intraepithelial squamous neoplasia;
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM gene therapy; murine; mouse; human; heavy chain variable domain.
XX Unidentified.
OS
XX MO2003048328-A2.
PN
XX 12-JUN-2003.
PD
XX 02-DEC-2002; 2002WO-US038550.
PF
XX 03-DEC-2001; 2001US-0337275P.
PR
XX (ABGE-) ABGENIX INC.
PA
XX Gudas J, Foltz I, Handa M, Gallo M;
PI WPI; 2003-523295/49.
DR
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or oesophageal tumors.
PS Example 2; SEQ ID NO 140; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumor antigen. The antibody of the invention
CC demonstrates cytosstatic activity and may be useful for treating a tumor,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
CC
XX
SQ Sequence 119 AA;

Query Match 84.3%; Score 517.5; DB 7; Length 119;
Best Local Similarity 86.8%; Pred. No. 1.1e-36;
Matches 99; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 2 ESGPGLVSPQTLSTCTVSGSIRSGGYWMIROPKGLGEMIGIYHSGNTYVNSL 61
Db 6 ESGPGLVSPQTLSTCTVSGSIRSGGYWMIROPKGLGEMIGIYHSGNTYVNSL 65

QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAIVVYCARSD-GYTLDNMGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNHFSLRLSSVTADTAIVVYCARGNVYGMVDWGQGLTVTVSS 119

RESULT 15
AAW78433
ID AAW78433 standard; protein; 123 AA.
XX
AC AAW78433;
XX
DT 11-MAY-1999 (first entry)
XX
DE Antibody heavy chain targeted to obr clone 26.
XX
KM Variant; antibody; heavy chain; light chain; immunoassay;
KM diagnosis; cancer; primer; PCR; amplification; diagnostic.
XX
OS Synthetic.
XX
PN WO9850431-A2.
XX

PD 12-NOV-1998.
XX
XX 30-APR-1998; 98WO-US008762.
PF
XX 02-MAY-1997; 97US-00850058.
PR 24-JUN-1997; 97US-0050661P.
XX
XX (GETH) GENENTECH INC.
PA
XX Arathoon R, Carter PJ, Merchant AM, Presta LG;
PI WPI; 1999-070091/06.
DR
XX
XX Selective preparation of multispecific antibodies - with heteromultimeric
PT heavy chain and common light chain components, useful for, e.g. in vivo
PT diagnosis of cancer.
PS Example 4; Fig 5; 69pp; English.
XX
XX This sequence represents the heavy chain variable region for an antibody
CC that binds to the obr clone 26 protein. The sequence encoding the chain
CC is generated by a new method for preparing a multispecific Ab comprising
CC a first polypeptide (PP) and at least 1 extra PP, where: (i) the first PP
CC comprises a multimerisation domain (MD) forming an interface positioned
CC to interact with an interface of a MD of the extra PP; and (ii) the first
CC and extra PPs each have a binding domain, which comprises a heavy chain
CC and a light chain, where the variable light chains of the first and extra
CC PPs comprise a common sequence. The method comprises: (a) culturing a
CC host cell comprising nucleic acid encoding the first PP and extra PP, and
CC the variable light chain, such that the nucleic acid is expressed; and
CC (b) recovering the multispecific Ab from the culture. The method prepares
CC heteromultimeric PPs, such as bispecific Abs, bispecific immunoconjugates
CC and Ab-immunoconjugate chimeras. The method allows for the enhanced
CC formation of the desired heteromultimer relative to the undesired
CC heteromultimers and homomultimers. The Abs can be used in immunoassays
CC and for the in vitro or in vivo diagnosis of various diseases, such as
CC cancer.
XX
SQ Sequence 123 AA;

Query Match 84.1%; Score 516.5; DB 2; Length 123;
Best Local Similarity 84.0%; Pred. No. 1.4e-36;
Matches 100; Conservative 5; Mismatches 9; Indels 5; Gaps 1;

QY 1 LESGPGLVSPQTLSTCTVSGSIRSGGYWMIROPKGLGEMIGIYHSGNTYVNS 60
Db 5 VESGPGLVSPQTLSTCTVSGSIRSGGYWMIROPKGLGEMIGIYHSGNTYVNS 64

QY 61 LKSRVTMSVDTSKNHFSLRLSSVTADTAIVVYCARSD-----GYTLDNMGQGLTVTVSS 114
Db 65 LKSRVTISVDTSKNHFSLRLSSVTADTAIVVYCARVLEDDYGSGASDYGQGLTVTVSS 123

Search completed: July 26, 2005, 09:19:19
Job time : 86.3273 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:26:32 ; Search time 72.5455 Seconds

(without alignments)
611.274 Million cell updates/sec

Title: US-10-027-725A-9

Perfect score: 614
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	614	100.0	114	US-10-027-725A-9	Sequence 9, Appl1
2	600	97.7	114	US-10-027-725A-8	Sequence 8, Appl1
3	556	90.6	114	US-10-027-725A-7	Sequence 7, Appl1
4	524.5	85.4	121	US-10-309-762-152	Sequence 152, App
5	524	85.3	118	US-10-309-762-138	Sequence 138, App
6	523.5	85.3	123	US-10-309-762-10	Sequence 10, Appl
7	521	84.9	120	US-10-309-762-13	Sequence 13, Appl
8	521	84.9	120	US-10-309-762-144	Sequence 144, App
9	520	84.7	122	US-10-309-762-147	Sequence 147, App
10	520	84.7	221	US-09-972-656-80	Sequence 80, Appl
11	519.5	84.6	121	US-10-309-762-151	Sequence 151, App

12	519.5	84.6	125	US-10-309-762-11	Sequence 11, Appl
13	518	84.4	121	US-10-805-177-56	Sequence 56, Appl
14	517.5	84.3	119	US-10-309-762-140	Sequence 140, App
15	517	84.2	123	US-10-805-177-53	Sequence 53, Appl
16	516.5	84.1	123	US-10-309-762-12	Sequence 12, Appl
17	516.5	84.1	144	US-10-893-576-35	Sequence 35, Appl
18	516	84.0	124	US-10-309-762-75	Sequence 75, Appl
19	516	84.0	143	US-10-309-762-96	Sequence 96, Appl
20	515.5	84.0	117	US-10-330-613-13	Sequence 13, Appl
21	515.5	84.0	117	US-10-330-613-13	Sequence 13, Appl
22	515.5	84.0	117	US-10-660-357-13	Sequence 13, Appl
23	514	83.7	120	US-10-309-762-128	Sequence 128, App
24	514	83.7	120	US-10-309-762-139	Sequence 139, App
25	514	83.7	121	US-10-308-817-137	Sequence 137, App
26	514	83.7	121	US-10-453-698-137	Sequence 137, App
27	514	83.7	122	US-10-984-960A-56	Sequence 56, Appl
28	513	83.6	116	US-10-309-762-127	Sequence 127, App
29	512.5	83.5	125	US-10-309-762-8	Sequence 8, Appl1
30	512.5	83.5	125	US-10-309-762-16	Sequence 16, Appl
31	512.5	83.5	480	US-10-910-901-6	Sequence 6, Appl1
32	511.5	83.3	119	US-10-309-762-131	Sequence 131, App
33	511.5	83.3	140	US-10-893-576-41	Sequence 41, Appl
34	511	83.2	110	US-10-309-762-74	Sequence 74, Appl
35	510.5	83.1	123	US-10-309-762-9	Sequence 9, Appl1
36	510.5	83.1	127	US-10-309-762-14	Sequence 14, Appl
37	510.5	83.1	148	US-10-893-576-31	Sequence 31, Appl
38	509	82.9	149	US-10-910-901-22	Sequence 22, Appl
39	508.5	82.8	123	US-10-893-576-190	Sequence 190, App
40	508.5	82.8	123	US-10-309-762-153	Sequence 153, App
41	508	82.7	128	US-10-727-155-2	Sequence 2, App
42	508	82.7	128	US-10-727-155-10	Sequence 10, Appl
43	508	82.7	128	US-10-727-155-30	Sequence 30, Appl
44	508	82.7	172	US-10-153-382-21	Sequence 21, Appl
45	508	82.7	172	US-10-612-497-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-10-027-725A-9
; Sequence 9, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific Ige-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-9

Query Match	100.0%	Score 614;	DB 14;	Length 114;
Best Local Similarity	100.0%	Pred. No. 1,1e-47;		
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QY	61	LKSRVTMSVDSKHFSLRLSGVTADTAIVYVCASDGTLDNMGQGLTVTVSS	114	
DB	61	LKSRVTMSVDSKHFSLRLSGVTADTAIVYVCASDGTLDNMGQGLTVTVSS	114	

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US-10-027-725A-8
; Sequence 8, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-8
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Query Match          97.7%; Score 600; DB 14; Length 114;
Best Local Similarity 96.5%; Pred. No. 2e-46;
Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 LESGPGLVKPSQTLSTCTVSGSIRSGYVSWIRQPGKLEWIGIYHSGNTYVPS 60
Db 1 LESGPGLVKPSQTLSTCTVSGSIRSGYVSWIRQPGKLEWIGIYHSGNTYVPS 60
Qy 61 LKSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDGYTLDMNGQGLTVTVSS 114
Db 61 LKSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDGYTLDMNGQGLTVTVSS 114
```

```
RESULT 3
US-10-027-725A-7
; Sequence 7, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-7
```

```
Query Match          90.6%; Score 556; DB 14; Length 114;
Best Local Similarity 90.4%; Pred. No. 1.8e-42;
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy 1 LESGPGLVKPSQTLSTCTVSGSIRSGYVSWIRQPGKLEWIGIYHSGNTYVPS 60
Db 1 LESGPGLVKPSQTLSTCTVSGSIRSGYVSWIRQPGKLEWIGIYHSGNTYVPS 60
Qy 61 LKSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDGYTLDMNGQGLTVTVSS 114
Db 61 LKSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDGYTLDMNGQGLTVTVSS 114
```

```
RESULT 4
US-10-309-762-152
; Sequence 152, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudus, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
```

```
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309, 762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-152
```

```
Query Match          85.4%; Score 524.5; DB 15; Length 121;
Best Local Similarity 86.2%; Pred. No. 1.3e-39;
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;
```

```
Qy 2 ESGPGLVKPSQTLSTCTVSGSIRSGYVSWIRQPGKLEWIGIYHSGNTYVPSL 61
Db 6 ESGPGLVKPSQTLSTCTVSGSIRSGYVSWIRQPGKLEWIGIYHSGNTYVPSL 65
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSD--GYTLDMNGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNHFSLRLSSVTADTAVYYCAYDILITGYAFDIDWQGLTVTVSS 121
```

```
RESULT 5
US-10-309-762-138
; Sequence 138, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudus, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309, 762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-138
```

```
Query Match          85.3%; Score 524; DB 15; Length 118;
Best Local Similarity 86.5%; Pred. No. 1.4e-39;
Matches 100; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
```

```
Qy 2 ESGPGLVKPSQTLSTCTVSGSIRSGYVSWIRQPGKLEWIGIYHSGNTYVPSL 61
Db 6 ESGPGLVKPSQTLSTCTVSGSIRSGYVSWIRQPGKLEWIGIYHSGNTYVPSL 65
Qy 62 KSRVTMSVDTSKNHFSLRLSSVTADTAVYYCARSDGYTLDMNGQGLTVTVSS 114
Db 66 KSRVTISVDTSKNHFSLRLSSVTADTAVYYCAYDILITGYAFDIDWQGLTVTVSS 118
```

```
RESULT 6
US-10-309-762-10
; Sequence 10, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudus, Jean
; APPLICANT: Foltz, Ian
```

```
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-10
```

```
Query Match      85.3%; Score 523.5; DB 15; Length 123;
Best Local Similarity 85.6%; Pred. No. 1.7e-39;
Matches 101; Conservative 5; Mismatches 7; Indels 5; Gaps 1;
```

```
QY 2 ESGPGLVPSQTLILCTVSGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNSPL 61
DB 6 ESGPGLVPSQTLILCTVSGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNSPL 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAADTAAYVYCARSDGTT---LDNWGGGTLVTYSS 114
DB 66 KSRVTISVDTSKNPFSLKLSLSSVTADTAADTAAYVYCARSDGTT---LDNWGGGTLVTYSS 123
```

```
RESULT 7
US-10-309-762-13
```

```
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-13
```

```
Query Match      84.9%; Score 521; DB 15; Length 120;
Best Local Similarity 87.1%; Pred. No. 2.7e-39;
Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;
```

```
QY 2 ESGPGLVPSQTLILCTVSGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNSPL 61
DB 6 ESGPGLVPSQTLILCTVSGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNSPL 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAADTAAYVYCARSDGTT---LDNWGGGTLVTYSS 114
DB 66 KSRVTISVDTSKNPFSLKLSLSSVTADTAADTAAYVYCARSDGTT---LDNWGGGTLVTYSS 120
```

```
RESULT 8
US-10-309-762-14
; Sequence 14, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
```

```
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-14
```

```
Query Match      84.9%; Score 521; DB 15; Length 120;
Best Local Similarity 87.1%; Pred. No. 2.7e-39;
Matches 101; Conservative 5; Mismatches 6; Indels 4; Gaps 2;
```

```
QY 2 ESGPGLVPSQTLILCTVSGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNSPL 61
DB 6 ESGPGLVPSQTLILCTVSGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNSPL 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAADTAAYVYCARSDGTT---LDNWGGGTLVTYSS 114
DB 66 KSRVTISVDTSKNPFSLKLSLSSVTADTAADTAAYVYCARSDGTT---LDNWGGGTLVTYSS 120
```

```
RESULT 9
US-10-309-762-147
```

```
; Sequence 147, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-147
```

```
Query Match      84.9%; Score 521; DB 15; Length 122;
Best Local Similarity 85.5%; Pred. No. 2.8e-39;
Matches 100; Conservative 5; Mismatches 8; Indels 4; Gaps 1;
```

```
QY 2 ESGPGLVPSQTLILCTVSGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNSPL 61
DB 6 ESGPGLVPSQTLILCTVSGSIRSGGYWSWIRPPGKLEWIGYIYHSGNTYNSPL 65
QY 62 KSRVTMSVDTSKNHFSLRLSSVTADTAADTAAYVYCARSDGTT---SDGTTLDNWGGGTLVTYSS 114
DB 66 KSRVTISVDTSKNPFSLKLSLSSVTADTAADTAAYVYCARSDGTT---SDGTTLDNWGGGTLVTYSS 122
```

```
RESULT 10
US-09-972-656-80
; Sequence 80, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Deshpande, Rajendra
; APPLICANT: Isai, Mel-Wel
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-80
```

```

Query Match      84.7%; Score 520; DB 10; Length 221;
Best Local Similarity 86.7%; Pred. No. 6,2e-39;
Matches 98; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
```

```

QY 2 ESGPGLVPSQTLSTCTVSGSIRSGLYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 61
DB 6 ESGPGLVPSQTLSTCTVSGSIRSGLYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 65
QY 62 KSRVTMSVDTSKNHPSLRSLSSVTADTAAYVYCARSDGTYTLDNWGCGTLVTYSS 114
DB 66 KSRVTISVDTSKNQPSLKLSSVTADTAAYVYCARSDGTYTLVTYSS 118
```

RESULT 11

```

US-10-309-762-151
; Sequence 151, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masaahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-151
```

```

Query Match      84.6%; Score 519.5; DB 15; Length 121;
Best Local Similarity 86.2%; Pred. No. 3.7e-39;
Matches 100; Conservative 5; Mismatches 8; Indels 3; Gaps 1;
```

```

QY 2 ESGPGLVPSQTLSTCTVSGSIRSGLYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 61
DB 6 ESGPGLVPSQTLSTCTVSGSIRSGLYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 65
QY 62 KSRVTMSVDTSKNHPSLRSLSSVTADTAAYVYCARSDGTYTLDNWGCGTLVTYSS 114
DB 66 KSRVTISVDTSKNQPSLKLSSVTADTAAYVYCARSLTLMFGYGMVWGCGTLVTYSS 121
```

RESULT 12

```

US-10-309-762-11
; Sequence 11, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masaahisa
```

```

; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-11
```

```

Query Match      84.6%; Score 519.5; DB 15; Length 125;
Best Local Similarity 83.3%; Pred. No. 3.9e-39;
Matches 100; Conservative 6; Mismatches 7; Indels 7; Gaps 2;
```

```

QY 2 ESGPGLVPSQTLSTCTVSGSIRSGLYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 61
DB 6 ESGPGLVPSQTLSTCTVSGSIRSGLYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 65
QY 62 KSRVTMSVDTSKNHPSLRSLSSVTADTAAYVYCARSDGTYTLDNWGCGTLVTYSS 114
DB 66 KSRVTISVDTSKNQPSLKLSSVTADTAAYVYCARSDGTYTLVTYSS 125
```

RESULT 13

```

US-10-805-177-56
; Sequence 56, Application US/10805177
; Publication No. US2005008449A1
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Chen, Francine
; APPLICANT: Berzbeh, Binyam
; APPLICANT: Tse, Kam Fai
; APPLICANT: Foltz, Ian
; APPLICANT: Measri, Michael
; APPLICANT: Measri, Michael
; APPLICANT: Starling, Gary
; APPLICANT: Meares, Peter
; APPLICANT: Khramtsov, Nikolai
; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
; TITLE OF INVENTION: DOMAIN AND MUCLIN DOMAIN 1 (TIM-1) ANTIGEN AND USES THEREOF
; FILE REFERENCE: ABXCUR.006A
; CURRENT APPLICATION NUMBER: US/10/805,177
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/456,652
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-805-177-56
```

```

Query Match      84.4%; Score 518; DB 17; Length 121;
Best Local Similarity 84.3%; Pred. No. 5.1e-39;
Matches 97; Conservative 9; Mismatches 7; Indels 2; Gaps 1;
```

```

QY 2 ESGPGLVPSQTLSTCTVSGSIRSGLYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 61
DB 6 ESGPGLVPSQTLSTCTVSGSIRSGLYWSWIRPPGKLEWIGYIYHSGNTYNPSTL 65
QY 62 KSRVTMSVDTSKNHPSLRSLSSVTADTAAYVYCARSDGTYTLDNWGCGTLVTYSS 114
DB 66 KSRVTISVDTSKNQPSLKLSSVTADTAAYVYCARSDGTYTLVTYSS 120
```

RESULT 14

US-10-309-762-140
; Sequence 140, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX 027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-140

Query Match 84.3%; Score 517.5; DB 15; Length 119;
Best Local Similarity 86.8%; Pred. No. 5.6e-39;
Matches 99; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Qy 2 ESGGGLVPSQTLSTCTVSGSGSIRSGGYWWSWIRQPPKGLIEWIGYTHSGNTYYNPSL 61
Db 6 ESGGGLVPSQTLSTCTVSGSGSISGGYWWSWIRQHPKGLIEWIGYTHSGNTYYNPSL 65

Qy 62 KSRVTMSVDTSKNHSRLSSVTADTAIVYYCARSD-GYTLDMWGQGLVTVSS 114
Db 66 KSRVTISVDTSKNQPSLKLSSVTADTAIVYYCARNTYYGMDWVGQGLTVTVSS 119

RESULT 15

US-10-805-177-53
; Sequence 53, Application US/10805177
; Publication No. US20050084449A1
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Chen, Francine
; APPLICANT: Bezabeh, Binyam
; APPLICANT: Foltz, Ian
; APPLICANT: Jeffers, Michael
; APPLICANT: Meeri, Mehdi
; APPLICANT: Starling, Gary
; APPLICANT: Mezes, Peter
; APPLICANT: Khramtsov, Nikolai
; TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN
; FILE REFERENCE: AEXCUR.006A
; CURRENT APPLICATION NUMBER: US/10/805,177
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/456,652
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-805-177-53

Query Match 84.2%; Score 517; DB 17; Length 125;
Best Local Similarity 83.2%; Pred. No. 6.5e-39;
Matches 99; Conservative 7; Mismatches 7; Indels 6; Gaps 1;

Qy 2 ESGGGLVPSQTLSTCTVSGSGSIRSGGYWWSWIRQPPKGLIEWIGYTHSGNTYYNPSL 61
Db 6 ESGGGLVPSQTLSTCTVSGSGSISGGYWWSWIRQHPKGLIEWIGYTHSGNTYYNPSL 65

Qy 62 KSRVTMSVDTSKNHSRLSSVTADTAIVYYCARSDGYT-----LDNWGQGLVTVSS 114
Db 66 KSRVTISVDTSKNQPSLKLSSVTADTAIVYYCARNNNNSSSWNNNFDYWGQGLVTVSS 124

Search completed: July 26, 2005, 10:05:19
Job time : 73.7121 secs

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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:09:56 ; Search time 21.5909 Seconds
(without alignments)
394.147 Million cell updates/sec

Title: US-10-027-725a-8

Perfect score: 614

Sequence: 1 LBEGPGLVKSQSLTLCV.....RSDGYLDMNGGTLTVSS 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	507	82.6	473	3	US-09-049-672A-4
2	494	80.5	122	1	US-08-360-125-11
3	494	80.5	122	2	US-08-450-578-11
4	494	80.5	122	2	US-09-017-628-11
5	494	80.5	122	2	US-09-014-880-11
6	494	80.5	122	2	US-08-450-363-11
7	494	80.5	122	4	US-09-467-903-11
8	494	80.5	172	4	US-09-472-087-7
9	494	80.5	172	4	US-09-472-087-86
10	490.5	79.9	117	4	US-09-720-493-2
11	488.5	79.6	119	3	US-09-025-769B-39
12	488.5	79.6	119	3	US-09-025-769B-65
13	488.5	79.6	119	3	US-09-490-070A-39
14	488.5	79.6	119	4	US-09-490-070A-65
15	488.5	79.6	119	4	US-09-490-153-39
16	488.5	79.6	119	4	US-09-490-153-65
17	488.5	79.6	119	4	US-09-490-324-39
18	488.5	79.6	119	4	US-09-490-324-65
19	488	79.5	118	3	US-09-025-769B-25
20	488	79.5	118	4	US-09-490-070A-25
21	488	79.5	118	4	US-09-490-153-25
22	488	79.5	118	4	US-09-490-153-39
23	478	77.9	487	4	US-09-800-729-145
24	477	77.7	120	4	US-09-424-840B-20
25	473.5	77.1	119	1	US-08-360-125-5
26	473.5	77.1	119	2	US-08-450-578-5
27	473.5	77.1	119	2	US-09-017-628-5

28	473.5	77.1	119	2	US-09-014-880-5	Sequence 5, Appli
29	473.5	77.1	119	4	US-08-450-363-5	Sequence 5, Appli
30	473.5	77.1	119	4	US-09-467-903-5	Sequence 5, Appli
31	459.5	74.8	142	2	US-08-480-774A-2	Sequence 2, Appli
32	458	74.6	244	3	US-08-918-148-79	Sequence 79, Appli
33	458	74.6	244	4	US-09-138-091A-77	Sequence 77, Appli
34	453	73.8	118	3	US-08-545-809A-116	Sequence 116, App
35	453	73.8	118	1	US-08-276-852-142	Sequence 142, App
36	453	73.8	126	1	US-08-899-575-142	Sequence 142, App
37	453	73.8	126	1	US-08-899-575-142	Sequence 142, App
38	453	73.8	126	5	PCT-US95-08743-142	Sequence 142, App
39	451.5	73.5	155	4	US-09-471-276-888	Sequence 888, App
40	446.5	72.7	119	2	US-08-652-816A-10	Sequence 10, Appli
41	446	72.6	118	3	US-08-545-809A-123	Sequence 123, App
42	446	72.6	278	3	US-09-260-527-3	Sequence 3, Appli
43	445.5	72.6	123	3	US-08-793-450-4	Sequence 4, Appli
44	445.5	72.6	472	3	US-08-793-450-8	Sequence 8, Appli
45	445	72.5	118	4	US-09-343-698-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-049-672A-4
Sequence 4, Application US/09049672A
Patent No. 6115941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HERewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ceirone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANTU01

```
CLONE: 1513264
US-09-049-672A-4

Query Match      82.6%; Score 507; DB 3; Length 473;
Best Local Similarity 79.8%; Pred. No. 1e-42;
Matches 95; Conservative 9; Mismatches 9; Indels 6; Gaps 1;

Cy 2 ESGPGLVKEPSQTLSTLTCTVSGGSIIRSGGYMSWVRQPGKGLWIGNIYHSQNTYVPSL 61
Db 25 ESGPGLVKEPSQTLSTLTCTVSGGSIIRSGGYMSWVRQPGKGLWIGNIYHSQNTYVPSL 84

Cy 62 KSRITMSVDPSTKXHFSLRTSVTAADTAAYVYCARSD-----GYTLDMNGGGLVTYSS 114
Db 85 KSRVITISVDTSKQFSLKLSSTVTAADTAAYVYCARSDVGLRGNGYGMVWGQGLVTYSS 143

RESULT 2
US-08-360-125-11
Sequence 11, Application US/08360125
Patent No. 5767246
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360.125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-11

Query Match      80.5%; Score 494; DB 1; Length 122;
Best Local Similarity 78.6%; Pred. No. 4.1e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

Cy 2 ESGPGLVKEPSQTLSTLTCTVSGGSIIRSGGYMSWVRQPGKGLWIGNIYHSQNTYVPSL 61
Db 6 ESGPGLVKEPSQTLSTLTCTVSGGSIIRSGGYMSWVRQPGKGLWIGNIYHSQNTYVPSL 65

Cy 62 KSRITMSVDPSTKXHFSLRTSVTAADTAAYVYCARSD-----GYTLDMNGGGLVTYSS 114
Db 66 KSRVITISVDTSKQFSLKLSSTVTAADTAAYVYCARSGYGYGMVWGQGLVTYSS 122

RESULT 3
US-08-450-578-11
Sequence 11, Application US/08450578
Patent No. 5837845
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450.578
```


PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
US-09-014-880-11

Query Match 80.5%; Score 494; DB 2; Length 122;
Best Local Similarity 78.6%; Pred. No. 4,1e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

Qy 2 ESGPGLVKEPSQTLSTLTCTVSGSIRSGGYMSWVRQPGKLEWIGNIYHSGNTYNPSTL 61
Db 6 ESGPGLVKEPSQTLSTLTCTVSGSIRSGGYMSWVRQPGKLEWIGNIYHSGNTYNPSTL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSD---GYTLDMWGQGLTVVSS 114
Db 66 KSRVITSVDTSKNHFSLRLTSVTAADTAAYVYCARSGYGYGMDWVGQGLTVVSS 122

RESULT 6

US-08-450-363-11
Sequence 11, Application US/08450363
Patent No. 6436434
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 6436434hiko ITO
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,363
FILING DATE: May 25, 1995
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:

US-08-450-363-11

Query Match 80.5%; Score 494; DB 4; Length 122;
Best Local Similarity 78.6%; Pred. No. 4,1e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;

Qy 2 ESGPGLVKEPSQTLSTLTCTVSGSIRSGGYMSWVRQPGKLEWIGNIYHSGNTYNPSTL 61
Db 6 ESGPGLVKEPSQTLSTLTCTVSGSIRSGGYMSWVRQPGKLEWIGNIYHSGNTYNPSTL 65
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSD---GYTLDMWGQGLTVVSS 114
Db 66 KSRVITSVDTSKNHFSLRLTSVTAADTAAYVYCARSGYGYGMDWVGQGLTVVSS 122

RESULT 7

US-09-467-903-11
Sequence 11, Application US/09467903
Patent No. 6787153
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA

No. 67817531hiko ITO
Kazuhiko NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
Specifically Binding to Surface Antigen of Cancer
Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 203 K Street, N.W., #800
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,903
FILING DATE: 21-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,363
FILING DATE: May 25, 1995
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER: JP158859/1991
FILING DATE: June 28, 1991
APPLICATION NUMBER: JP158860/1991
FILING DATE: June 28, 1991
APPLICATION NUMBER: JP158861/1991
FILING DATE: June 28, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: <Unknown>
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
HYPOTHEICAL: <Unknown>
ANTI-SENSE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: <Unknown>
STRAIN: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:

OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-467-903-11
Query Match 80.5%; Score 494; DB 4; Length 122;
Best Local Similarity 78.6%; Pred. No. 4; 1e-42;
Matches 92; Conservative 10; Mismatches 11; Indels 4; Gaps 1;
QY 2 ESGPGLVPSQTLSTCTVSGSIRSGGYWVWROPKGLWIGNIYHSGNTYVPSL 61
DB 6 ESGPGLVPSQTLSTCTVSGSIRSGGYWVWROPKGLWIGNIYHSGNTYVPSL 65
QY 62 KSRITMSVDTSKNHFSRLTSVTAADTAIVYVCARSD---GYLDNMGQGLTVVSS 114
DB 66 KSRITMSVDTSKNHFSRLTSVTAADTAIVYVCARSGSYGYVYGMVDWGGGTVTVSS 122
RESULT 8
US-09-472-087-7
Sequence 7, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, BILLEN E.
APPLICANT: HANKS, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-7
Query Match 80.5%; Score 494; DB 4; Length 172;
Best Local Similarity 81.6%; Pred. No. 6; 1e-42;
Matches 93; Conservative 8; Mismatches 11; Indels 2; Gaps 1;
QY 3 SGPLVPSQTLSTCTVSGSIRSGGYWVWROPKGLWIGNIYHSGNTYVPSL 62
DB 1 SGPLVPSQTLSTCTVSGSIRSGGYWVWROPKGLWIGNIYHSGNTYVPSL 60
QY 63 SRTMSVDTSKNHFSLRLTSVTAADTAIVYVCARSDG--YTLDMGQGLTVVSS 114
DB 61 SRTMSVDTSKNHFSLRLTSVTAADTAIVYVCARSDGYGIDWGGGTVTVSS 114
RESULT 9
US-09-472-087-86
Sequence 86, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:

APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MOELLER, EILEEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 86
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-86

Query Match 80.5%; Score 494; DB 4; Length 172;
Best Local Similarity 81.6%; Pred. No. 6.1e-42;
Matches 92; Conservative 8; Mismatches 11; Indels 2; Gaps 1;

QY 3 SGGGLVPSQTLSTCTVSGSIRSGYYSWVRQPPGKLEWIGNIYHSGNTYYPSSLK 62
DB 1 SGGGLVPSQTLSTCTVSGSIRSGYYSWVRQPPGKLEWIGNIYHSGNTYYPSSLK 60
QY 63 SRTTMSVDTSKNHFSLRTSVTAADTAAYVCARSDG--YTLDMNGOGLTVTVSS 114
DB 61 SRTTISVDTSKNHFSLKLSVTAADTAAYVCARSDGYIGIDVWGOGTLTVTVSS 114

RESULT 10
US-09-720-493-2
Sequence 2, Application US/09720493
Patent No. 6827925
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Williams, Andrew J
APPLICANT: Tempest, Philip R
APPLICANT: Holter, Thor L
APPLICANT: Main, Sarah H
APPLICANT: Jackson, Helen
APPLICANT: Daxmolai, Olaalekan
TITLE OF INVENTION: Improvements relating to antibodies
FILE REFERENCE: AHB/CP575333
CURRENT APPLICATION NUMBER: US/09/720,493
CURRENT FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: GB 9814383.7
PRIOR FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-09-720-493-2

Query Match 79.9%; Score 490.5; DB 4; Length 117;
Best Local Similarity 81.4%; Pred. No. 8.7e-42;
Matches 92; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 2 ESGGGLVPSQTLSTCTVSGSIRSGYYSWVRQPPGKLEWIGNIYHSGNTYYPSSL 61
DB 6 ESGGGLVPSQTLSTCTVSGSIRSGYYSWVRQPPGKLEWIGNIYHSGNTYYPSSL 64
QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAAYVCARSDGYTLDMNGOGLTVTVSS 114
DB 65 KSRITISVDTSKNHFSLKLSVTAADTAAYVCARSKMSPFDYWGOGTLTVTVSS 117

RESULT 11
US-09-025-769B-39
Sequence 39, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-39

Query Match 79.6%; Score 488.5; DB 3; Length 119;
Best Local Similarity 81.9%; Pred. No. 1.4e-41;
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;

QY 2 ESGGGLVPSQTLSTCTVSGSIRSGYYSWVRQPPGKLEWIGNIYHSGNTYYPSSL 61
DB 6 ESGGGLVPSQTLSTCTVSGSIRSGYYSWVRQPPGKLEWIGNIYHSGNTYYPSSL 63
QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAAYVCAR--SDG--YTLDMNGOGLTVTVSS 114
DB 64 KSRITISVDTSKNHFSLKLSVTAADTAAYVCARWGSDGFYADYWGOGTLTVTVSS 119

RESULT 12
US-09-025-769B-65
Sequence 65, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10021
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/025,769B
;; FILING DATE: 18-FEB-1998
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: EP 95 11 3021.0
;; FILING DATE: 18-AUG-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: James F. Haley, Jr., Esq.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: MORPHO/5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)596-9000
;; TELEFAX: (212)596-9090
;;
;; INFORMATION FOR SEQ ID NO: 65:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
;; US-09-025-769B-65

Query Match 79.6%; Score 488.5; DB 3; Length 119;
Best Local Similarity 81.9%; Pred. No. 1.4e-41;
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;

Qy 2 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWVROPKGLKLEWIGNIYHSGNTYNSPL 61
Db 6 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWVROPKGLKLEWIGNIYHSGNTYNSPL 63
Qy 62 KSRITMSVDTSKNHFSLRTSVTAADTAIVYYCAR--SDG-YTLDMWQGLTVTVSS 114
Db 64 KSRVITISVDTSKNHFSLRTSVTAADTAIVYYCARWGDGDFYAMDYWGGLTVTVSS 119

RESULT 13
US-09-490-070A-39
; Sequence 39, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Plueckthun, Andreas
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/490,070A
;; FILING DATE: 24-Jan-2000
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 95 11 3021.0
;; FILING DATE: 18-AUG-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Colin G. Sandercock, Esq.
;; REGISTRATION NUMBER: 31,298
;; REFERENCE/DOCKET NUMBER: 37629-0005
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 912-2000
;; TELEFAX: (202) 912-2020
;;
;; INFORMATION FOR SEQ ID NO: 39:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
;;
;; US-09-490-070A-39

Query Match 79.6%; Score 488.5; DB 4; Length 119;
Best Local Similarity 81.9%; Pred. No. 1.4e-41;
Matches 95; Conservative 9; Mismatches 7; Indels 5; Gaps 3;

Qy 2 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWVROPKGLKLEWIGNIYHSGNTYNSPL 61
Db 6 ESGPGLVPSQTLSTCTVSGSIRSGGYMSWVROPKGLKLEWIGNIYHSGNTYNSPL 63
Qy 62 KSRITMSVDTSKNHFSLRTSVTAADTAIVYYCAR--SDG-YTLDMWQGLTVTVSS 114
Db 64 KSRVITISVDTSKNHFSLRTSVTAADTAIVYYCARWGDGDFYAMDYWGGLTVTVSS 119

RESULT 14
US-09-490-070A-65
; Sequence 65, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Plueckthun, Andreas
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000

```

? TELEFAX: (202) 912-2020
? INFORMATION FOR SEQ ID NO: 65:
? SEQUENCE CHARACTERISTICS:
?     LENGTH: 119 amino acids
?     TYPE: amino acid
?     TOPOLOGY: linear
?     MOLECULE TYPE: protein
?     SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-070A-65

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Query Match	79.6%;	Score	488.5;	DB	4;	Length	119;
Best Local Similarity	81.9%;	Pred. No.	1.4e-41;				
Matches	95;	Conservative	9;	Mismatches	7;	Indels	5;
						Gaps	3;

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QY      62 KSRITMSVDTSKQHFSLRLTSVTAADTAIVYCAR--SDG-YTLDNNGGTLTVSS 114
      |||::||| |||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
Db      64 KSRVTISVDTSKQFSLRLTSVTAADTAIVYCARNGGDGYAMDYMGGTLTVSS 119

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Query Match	79.6%;	Score 488.5;	DB 4;	Length 119;
Best Local Similarity	81.9%;	Pred. No. 1.4e-41;		
Matches 95; Conservative	9;	Mismatches 7;	Indels 5;	Gaps 3;

Search completed: July 26, 2005, 09:29:59
Job time : 22.5909 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:26:32 ; Search time 72.5455 Seconds
(without alignments)
611.274 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614
Sequence: 1 LBSGPGLVKPSQTLSTCTV.....RSDGYTLDMWGQGLTVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubppaa/US11_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	614	100.0	114	US-10-027-725A-8	Sequence 8, Appl1
2	600	97.7	114	US-10-027-725A-9	Sequence 9, Appl1
3	546	88.9	114	US-10-027-725A-7	Sequence 7, Appl1
4	514.5	83.8	140	US-10-893-576-41	Sequence 41, Appl1
5	511	83.2	128	US-10-727-155-2	Sequence 2, Appl1
6	511	83.2	128	US-10-727-155-10	Sequence 10, Appl1
7	511	83.2	128	US-10-727-155-30	Sequence 30, Appl1
8	510.5	83.1	121	US-10-309-762-152	Sequence 152, App
9	510	83.1	118	US-10-309-762-138	Sequence 138, App
10	509.5	83.0	123	US-10-309-762-10	Sequence 10, Appl1
11	507.5	82.7	125	US-10-309-762-11	Sequence 11, Appl1

12	507	82.6	120	US-10-309-762-13	Sequence 13, Appl1
13	507	82.6	120	US-10-309-762-144	Sequence 144, App
14	507	82.6	122	US-10-309-762-147	Sequence 147, App
15	506.5	82.5	119	US-10-893-576-189	Sequence 189, App
16	506	82.4	221	US-09-972-656-80	Sequence 80, Appl1
17	505.5	82.3	121	US-10-309-762-151	Sequence 151, App
18	505	82.2	128	US-10-727-155-26	Sequence 26, Appl1
19	504.5	82.2	117	US-10-330-613-13	Sequence 13, Appl1
20	504.5	82.2	117	US-10-330-530-13	Sequence 13, Appl1
21	504.5	82.2	117	US-10-660-357-13	Sequence 13, Appl1
22	504	82.1	121	US-10-805-177-56	Sequence 56, Appl1
23	503.5	82.0	119	US-10-309-762-140	Sequence 140, App
24	503	81.9	125	US-10-805-177-53	Sequence 53, Appl1
25	502.5	81.8	123	US-10-309-762-12	Sequence 12, Appl1
26	502.5	81.8	144	US-10-893-576-35	Sequence 35, Appl1
27	502	81.8	122	US-10-984-660A-56	Sequence 56, Appl1
28	502	81.8	124	US-10-309-762-75	Sequence 75, Appl1
29	502	81.8	143	US-10-309-762-96	Sequence 96, Appl1
30	501	81.6	252	US-09-880-748-1329	Sequence 1329, App
31	501	81.6	252	US-10-293-418-1329	Sequence 1329, App
32	500	81.4	120	US-10-309-762-128	Sequence 128, App
33	500	81.4	120	US-10-309-762-139	Sequence 139, App
34	500	81.4	121	US-10-308-817-137	Sequence 137, App
35	500	81.4	121	US-10-453-698-137	Sequence 137, App
36	500	81.4	126	US-09-974-449-6	Sequence 6, Appl1
37	500	81.4	16	US-10-652-502A-18	Sequence 18, Appl1
38	499.5	81.4	135	US-10-388-214A-34	Sequence 34, Appl1
39	499	81.3	116	US-10-309-762-127	Sequence 127, App
40	499	81.3	120	US-10-706-689-40	Sequence 40, Appl1
41	499	81.3	120	US-10-988-360-40	Sequence 40, Appl1
42	498.5	81.2	125	US-10-309-762-8	Sequence 8, Appl1
43	498.5	81.2	135	US-10-309-762-16	Sequence 16, Appl1
44	498.5	81.2	480	US-10-910-901-6	Sequence 6, Appl1
45	498	81.1	135	US-10-910-901-23	Sequence 23, Appl1

ALIGNMENTS

RESULT 1
US-10-027-725A-8
; Sequence 8, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OR INVENTION: Group 2 Allergen Specific IGF-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259, 436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-8
Query Match 100.0%; Score 614; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 7, 8e-48;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 LBSGPGLVKPSQTLSTCTVSGSIRSGGYWVWRPPGKGLMIGNIYHSNTYNP 60
Db 1 LBSGPGLVKPSQTLSTCTVSGSIRSGGYWVWRPPGKGLMIGNIYHSNTYNP 60
Cy 61 LKSRITSVDTSKNHFSLRTSVTAADTAAYYCARSDGYTLDMWGQGLTVSS 114
Db 61 LKSRITSVDTSKNHFSLRTSVTAADTAAYYCARSDGYTLDMWGQGLTVSS 114
RESULT 2

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US-10-027-725A-9
; Sequence 9, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-9
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Query Match          97.7%; Score 600; DB 14; Length 114;
Best Local Similarity 96.5%; Pred. No. 1,4e-46;
Matches 110; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYVNS 60
DB 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYVNS 60
```

```
QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDMNGGTLVTSS 114
DB 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDMNGGTLVTSS 114
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RESULT 3
US-10-027-725A-7
; Sequence 7, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-7
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Query Match          88.9%; Score 546; DB 14; Length 114;
Best Local Similarity 89.5%; Pred. No. 1.1e-41;
Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
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QY 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYVNS 60
DB 1 LESGPGLVKPSQTLSTCTVSGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYVNS 60
```

```
QY 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDMNGGTLVTSS 114
DB 61 LKSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDMNGGTLVTSS 114
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RESULT 4
US-10-893-576-41
; Sequence 41, Application US/10893576
; Publication No. US20050118643A1
; GENERAL INFORMATION:
; APPLICANT: BURGESS, TERESA L.
; APPLICANT: COXON, ANGELA
; APPLICANT: GREEN, LARRY L.
```

```
; APPLICANT: ZHANG, KE
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
; FILE REFERENCE: 06843.0051-00000
; CURRENT APPLICATION NUMBER: US/10/893, 576
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/488,681
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 41
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HGF 2.40.1
; OTHER INFORMATION: Heavy chain V region (Vh, Vg 4-31)-hmg2 C region
US-10-893-576-41
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Query Match          83.8%; Score 514.5; DB 17; Length 140;
Best Local Similarity 84.5%; Pred. No. 9.3e-39;
Matches 98; Conservative 5; Mismatches 10; Indels 3; Gaps 1;
```

```
QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYVNSL 61
DB 25 ESGPGLVKPSQTLSTCTVSGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYVNSL 84
```

```
QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDMNGGTLVTSS 114
DB 85 KSRITMSVDTSKNHFSLRLTSVTAADTAVYYCARSDGYTLDMNGGTLVTSS 140
```

```
RESULT 5
US-10-727-155-2
; Sequence 2, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orli Foodt
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Ratchanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenko
; APPLICANT: Raffaela Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FILE REFERENCE: AGENIX 073A
; CURRENT APPLICATION NUMBER: US/10/727, 155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-2
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```
Query Match          83.2%; Score 511; DB 17; Length 128;
Best Local Similarity 78.9%; Pred. No. 1.8e-38;
Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;
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```
QY 2 ESGPGLVKPSQTLSTCTVSGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYVNSL 61
DB 6 ESGPGLVKPSQTLSTCTVSGSIRSGGYWVWROPFGKLEWIGNIYHSGNTYVNSL 65
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QY	62	KSIIITMSVPTS	KHIFSLRLTS	VTAADTAVYYCARSDG-----	YTLDNMGCGTLVT	111
Dd	66	KSATVISVDPTSK	KNQFSLKLSL	VTADTAVYYCARDSNQNNNDVEYDYGIDLVWGCGITTVI		125
QY	112	VSS				
Dd	126	VSS				
		128				

RESULT 6
US-10-727-155-10

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Sequence 10, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
APPLICANT: John S. Babcock
APPLICANT: Jaspal S. Kang
APPLICANT: Orit Food
APPLICANT: Larry Green
APPLICANT: Xiao Feng
APPLICANT: Scott Klampp
APPLICANT: Mary Haak-Frendscho
APPLICANT: Palaniswami Rathanaswami
APPLICANT: Craig Pigott
APPLICANT: Meina Liang
APPLICANT: Rozanne Lee
APPLICANT: Kathy Manchulenchio
APPLICANT: Raffaella Faggiani
APPLICANT: Giorgio Senaldi
APPLICANT: Qiaojuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
FILE REFERENCE: FACTOR AND USES THEREOF
FILE REFERENCE: AGENIX-073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 128
TYPE: PRT
ORGANISM: Homo sapiens
US-10-727-155--10

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Query Match	83.2%	Score 511;	DB 17;	Length 128;
Best Local Similarity	78.9%	Pred. No. 1.8e-38;		
Matches 97;	Conservative 7;	Mismatches 9;	Indels 10;	Gaps 1;

QY 2 ESQSGVLKPSQTLSTLCYSGSGIRSGGYWMEVWQPGKGLMEWIGNIYHSGNTYVPSL 61
Db 6 ESQSGVLKPSQTLSTLCYSGSGISSGGYWMEWINGHKGKGLMEWIGNIYHSGNTYVPSL 65
QY 62 KSRITLTVSDPSKRNHESLRLTSTAAADTAAYYCARSDG-----YTLDNMGCGTLTY 111
Db 66 KSRITLTVSDPSKQPSLKLSTVAADTAAYYCARSDNQNTNNDVEYDYGLDVWQGGITVT 125
QY 112 VSS 114
Db 126 VSS 128

RESULT 7
US-10-727-155-30

Sequence 30, Application USA/10737155
Publication No. US20050049402A1
GENERAL INFORMATION:
APPLICANT: John S. Babcock
APPLICANT: Jaspal S. Kang
APPLICANT: Orle Food
APPLICANT: Larry Green
APPLICANT: Xiao Feng
APPLICANT: Scott Klakamp

```

1  APPLICANT: Mary Haak-Frendescho
2  APPLICANT: Palaniswami Rathanaswami
3  APPLICANT: Craig Pigott
4  APPLICANT: Weina Liang
5  APPLICANT: Rozanne lee
6  APPLICANT: Kathy Manchulenco
7  APPLICANT: Raffiella Paggioli
8  APPLICANT: Giorgio Senaldi
9  APPLICANT: Qiaojuan Jane Su
10 TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
11 FILE REFERENCE: FACTOR AND USES THEREOF
12 FILE REFERENCE: AGENIX 073A
13 CURRENT APPLICATION NUMBER: US/10/727,155
14 CURRENT FILING DATE: 2003-12-02
15 PRIOR APPLICATION NUMBER: 60/430729
16 PRIOR FILING DATE: 2002-12-02
17 NUMBER OF SEQ. ID NOS.: 320
18 SOFTWARE: FastSeq for Windows Version 4.0
19 SEQ. ID NO 30
20 LENGTH: 128
21 TYPE: PRT
22 ORGANISM: Homo sapiens
23 US-10-727-155-30

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Query Match	83.2%;	Score 511;	DB 17;	Length 128;
Best Local Similarity	78.9%;	Pred. No. 1.8e-38;		
Matches 97;	Conservative 7;	Mismatches 9;	Indels 10;	Gaps 1;

Qy	2	ESPEGLVWRKSQTLSTLCTVSGGSISSGGGYMSWVRPGKGLWIMIGNIYHSGNTYYNPSL	61
Db	6	ESPEGLVWRKSQTLSTLCTVSGGSISSGGGYMSWVRPGKGLWIMIGNIYHSGNTYYNPSL	65
Qy	62	KSRITMSVDTSKNHFSLRLTSTVTAADFVAVYCARSDG-----YTLDNMGOGTLVT	111
Db	66	KSRVITLSDVTSKNQPSLKLSTVTAADTAVIYTCARDSNQINMNDVEYDGLDWGGTIVT	125
Qy			
Qy	112	VSS	
Db	126	VSS 128	

RESULT 8
US-10-309-762-152

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Sequence 152, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Cudas, Jean
APPLICANT: Poltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
FILE REFERENCE: ABGENIX, 027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 152
LENGTH: 121
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-152

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Query Match	83.1%	Score 510.5;	DB 15;	Length 121;
Best Local Similarity	82.8%	Pred. No. 1.8e-38;		
Matches	96;	Conservative	8;	Mismatches 9;
				Indels 3;
				Gaps 1;

Qy 2 ESGPGLVKPQTLSTLCTVSGSIRSGCYWMSVTRQPPCKGLEINIGNIYHSGNITYNPSL 61

Db 6 ESGPGLVKPQTLSTLCTVSGSIRSGCYWMSVTRQPPCKGLEINIGNIYHSGNITYNPSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYCARSD---GYTLDMGCGTLVTYSS 114
Db 66 KSRVITISVDTSKNQFSLKLSSTVTAADTAIVYCCAYYDILTGAFDIMGCGTMTYSS 121

RESULT 9
US-10-309-762-138

Sequence 138, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 138
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-138

Query Match 83.1%; Score 510; DB 15; Length 118;
Best Local Similarity 85.0%; Pred. No. 2e-38;

Matches 96; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 2 ESGPGLVKPSQTLSTLCTVSGSIRSGLYWSWVROPKGLKLEWIGNIYHSGNTYYNPSL 61
Db 6 ESGPGLVKPSQTLSTLCTVSGSIRSGLYWSWVROPKGLKLEWIGNIYHSGNTYYNPSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYCARSDGYTLDMGCGTLVTYSS 114
Db 66 KSRVITISVDTSKNQFSLKLSSTVTAADTAIVYCCAYYSGSDYWGCGTLVTYSS 118

RESULT 10

US-10-309-762-10
Sequence 10, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-10

Query Match 83.0%; Score 509.5; DB 15; Length 123;
Best Local Similarity 82.2%; Pred. No. 2.3e-38;

Matches 97; Conservative 8; Mismatches 8; Indels 5; Gaps 1;

Qy 2 ESGPGLVKPSQTLSTLCTVSGSIRSGLYWSWVROPKGLKLEWIGNIYHSGNTYYNPSL 61
Db 6 ESGPGLVKPSQTLSTLCTVSGSIRSGLYWSWVROPKGLKLEWIGNIYHSGNTYYNPSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYCARSD---DGYTLDMGCGTLVTYSS 114
Db 66 KSRVITISVDTSKNQFSLKLSSTVTAADTAIVYCCARAGKYSGSLDYWGCGTLVTYSS 123

RESULT 11

US-10-309-762-11
Sequence 11, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-11

Query Match 82.7%; Score 507.5; DB 15; Length 125;
Best Local Similarity 81.7%; Pred. No. 3.5e-38;

Matches 98; Conservative 7; Mismatches 8; Indels 7; Gaps 2;

Qy 2 ESGPGLVKPSQTLSTLCTVSGSIRSGLYWSWVROPKGLKLEWIGNIYHSGNTYYNPSL 61
Db 6 ESGPGLVKPSQTLSTLCTVSGSIRSGLYWSWVROPKGLKLEWIGNIYHSGNTYYNPSL 65

Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAIVYCARSD---DGYTLDMGCGTLVTYSS 114
Db 66 KSRVITISVDTSKNQFSLKLSSTVTAADTAIVYCCARTYYDFLTGYPDAFDIMGCGTMTYSS 125

RESULT 12

US-10-309-762-13
Sequence 13, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 120
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-13

Query Match 82.6%; Score 507; DB 15; Length 120;
Best Local Similarity 83.6%; Pred. No. 3.8e-38;

Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;

Qy 2 ESGPGLVKPSQTLSTLCTVSGSIRSGLYWSWVROPKGLKLEWIGNIYHSGNTYYNPSL 61
Db 6 ESGPGLVKPSQTLSTLCTVSGSIRSGLYWSWVROPKGLKLEWIGNIYHSGNTYYNPSL 65

Db 6 ESGPGLVKSQTLSTLCTVSGGSISGGYWSWIRQHPGKLEWIGITYYSGSTYNP SL 65
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCARSDGT---LDNMGQGLTVTVSS 114
Db 66 KSRVTVSDTSKNQFSLKLSSTVTAADTAAYYCAR-DGYNYWYFDLMGRGLTVTVSS 120

RESULT 13
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-144

Query Match 82.6%; Score 507; DB 15; Length 120;
Best Local Similarity 83.6%; Pred. No. 3.8e-38;
Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;
Qy 2 ESGPGLVKSQTLSTLCTVSGGSISGGYWSWIRQHPGKLEWIGITYYSGSTYNP SL 61
Db 6 ESGPGLVKSQTLSTLCTVSGGSISGGYWSWIRQHPGKLEWIGITYYSGSTYNP SL 65
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCARSDGT---LDNMGQGLTVTVSS 114
Db 66 KSRVTVSDTSKNQFSLKLSSTVTAADTAAYYCAR-DGYNYWYFDLMGRGLTVTVSS 120

RESULT 14
US-10-309-762-147
; Sequence 147, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-147

Query Match 82.6%; Score 507; DB 15; Length 122;
Best Local Similarity 82.1%; Pred. No. 3.8e-38;
Matches 96; Conservative 8; Mismatches 9; Indels 4; Gaps 1;
Qy 2 ESGPGLVKSQTLSTLCTVSGGSISGGYWSWIRQHPGKLEWIGITYYSGSTYNP SL 61

Db 6 ESGPGLVKSQTLSTLCTVSGGSISGGYWSWIRQHPGKLEWIGITYYSGSTYNP SL 65
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCAR---SDGYTLDNMGQGLTVTVSS 114
Db 66 KSRVTVSDTSKNQFSLKLSSTVTAADTAAYYCARYYDILLYGMDWGGQGLTVTVSS 122

RESULT 15
US-10-893-576-189
; Sequence 189, Application US/10893576
; Publication No. US20050118643A1
; GENERAL INFORMATION:
; APPLICANT: BURGESS, TERESA L.
; APPLICANT: COXON, ANGELA
; APPLICANT: GREEN, LARRY L.
; APPLICANT: ZHANG, KE
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
; FILE REFERENCE: 06843.0051-00000
; CURRENT APPLICATION NUMBER: US/10/893,576
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/488,681
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 189
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic gamma heavy
US-10-893-576-189

Query Match 82.5%; Score 506.5; DB 17; Length 119;
Best Local Similarity 84.2%; Pred. No. 4.1e-38;
Matches 96; Conservative 5; Mismatches 10; Indels 3; Gaps 1;
Qy 2 ESGPGLVKSQTLSTLCTVSGGSISGGYWSWIRQHPGKLEWIGITYYSGSTYNP SL 61
Db 6 ESGPGLVKSQTLSTLCTVSGGSISGGYWSWIRQHPGKLEWIGITYYSGSTYNP SL 65
Qy 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYYCARSDGT---DGYTLDNMGQGLTVTV 112
Db 66 KSRVTVSDTSKNQFSLKLSSTVTAADTAAYYCARDPYGYGFPDPCGGLTVTV 119

Search completed: July 26, 2005, 10:05:18
Job time: 72.7121 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 09:09:56 ; Search time 21.5909 Seconds
(without alignment)
394.147 Million cell updates/sec

Title: US-10-027-725A-7

Perfect score: 609

Sequence: 1 LESGPGLVKPAQTLISCAV.....RLDGYTLIDWQGTLYTVSS 114

Scoring table: BLOSUM62

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCBUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	499	81.9	473	3	US-09-049-672A-4
2	496	81.4	172	4	US-09-472-087-7
3	496	81.4	172	4	US-09-472-087-86
4	482	79.1	487	1	US-09-800-729-145
5	471.5	77.4	119	1	US-08-360-125-5
6	471.5	77.4	119	2	US-08-450-578-5
7	471.5	77.4	119	2	US-09-017-628-5
8	471.5	77.4	119	2	US-09-014-880-5
9	471.5	77.4	119	3	US-09-025-769B-39
10	471.5	77.4	119	3	US-09-025-769B-65
11	471.5	77.4	119	4	US-08-450-363-5
12	471.5	77.4	119	4	US-09-490-070A-39
13	471.5	77.4	119	4	US-09-490-070A-65
14	471.5	77.4	119	4	US-09-490-153-39
15	471.5	77.4	119	4	US-09-490-153-65
16	471.5	77.4	119	4	US-09-467-903-5
17	471.5	77.4	119	4	US-09-490-324-39
18	471.5	77.4	119	4	US-09-490-324-65
19	468	76.8	120	1	US-09-424-840B-20
20	466	76.5	122	1	US-08-360-125-11
21	466	76.5	122	2	US-08-450-578-11
22	466	76.5	122	2	US-09-017-628-11
23	466	76.5	122	2	US-09-014-880-11
24	466	76.5	122	4	US-08-450-363-11
25	466	76.5	122	4	US-09-467-903-11
26	465.5	76.4	117	4	US-09-720-493-2
27	455	74.7	118	3	US-09-025-769B-25

28	455	74.7	118	4	US-09-490-070A-25	Sequence 25, Appl
29	455	74.7	118	4	US-09-490-153-25	Sequence 25, Appl
30	455	74.7	118	4	US-09-490-324-25	Sequence 116, Appl
31	453	74.4	118	3	US-08-545-809A-116	Sequence 79, Appl
32	445	73.1	244	3	US-08-918-148-79	Sequence 77, Appl
33	445	73.1	244	4	US-09-138-091A-77	Sequence 2, Appl
34	442.5	72.7	142	2	US-08-480-774A-2	Sequence 888, App
35	441.5	72.5	155	4	US-09-471-276-888	Sequence 3, Appl
36	438	71.9	278	3	US-09-260-527-3	Sequence 10, Appl
37	429.5	70.5	119	2	US-08-652-816A-10	Sequence 14, Appl
38	429	70.4	150	4	US-09-582-337-14	Sequence 6, Appl
39	427	70.1	118	4	US-09-343-698-6	Sequence 6, Appl
40	427	70.1	118	4	US-08-325-955-6	Sequence 12, Appl
41	425.5	69.9	119	4	US-09-424-840B-2	Sequence 12, Appl
42	425.5	69.9	476	3	US-08-487-550-12	Sequence 12, Appl
43	425.5	69.9	476	4	US-09-526-098-12	Sequence 12, Appl
44	425.5	69.9	476	4	US-09-383-916-12	Sequence 12, Appl
45	424.5	69.7	117	4	US-09-232-290-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-09-049-672A-4
; Sequence 4, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREMITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ceirone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 473 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PANTUT01

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1 CLONE: 1513264
2 US-09-049-672A-4
3
4 Query Match 81.9%; Score 499; DB 3; Length 473;
5 Best Local Similarity 78.2%; Pred. No. 6,3e-43;
6 Matches 93; Conservative 13; Mismatches 7; Indels 6; Gaps 1;
7
8 Qy 2 ESGGGLVKAPOATLSLSCAVSGGSGIRSGGYWSWIRHFGKGLWMTGYTHSGNTYINPSL 61
9 Db 25 ESGGGLVKAPOATLSLSCAVSGGSGIRSGGYWSWIRHFGKGLWMTGYTHSGNTYINPSL 84
10
11 Qy 62 KSRIAMSVDTSENKPSLRINSVTAADTAIVYVCARLD-----GYTLDIWGQGLTVYSS 114
12 Db 85 KSRIAMSVDTSENKPSLRINSVTAADTAIVYVCARLDVGLRGAGMDVWGQGLTVYSS 143
13
14 RESULT 2
15 US-09-472-087-7
16 Sequence 7, Application US/09472087
17 Patent No. 6682736
18 GENERAL INFORMATION:
19 APPLICANT: HANSON, DOUGLAS C.
20 APPLICANT: NEVEU, MARK J.
21 APPLICANT: MUELLER, ELLEN E.
22 APPLICANT: HANKE, JEFFREY H.
23 APPLICANT: GILMAN, STEVEN C.
24 APPLICANT: DAVIS, C. GEOFFREY
25 APPLICANT: CORVALAN, JOSE R.
26 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
27 FILE REFERENCE: ABX-PFI
28 CURRENT FILING DATE: 1999-12-23
29 PRIOR FILING DATE: 1998-12-23
30 NUMBER OF SEQ ID NOS: 147
31 SOFTWARE: PatentIn Ver. 2.1
32 SEQ ID NO 7
33 LENGTH: 172
34 TYPE: PRT
35 ORGANISM: Homo sapiens
36 US-09-472-087-7
37
38 Query Match 81.4%; Score 496; DB 4; Length 172;
39 Best Local Similarity 79.8%; Pred. No. 3.8e-43;
40 Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;
41
42 Qy 3 SGPGLVKAPOATLSLSCAVSGGSGIRSGGYWSWIRHFGKGLWMTGYTHSGNTYINPSL 62
43 Db 1 SGPGLVKAPOATLSLSCAVSGGSGIRSGGYWSWIRHFGKGLWMTGYTHSGNTYINPSL 60
44
45 Qy 63 SRIMASVDTSENKPSLRINSVTAADTAIVYVCARLDG--YTLDIWGQGLTVYSS 114
46 Db 61 SRIMASVDTSENKPSLRINSVTAADTAIVYVCARLDGSDYIGIDVWGQGLTVYSS 114
47
48 RESULT 3
49 US-09-472-087-86
50 Sequence 86, Application US/09472087
51 Patent No. 6682736
52 GENERAL INFORMATION:
53 APPLICANT: HANSON, DOUGLAS C.
54 APPLICANT: NEVEU, MARK J.
55 APPLICANT: MUELLER, ELLEN E.
56 APPLICANT: HANKE, JEFFREY H.
57 APPLICANT: GILMAN, STEVEN C.
58 APPLICANT: DAVIS, C. GEOFFREY
59 APPLICANT: CORVALAN, JOSE R.
60 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
61 FILE REFERENCE: ABX-PFI
62 CURRENT FILING DATE: 1999-12-23
63 PRIOR FILING DATE: 1998-12-23
64 PRIOR APPLICATION NUMBER: 60/113,647
65 PRIOR FILING DATE: 1998-12-23

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; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 86
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-86

Query Match      81.4%; Score 496; DB 4; Length 172;
Best Local Similarity 79.8%; Pred. No. 3,8e-43;
Matches 91; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

QY      3  SGEPLVNPACQLSLSCAVSGGSITSGGYWMIROHKGKLEWIGIYHSNTYNNPSL 62
DB      1  SGPPLVNPQSLLSLTCTVSGGSISGGHWMIROHKGKLEWIGIYIGNTYNPSLK 60

QY      63  SRIMASVDTSENKFSRLNVSYTAADTAVVYCARLDG--YTLDDIMGGGLTVVSS 114
DB      61  SRVITISVDISKNPSLKLSSVTAADTAVVYCARSDGYIGIDVWGGITTVVSS 114

RESULT 4
US-09-800-729-145
; Sequence 145, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 145
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-145

Query Match      79.1%; Score 482; DB 4; Length 487;
Best Local Similarity 74.8%; Pred. No. 3,6e-41;
Matches 92; Conservative 12; Mismatches 9; Indels 10; Gaps 2;

QY      2  EESGGLYKPAOTLSLSCAVSGGSITSGGYWMIROHKGKLEWIGIYHSNTYNNPSL 61
DB      25  EESGGLYKPSSTLSLTCTVSGGSISGGHWMIROHKGKLEWIGIYISNGVITYNPSL 84

QY      62  KSRFAMSVDTSENKFSRLNVSYTAADTAVVYCAR-----LDGYTL-----DIMGGGLTVT 111
DB      85  KSRVITISVDISQNPFSRLNVSYTAADTAVVYCARQKHRRATRDGYOLETRGDFYWGQILVT 144

QY      112 VSS 114
DB      145 VSS 147

RESULT 5
US-08-360-125-5
; Sequence 5, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: SAIKO HOSOKAWA
; APPLICANT: TOSHIAKI TAGAWA
; APPLICANT: YOKO HIRAKAWA
; APPLICANT: No. 5767246;hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane

```

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Menderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL LINE: antibody GAH
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLES:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:

PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-5
Query Match 77.4%; Score 471.5; DB 1; Length 119;
Best Local Similarity 75.9%; Pred. No. 7.9e-41;
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;
Qy 2 ESGPGLVPAQTSLSCAVSGSIRSGYVSWIRHFGKLEWIGYIYHSGNTYVPSL 61
Db 6 ESGPGLVPAQTSLTCTVSGSISSCGFYVWIRHFGKLEWIGYIYHSGNTYVPSL 65
Qy 62 KSRIAMSVDTSEKFSRLNSVTADTAIVYCA--RIDGYTLDIWCGTILVTVSS 114
Db 66 KSRVTISLDTSKSQFSIKLSLTADTAIVYCASTRLRG--ADYWGCGTWTVTSS 119
RESULT 6
US-08-450-578-5
Sequence 5, Application US/08450578
Patent No. 5837845
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845;hiko ITO
APPLICANT: Kazuhito NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Menderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:

STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL LINE: antibody GAH
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-5

Query Match 77.4%; Score 471.5; DB 2; Length 119;
Best Local Similarity 75.9%; Pred. No. 7.9e-41;
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

Qy 2 ESGGLVPAQTLISCAVSGSIRSGYWSWIRQHPGKLEWIGYIYHSGNTYVNSL 61
Db 6 ESGGLVPAQTLISCAVSGSIRSGYWSWIRQHPGKLEWIGYIYHSGNTYVNSL 65

Qy 62 KSRIVMSVTSSEKFSRLNSVTADTAIVYCA---RLDGYTLDIWGGTLVTVSS 114
Db 66 KSRVTSIDTSKQFSLKSLSLTADTAIVYCASTRIRG--ADYWGQGMVTVSS 119

RESULT 7
US-09-017-628-5
Sequence 5, Application US/09017628
Patent No. 5990287
GENERAL INFORMATION:
APPLICANT: HOSOKAWA, Saiko
APPLICANT: TAGAWA, Toshiaki
APPLICANT: HIRAKAWA, Yoko
APPLICANT: ITO, No. 5990287Ihiko
APPLICANT: NAGAIKE, Kazuhiko
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
SURFACE ANTIGEN OF CANCER CELL MEMBRANE
FILE REFERENCE: 177/527361KH
CURRENT APPLICATION NUMBER: US/09/017, 628
CURRENT FILING DATE: 1998-02-02
EARLIER APPLICATION NUMBER: 08/360,125
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 119
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody GAH

US-09-017-628-5

Query Match 77.4%; Score 471.5; DB 2; Length 119;
Best Local Similarity 75.9%; Pred. No. 7.9e-41;
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

Qy 2 ESGGLVPAQTLISCAVSGSIRSGYWSWIRQHPGKLEWIGYIYHSGNTYVNSL 61
Db 6 ESGGLVPAQTLISCAVSGSIRSGYWSWIRQHPGKLEWIGYIYHSGNTYVNSL 65

Qy 62 KSRIVMSVTSSEKFSRLNSVTADTAIVYCA---RLDGYTLDIWGGTLVTVSS 114
Db 66 KSRVTSIDTSKQFSLKSLSLTADTAIVYCASTRIRG--ADYWGQGMVTVSS 119

RESULT 8
US-09-014-880-5
Sequence 5, Application US/09014880
Patent No. 590297
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: May 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
US-09-014-880-5

Query Match 77.4%; Score 471.5; DB 2; Length 119;
Best Local Similarity 75.9%; Pred. No. 7.9e-41;
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;

QY	2	ESGGLVAKPQQTLLSLCAVSGGSLRSQGYWSNRHPQGGGLMIGIYHSGNTYNP	6
		: : : : : : : : :	
Db	6	ESGGVLAKPQQTLLSLCTVSGGSLSSCGFLMNRIQRHKGGLMIGIYHSSSTYNP	65
		: : : : : : : :	
QY	62	KSRIAMVDNSEKFEISRLNSVTRADPAVYYCA---RLDGYTLIDINGCGILTV	114
		: : : : : : : :	
Db	66	KSRIATLIDSSQPSFLKSLSSLTADPAVYYCARSTRLRG--ADYWGQGMVTV	119
		: : : : : : : :	

RESULT 9
US-09-025-769B-39
; Sequence 39, Application US/09025769B

```

: GENERAL INFORMATION:
: APPLICANT: Knappik, Achim
: APPLICANT: Beck, Peter
: APPLICANT: Ilag, Vic
: APPLICANT: Ge, Liming
: APPLICANT: Moroney, Simon
: APPLICANT: Plueckthun, Andreas
: TITLE OF INVENTION: Protein/(poly)peptide libraries
: NUMBER OF SEQUENCES: 373
: CORRESPONDENCE ADDRESS:
:

```

```

: ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave
: STREET: 1251 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10021

```

```

; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;

```

APPLICATION NUMBER: US/09/025,769E

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 27,794

TELECOMMUNICATION INFORMATION:

TELEFAX: (212) 596-9090

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

TOPOLOGY: linear

US-09-025-769B-39

Query Match	77.4%	Score 471.5;	DB 3;	Length 119;
Best Local Similarity	77.6%	Pred. No. 7.9e-41;		
Matches 90; Conservative	12;	Mismatches 9;	Indels 5;	Gaps 2

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QY      2  ESGPGLVKPAQTLTSLSCAVSGGSLRSGGYWMSWRQHPGKGLIEWIGIYIHSGNTYVNPSL 61
      |||||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      6  ESGPGLVKPSETLSLTCTVSGGSLSS--YWMSWIRQPPGKGLIEWIGIYIHSGSTNYPVSL 63

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```

QY      62 KSR IAMSVDTSENKFSRLNSVTADTA VVYCARLDG---YLLDIWGGLTVTVSS 114
      |||:::||||:::|||||:::|:|||||
Db      64 KSRVTSVDTSKNQFSLKLSVTADTA VVYCARWGGDGFYAMDYWGGLTVTVSS 119

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RESULT 10
US-09-025-769B-65
; Sequence 65, Application US/09025769B
; Patent No. 6300064

```

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Illag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EBO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEO ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-65

Query Match 77.4%; Score 471.5; DB 3; Length 119;
Best Local Similarity 77.6%; Pred. No. 7.9e-41;
Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2;

OY 2 ESGGGLVKNPQNTSLSCAVSGGSGTRSGGYWWSWTRHPKGLKLEIGTYHSGNTYVPSL 61
DB 6 ESGGGLVKNPSETSLTCTVSGGSSIS--YYWSWTRPPGKLEIGTYHSGSTYVPSL 63
OY 62 KSRIVSVDSSENKFSRLNSVTADPAVYYCARLDG---YTLDPMGOGTLVTVSS 114
DB 64 KSRVTISVDSKDFSLKLSVTHADPAVYYCARMGDGRYAMDYMGOGTLVTVSS 119

RESULT 11
US-08-450-363-5
Sequence 5, Application US/08450363
Patent No. 6436434
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 6436434ihiko ITO
APPLICANT: Kazuhito NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
SPECIFICALLY BINDING TO SURFACE ANTIGEN OF CANCER
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington

```

RESULT 11
US-08-450-363-5
Sequence 5, Application US/08450363
Patent No. 6436434
GENERAL INFORMATION:
APPLICANT: SAIKO HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 6436434-Ihiko ITO
APPLICANT: Kazuhiko NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,363
FILING DATE: May 25, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8650
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL LINE: antibody G4H
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-5

Query Match 77.4%; Score 471.5; DB 4; Length 119;
Best Local Similarity 75.9%; Pred. No. 7,9e-41;
Matches 88; Conservative 16; Mismatches 7; Indels 5; Gaps 2;
Qy 2 ESGPGLVPAQOTLSLSCAVSGGSIKSGYWSWIRQHGKLEWIGYIYHSGNTYNPSTL 61
Db 6 ESGPGLVPSQTLSTCTVSGGSISSCGFYWMNRQHPGKLEWIGYIYHSGNTYNPSTL 65
Qy 62 KSRIVMSVDTSENKFSRLNSVTAAADTAAYVCA---RLDGYTLDIWOGTLVTYSS 114
Db 66 KSRVTISLDTSKSQFSLKSLTAADTAAYVCAKSTRLRG--ADYWGQGMVTYSS 119
RESULT 12
US-09-490-070A-39
Sequence 39, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & Maulliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-490-070A-39
Query Match 77.4%; Score 471.5; DB 4; Length 119;
Best Local Similarity 77.6%; Pred. No. 7,9e-41;
Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2;
Qy 2 ESGPGLVPAQOTLSLSCAVSGGSIKSGYWSWIRQHGKLEWIGYIYHSGNTYNPSTL 61
Db 6 ESGPGLVPSQTLSTCTVSGGSIS--YYWSWIRQHPGKLEWIGYIYHSGNTYNPSTL 63
Qy 62 KSRIVMSVDTSENKFSRLNSVTAAADTAAYVCAKSTRLRG---YTLDIWOGTLVTYSS 114
Db 64 KSRVTISVDTSKQFSLKSLTAADTAAYVCAKSTRLRG---YTLDIWOGTLVTYSS 119

```

RESULT 13
US-09-490-070A-65
; Sequence 65, Application US/09490070A
; Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
            Knapp, Peter
            Ilag, Vic
            Ge, Liming
            Moroney, Simon
            Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
    ADDRESS: Colin G. Sandercock, Esq. c/o Heller Ehrman
            White & McAuliffe
    STREET: 1666 K Street, N.W., Suite 300
    CITY: Washington
    STATE: D.C.
    COUNTRY: USA
    ZIP: 20006
COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Releasee #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/490,070A
    FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: EP 95 11 3021.0
    FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
    NAME: Colin G. Sandercock, Esq.
    REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
    TELEPHONE: (202) 912-2000
    TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
    LENGTH: 119 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-490-070A-65

Query Match          77.4%; Score 471.5; DB 4; Length 119;
Best Local Similarity 77.6%; Pred. No. 7.9e-41;
Matches 90; Conservative 12; Mismatches 9; Indels 5; Gaps 2

QY      2  ESGPGLVYPAQTLTSLSCAVSGSGSINSIGYMWIMQHPRKGLIEMIGYIHSNTYYNSL 61
      |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      6  ESGPGLVYPSRSLTSLCTVSGSGISS--YVWSMIRQPKGLIEMIGYIYSGSTVYNSL 63
QY      62  KSRIMASVDTSENKPSLRINSVTAADTAVYVCARDG--YTLDIWGGGLTVTVSS 114
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      64  KSRVITSVDTSKNPSLKLSSVTAADTAVYVCARNGGDGFYMDYWGQGLTVTVSS 119
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

RESULT 14
US-09-490-153-39
; Sequence 39, Application US/09490153
; Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
            Knapp, Peter
            Ilag, Vic
            Ge, Liming
            Moroney, Simon

```

```

1 Plueckthun, Andreas
2 TITLE OF INVENTION: Protein/(Poly)peptide libraries
3 NUMBER OF SEQUENCES: 373
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
6 STREET: 1251 Avenue of the Americas
7 CITY: New York
8 STATE: New York
9 COUNTRY: USA
10 ZIP: 10021
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
17
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/490,153
20 FILING DATE: 24-Jan-2000.
21
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US/09/025,769B
24 FILING DATE: 18-FEB-1998
25 APPLICATION NUMBER: EP 95 11 3021.0.
26 FILING DATE: 18-AUG-1995
27
28 ATTORNEY/AGENT INFORMATION:
29 NAME: James F. Haley, Jr., Esq.
30 REGISTRATION NUMBER: 27,794
31 REFERENCE/DOCKET NUMBER: WOPHO/5
32
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (212)596-9000
35 TELEFAX: (212)596-9090
36
37 INFORMATION FOR SEQ ID NO: 39:
38
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 119 amino acids
41 TYPE: amino acid
42 STRANDEDNESS: <Unknown>
43 TOPOLOGY: linear
44
45 MOLECULE TYPE: protein
46
47 SEQUENCE DESCRIPTION: SEQ ID NO: 39:
48
49 US-09-490-153-39
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS

SOFTWARE: PatentIn Release #1.0

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:

ENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILED DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998

FILING DATE: 18-FEB-1998
 APPLICATION NUMBER: EP 95 11 3021.C

FILING DATE: 18-AUG-1995

ORNEY/AGENT INFORMATION:

NAME: James F. Haley,

REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MOPHC

REFERENCE/DOC#1 NUMBER: MORPHO/3
COMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

ON FOR SEQ ID NO: 65:

SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids

LENGTH: 113 amino acids
TYPE: amino acid

TOPOLOGY: linear

CULE TYPE: protein

SEQUENCE DESCRIPTION:

0-153-65

Query Match 77.4%: Score 471.5

US-09-490-153-65

Query Match 77.4%; Score 471.5; DB 4; Length 119;

Best Local Similarity 77.6%; Pred. No. 7.9e-41;

Matches	90;	Conservative	12;	Mismatches	9;	Indels	5;	Gaps	2;
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[illegible]

Search completed: July 26, 2005, 09:29:58
Job time : 22.5909 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:07:26 ; Search time 14.6818 Seconds

(without alignments)
747.095 Million cell updates/sec

Title: US-10-027-725A-8

Perfect score: 614
Sequence: 1 LESGPGLVKPSQSLSTCTV.....RSDGYTLDMWGQGLTVVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	499.5	81.4	135	2 S78051	Ig heavy chain pre
2	495.5	80.7	147	2 S13519	Ig heavy chain V r
3	487	79.3	130	2 S30534	Ig heavy chain V r
4	480.5	78.3	121	2 S44113	Ig heavy chain V r
5	478.5	77.9	140	2 S37782	Ig variable region
6	477.5	77.8	146	2 S09710	Ig heavy chain V r
7	474.5	77.3	116	2 S37456	Ig mu chain - huma
8	474.5	77.3	130	2 S31690	Ig heavy chain V r
9	474	77.2	122	2 S69912	Ig heavy chain V r
10	473.5	77.1	128	2 S31514	Ig V-D-J region (N
11	472.5	77.0	127	2 S19668	Ig heavy chain - h
12	469	76.4	137	2 S31676	Ig heavy chain V r
13	468.5	76.3	123	2 S30530	Ig heavy chain V r
14	465.5	75.8	155	2 S31511	Ig heavy chain - h
15	463.5	75.5	155	2 S31512	Ig heavy chain - h
16	462	75.0	143	2 S31586	Ig heavy chain V r
17	460.5	75.0	146	2 S09711	Ig heavy chain V r
18	460	74.9	145	2 S78055	Ig heavy chain pre
19	459.5	74.8	109	2 PH1673	Ig heavy chain V r
20	457	74.4	110	2 S44110	Ig heavy chain V-D
21	455	74.1	99	2 S26803	Ig heavy chain V r
22	454	73.9	139	2 A41287	Ig heavy chain pre
23	453	73.8	99	2 S26801	Ig heavy chain V r
24	452	73.6	129	2 S44114	Ig heavy chain V r
25	450	73.3	99	2 S26802	Ig heavy chain V r
26	450	73.3	135	2 S31604	Ig heavy chain V r
27	447	72.8	118	2 S20780	Ig heavy chain V r
28	446	72.6	99	2 S12418	Ig heavy chain V r
29	444.5	72.4	139	2 S31696	Ig heavy chain V r

30	443	72.1	118	2 A26340	Ig heavy chain pre
31	442.5	72.1	140	2 A49045	Ig heavy chain V r
32	441.5	71.9	132	2 A38911	Ig heavy chain V r
33	441	71.8	99	2 S26800	Ig heavy chain V r
34	441	71.8	126	2 S47010	Ig heavy chain V4
35	440.5	71.7	129	1 D2HWA	Ig heavy chain V-I
36	440	71.7	97	2 PK0118	Ig heavy chain V-I
37	440	71.7	99	2 S26839	Ig heavy chain V r
38	439.5	71.6	98	2 S12421	Ig heavy chain V r
39	439.5	71.6	140	2 A24770	Ig heavy chain V r
40	439	71.5	140	2 S78052	hypothetical hybr
41	438.5	71.4	123	2 S30529	Ig heavy chain pre
42	438	71.3	120	2 PT0370	Ig heavy chain V r
43	437	71.2	124	2 S31684	Ig mu chain precu
44	435.5	70.9	134	2 S54906	Ig heavy chain V r
45	434.5	70.8	98	2 S26902	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S78051

Ig heavy chain precursor V-D-J region (clone mAb 61VH) - human (fragment)
C/Species: Homo sapiens (man)

C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C/Accession: S78051; S23716

R/Harindranath, N.
submitted to the EMBL Data Library, August 1990

A/Reference number: S78051

A/Accession: S78051

A/Molecule type: mRNA

A/Residues: 1-135 <HAR>

A/Cross-references: EMBL:X54437; NID:937814; PIDN:CA38306.1; PID:9930117

R/Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burratiero, S.E.; Wilder, R.L.; Notkins

Int. Immunol. 3, 865-875, 1991

A/Title: Complete sequence of the gene encoding the V(H) and V(L) regions of low- and h

patient.

A/Reference number: S23716; MUID:92031262; PMID:1718404

A/Accession: S23716

A/Molecule type: mRNA

A/Residues: 13-111 <HAW>

A/Cross-references: EMBL:X54437

C/Species: Homo sapiens (man)

C/Accession: S78051; S23716

C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C/Accession: S78051; S23716

C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

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C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

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C/Accession: S78051; S23716

C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C/Accession: S78051; S23716

C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

C/Accession: S78051; S23716

C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999

QY	62	KSRIMTSVDTSKNHFSLRITSTVAADTAYVCARSDDG-----TLDMNGGGLIVT	111
		: : : : : : : : : : : : : : :	
Dd	85	KSRVTISVDLTKNFNSLKLTSSVTAADTAYVYICTR-PRYGDSIVRKKEVMNMDLGGGTIVT	143
QY	112	VSS	114
Dd	144	VSS	146

```

RESULT 7
S37456
IG mu chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37456
R:McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data library, September 1993
A:Description: Cloning and analysis of human IGM anti-Thyroglobulin autoantibodies from
A:Reference number: S37453
A:Accession: S37456
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <MC1>
A:Cross-references: EMBL:X75924; NID:g404313; PIDD:CAA52932.1; PID:g758095
C:Superfamily: Immunoglobulin V region, Immunoglobulin Homology
C:Keywords: Immunoglobulin
C:6-90/Domain: immunoglobulin homology <IMM>

```

Query Match	77.3%;	Score 474.5;	DB 2;	Length 116;
Best Local Similarity	77.8%;	Pred. No. 1.8e-35;		
Matches 91;	Conservative 10;	Mismatches 7;	Indels 9;	Gaps 2

Qy	6	GLVPSQTLTSLTCTVSGSGSIRSGGYWSWVQCPGKGLMEIGNIYHSQATYNNPSLKSII	65
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	1	GLVPSQTLTSLTCTVSGSGSISGGYWSWIRQHPGKGLMEIGIYIYSGSYNNPSLKSIV	60
Qy	66	TMSTDSKKNHPSLRITSVTAADPAVYVYCAASDGYT-----LDWGGGTLVTVSS	114
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	61	TIYSDTKNQPSLKSISTVTAADPAVYVYCAAG-GISGYIYIYNNPDWVGKGTIVTVSS	116

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RESULT 8
S31690
IG heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1998 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31690
R:Cusinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
Submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31690
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <CUI>
A:Cross-references: EMBL:214199; NID:g30984; PIDN:CA878568.1; PID:g30985
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterodimer; immunoglobulin
F:120-102/Domain: immunoglobulin homology <IMM>

```

Query Match	77.3%;	Score 474.5;	DB 2;	Length 130;
Best Local Similarity	76.2%;	Pred. No. 2e-35;		
Matches 93;	Conservative 7;	Mismatches 11;	Indels 11;	Gaps 2

OY	2	ESGPGLVNPSCQLSLTCTCYGCGSISGGGYMVMWNPQPKGLEMGNIHNSNTFYNPEL	61
	:	: : : : : : : : : : : : : : : : :	
Dd	11	ESGPGLVNPSETLSTLCITVSGGIS--YYMWMSRQPQKGLEMGIIYYSGSTNNPSEL	68
OY	62	KSRIMSVDTSKNHFSRLRTSYTAADPTAYYCARSDG-----YTLDNMNGOGLTYLV	112
	:	: : : : : : : : : : : : : : : : :	
Dd	69	KSRVIISDTSKNQGSLEKLSTYTAADPTAYYCARSSVLLMFGELLITYDYDGOGTLTVV	128
OY	113	SS 114	

Db 129 SS 130

RESULT 9
S69912
IG V-D-J region (ND) - human
C:Species: Homo sapiens (man)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69912
R:Sanota, S.; Hamdlin, T.; Oscier, D.G.; Stevenson, F.K.
L:Leukemia 8, 1285-1289, 1994
A:Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multic
A:Reference number: S69909; MUID:9435315; PMID:8057663
A:Accession: S69912
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-122 <SAH>
A:Cross-references: EMBL:Z33398; NID:G871347; PIDD:CA83849.1; PIDD:G887460
A>Note: the sequence of residues 108-122 and the corresponding nucleic acid sequence are
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
;15-99/Domain: Immunoglobulin homology <IMM>

Query Match	77.2%;	Score 474;	DB 2;	Length 122;
Best Local Similarity	76.9%;	Pred. No. 2.1e-35;		
Matches 90; Conservative	11;	Mismatches 12;	Indels 4;	Gaps 1

QY	2	ESGGGLVKEPQTLSTLTCTVSGGSI	IRSGGIVSWVRP	PGKGLGEM	IGNI	YHSNGTYVNSL	6
		::: :::					
Db	6	ESGGGLVKEPQTLSTLTCTVSGGSI	SSSGHFMNIR	PGKGLGEM	IGNI	YFSGSSYNPSL	65
QY		62	KSRTITMVDPSKXHFSLRLTSVTAAP	DAVAVVYCAR	----	DGYLDMGGGTLTVTAS	114
			::: :::				
Db		66	KSRTISIVDTSSKQPSLRKLSVTAAP	DAIVFCAR	GGFFRGTYY	GLDWGGGTLVRLSS	122

```

RESULT 10
S31514
Ig heavy chain - human
C|Species: Homo sapiens (man)
C|Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C|Accession: S31514
R|Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A|Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA
A|Reference number: S31509
A|Accession: S31514
A|Status: preliminary
A|Molecule type: mRNA
A|Residues: 1-128 <CHA>
A|Cross-references: EMBL:X69862; NID:g33086; PIDN:CAA9496.1; PID:g33087
C|Superfamily: immunoglobulin V region; immunoglobulin homology
C|Keywords: heterotetramer; immunoglobulin
F|22-106/Domain: immunoglobulin homology <Imm>

```

Query Match	77.1%;	Score 473.5;	DB 2;	Length 128;
Best Local Similarity	77.6%;	Pred. No. 2.4e-35;		
Matches 90; Conservative	9;	Mismatches 14;	Indels 3;	Gaps 1

QY 2 ESAGGLVKEPQQLSLTCTVSGGSI RSGGYSWVWRPGPGGLMWIGNIYHSQNTYVPSL 6
 Db 13 ESGGLVKEPQQLSLTCTVSGGSI RSGGYSWVWRPGPGGLMWIGNIYHSQNTYVPSL 7
 QY 62 KSRITMSVDSKXHFSLRLTSVAADPAVYVYCAR---SDGYTLDMNGGGLLVVSS 114
 Db 73 KSRITMSVDSKXHFSLRLTSVAADPAVYVYCARIGNFGYGDPMGGGLLVVSS 128

```

RESULT 11
S19668
IG heavy chain V region (VH4DJH6) - human (fragment)
C1Species: Homo sapiens (man)
C1Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 20-Jun-2000

```

C:Accession: S19668; S24445
C:Marker: U.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on pH A:Reference number: S19663; MUID:92085276; PMID:1748994
A:Accession: S19668
A:Molecule type: mRNA
A:Residues: 1-127 <MAR>
A:Cross-references: EMBL:X61648
R:Jones, P.T.
Submitted to the EMBL Data Library, October 1991
A:Reference number: S24442
A:Accession: S24445
A:Molecule type: mRNA
A:Residues: 1-118, 'E', 120-121, 'T', 123-126, 'F' <DON>
A:Cross-references: EMBL:X61648; NID:g37722; PIDN:CAA43829.1; PID:g1335380
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 77.0%; Score 472.5; DB 2; Length 127;
Best Local Similarity 73.0%; Pred. No. 2.9e-35;
Matches 89; Conservative 12; Mismatches 12; Indels 9; Gaps 1;

Oy 2 ESGGGLVPSQTLSTCTVSGSGSIRSGYWSWVRQPPGKLEWIGNIYHSGNTYNPSTL 61
Db 6 QSGGGLVPSQTLSTCTVSGSDSISSGYSWSWRQPPGKLEWIGSHGSPYYPSTL 65

Oy 62 KSRITMSVDTSKNHPSLRSLTSVTADTAIVYCARSDG-----YTLDMWGQGLVTV 112
Db 66 KSRITMSVDTSKNQPSLKLKSVTAADTAIVYCARSGSTWRSLSYKHYMDVWGKTLVTV 125

Oy 113 SS 114
Db 126 SS 127

RESULT 12
S31676
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31676
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Pougereau, M.; Tonnelie, C.
Submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the A:Reference number: S31585
A:Accession: S31676
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137 <CU>
A:Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 469; DB 2; Length 137;
Best Local Similarity 80.0%; Pred. No. 6.5e-35;
Matches 92; Conservative 7; Mismatches 12; Indels 4; Gaps 2;

Oy 2 ESGGGLVPSQTLSTCTVSGSGSIRSGYWSWVRQPPGKLEWIGNIYHSGNTYNPSTL 61
Db 25 ESGGGLVPSQTLSTCTVSGSGSIS--YWSWIRQPPGKLEWIGRIYTSSTYNPSTL 82

Oy 62 KSRITMSVDTSKNHPSLRSLTSVTADTAIVYCARSDG-----YTLDMWGQGLVTVSS 114
Db 83 KSRITMSVDTSKNQPSLKLKSVTAADTAIVYCARAPLMTGMDVWGQGLVTVSS 137

RESULT 13
S30530
Ig heavy chain V region - human
C:Species: Homo sapiens (man)

C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C:Accession: S30530
R:Maricette, X.
Submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-123 <MAR>
A:Cross-references: EMBL:Z18316
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 468.5; DB 2; Length 123;
Best Local Similarity 75.6%; Pred. No. 6.4e-35;
Matches 90; Conservative 11; Mismatches 11; Indels 7; Gaps 2;

Oy 2 ESGGGLVPSQTLSTCTVSGSGSIRSGYWSWVRQPPGKLEWIGNIYHSGNTYNPSTL 61
Db 6 ESGGGLVPSQTLSTCTVSGYSI--SSGYWGWIRQPPGKLEWIGSHGSSYYPSTL 64

Oy 62 KSRITMSVDTSKNHPSLRSLTSVTADTAIVYCAR-----SDGYTLDMWGQGLVTVSS 114
Db 65 KSRITMSVDTSKNQPSLKLKSVTAADTAIVYCARGRYCSSTSCNMFPMWGQGLVTVSS 123

RESULT 14
S31511
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31511
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992.
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto- A:Reference number: S31509
A:Accession: S31511
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <CHA>
A:Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 75.8%; Score 465.5; DB 2; Length 155;
Best Local Similarity 74.2%; Pred. No. 1.5e-34;
Matches 89; Conservative 11; Mismatches 11; Indels 9; Gaps 2;

Oy 2 ESGGGLVPSQTLSTCTVSGSGSIRSGYWSWVRQPPGKLEWIGNIYHSGNTYNPSTL 61
Db 38 ESGGGLVPSQTLSTCTVSGSGSIS--YWSWIRQPPGKLEWIGRIYTSSTYNPSTL 95

Oy 62 KSRITMSVDTSKNHPSLRSLTSVTADTAIVYCARSDG-----YTLDMWGQGLVTVSS 114
Db 96 KSRITMSVDTSKNQPSLKLKSVTAADTAIVYCARGGGSISSWYDYGMDVWGQGLVTVSS 155

RESULT 15
S31512
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31512
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto A:Reference number: S31509
A:Accession: S31512
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <CHA>

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 08:52:21 ; Search time 71.6818 Seconds

(without alignments)
814.391 Million cell updates/sec

Title: US-10-027-725a-8

Perfect score: 614
Sequence: 1 LBSGPGLVKPSQTLSTLCTV.....RSDGYTLDMNGQTLVTWSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	492.5	80.2	476	2	O6GMX1 homo sapien
2	477	77.7	465	2	O6GMX6 homo sapien
3	476.5	77.6	492	2	O7Z374 homo sapien
4	470	76.5	478	2	O7Z379 homo sapien
5	466	75.9	150	2	O95973 homo sapien
6	466	75.9	496	2	O96KX8 homo sapien
7	463.5	75.5	119	2	O9UL73 homo sapien
8	457	74.4	477	2	O6GMX7 homo sapien
9	457	74.4	620	2	O96EY0 homo sapien
10	451	73.5	576	2	O6P418 homo sapien
11	440.5	71.7	130	1	HVZF_HUMAN
12	429	69.9	130	2	O81ZD7 homo sapien
13	427	69.5	139	2	O86SX2 homo sapien
14	426.5	69.5	595	2	O8WUX4 homo sapien
15	426.5	69.5	597	2	O6GMX5 homo sapien
16	426.5	69.5	597	2	O95U10 homo sapien
17	426.5	69.5	625	2	O96AA6 homo sapien
18	422.5	68.8	597	2	O9BQ88 homo sapien
19	417.5	68.0	478	2	O6MYH3 homo sapien
20	417	67.9	146	1	HVZ1_HUMAN
21	413	67.3	473	2	O8TC63 homo sapien
22	386	62.9	116	2	O7Z3Y6 homo sapien
23	383.5	62.5	476	2	O6WZX7 homo sapien
24	382.5	62.3	479	2	O99M22 mus musculu
25	381.5	62.1	117	1	HVGB_HUMAN
26	377	61.4	136	2	O6LBO5 mus musculu
27	365	59.4	122	2	O9UL75 homo sapien
28	363.5	59.2	137	1	HV46_MOUSE
29	360.5	58.7	262	2	O65Z11 mus musculu
30	352.5	57.4	144	1	HV43_MOUSE
31	347.5	56.6	113	1	HV47_MOUSE

32	346.5	56.4	121	2	O9UL96	O9UL96 homo sapien
33	341	55.5	118	2	O8LIU5	O8LIU5 mus musculu
34	339	55.2	121	2	O99NG4	O99NG4 mus musculu
35	338.5	55.1	116	1	HV61_MOUSE	P18532 mus musculu
36	335	54.6	117	1	HV62_MOUSE	P18533 mus musculu
37	335	54.6	482	2	O91X52	O91X52 mus musculu
38	332.5	54.2	116	1	HV60_MOUSE	P18531 mus musculu
39	325	52.9	135	1	HV02_XENLA	P20957 xenopus lae
40	315.5	51.4	118	2	O9UL74	O9UL74 homo sapien
41	314	51.1	120	1	HV2B_HUMAN	P01815 homo sapien
42	304.5	49.6	470	2	O6PJA4	O6PJA4 homo sapien
43	302.5	49.3	240	2	O65ZC9	O65ZC9 homo sapien
44	301	49.0	605	2	O6GN83	O6GN83 xenopus lae
45	300.5	48.9	466	2	O6IN78	O6IN78 homo sapien

ALIGNMENTS

RESULT 1	ID	Accession	PRELIMINARY	PRT	476 AA.
O6GMX1	O6GMX1				
AC	O6GMX1				
DT	05-JUL-2004	(TREMBLrel. 27, Created)			
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)			
DE	05-JUL-2004	(TREMBLrel. 27, Last annotation update)			
DE	Hypothetical protein.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Splice.				
RX	MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Ueda T.B., Toshimuki S., Carrincci P., Prange C.,				
RA	Rosa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,				
RA	Krzywinski M.I., Skalek U., Smallus D.E., Scherch A., Schein J.E.,				
RA	Jones S.J., Maita M.A.,				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Splice.				
RA	Strausberg R.,				
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC073773; AAH73773.1; -				
DR	InterPro; IPR003599; IG_1				
DR	InterPro; IPR007110; IG_1like				
DR	InterPro; IPR003597; IG_1				
DR	InterPro; IPR003006; IG_MHC				
DR	InterPro; IPR003596; IG_V				
DR	Pfam; PF07654; CI-sect; 3.				
DR	Pfam; PF00047; IG_4				
DR	SMART; SM00409; IG_2				
DR	SMART; SM00407; IG_1				
DR	SMART; SM00406; IGV_1				
DR	PROSITE; PS50835; IG_LIKE; 4.				
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.				

KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
Query Match 80.2%; Score 492.5; DB 2; Length 476;
Best Local Similarity 74.2%; Pred. No. 2,5e-41;
Matches 92; Conservative 13; Mismatches 6; Indels 13; Gaps 2;
QY 2 ESGGGLVPSQGLTSLTCTVSGSGSIRSGGYWVWVRQPPGKGLWIGNIYHSGNTYNPSTL 61
DB 25 ESGGGLVPSQGLTSLTCTVSGSGSISGQYWSWIRQPPGKGLWIGNIYHSGNTYNPSTL 84
QY KSRITMSVDSKKNHFSRLTSTVTAADPAVYYCARSDYITLDMNGGTLTVSS 110
DB 85 KSRITMSVDSKKNHFSRLTSTVTAADPAVYYCARSDYITLDMNGGTLTVSS 142
QY 111 TVSS 114
DB 143 TVSS 146
RESULT 2
Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC 06GMX6;
DT 05-JUN-2004 (TReMBLrel. 27, Created)
DT 05-JUN-2004 (TReMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casarini T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Vallatton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DB EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igcl; 3.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
Query Match 77.7%; Score 477; DB 2; Length 465;
Best Local Similarity 81.4%; Pred. No. 9e-40;
Matches 92; Conservative 6; Mismatches 13; Indels 2; Gaps 1;
QY 2 ESGGGLVPSQGLTSLTCTVSGSGSIRSGGYWVWVRQPPGKGLWIGNIYHSGNTYNPSTL 61
DB 25 ESGGGLVPSQGLTSLTCTVSGSGSIRSGGYWVWVRQPPGKGLWIGNIYHSGNTYNPSTL 82
QY KSRITMSVDSKKNHFSRLTSTVTAADPAVYYCARSDYITLDMNGGTLTVSS 114
DB 83 KSRITMSVDSKKNHFSRLTSTVTAADPAVYYCARSDYITLDMNGGTLTVSS 135
RESULT 3
Q7Z374 PRELIMINARY; PRT; 492 AA.
ID Q7Z374;
AC Q7Z374;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686C02218 (Fragment).
GN Name=DKFZp686C02218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecher H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DB EMBL; BX538077; CAD98001.1; -.
DR HSSP; P01820; 167J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 492 AA; 53776 MW; 1E7A15760F0CA74B CRC64;
Query Match 77.6%; Score 476.5; DB 2; Length 492;
Best Local Similarity 76.9%; Pred. No. 1.1e-39;
Matches 90; Conservative 11; Mismatches 11; Indels 5; Gaps 2;
QY 2 ESGGGLVPSQGLTSLTCTVSGSGSIRSGGYWVWVRQPPGKGLWIGNIYHSGNTYNPSTL 61
DB 37 ESGGGLVPSQGLTSLTCTVSGSGSVSNRNYYWGWIRQPPGKGLWIGNIYHSGNTYNPSTL 96
QY KSRITMSVDSKKNHFSRLTSTVTAADPAVYYCARSDYITLDMNGGTLTVSS 114
DB 97 KSRITMSVDSKKNHFSRLTSTVTAADPAVYYCARSDYITLDMNGGTLTVSS 152
RESULT 4
Q7Z379 PRELIMINARY; PRT; 478 AA.
ID Q7Z379;
AC Q7Z379;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686K04218 (Fragment).
GN Name=DKFZp686K04218;
OS Homo sapiens (Human).


```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecher H., Boeher M., Wewes H.W., Weil B., Amid C., Oanger A.,
RA Pobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538066; CAD97996.1; -.
DR HSP; P01820; IGI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-V.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00406; IGV. 1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG-MHC; UNKNOWN_2.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 478 AA; 51620 MW; 4AFB541F3217CA1 CRC64;

Query Match 76.5%; Score 470; DB 2; Length 478;
Best Local Similarity 75.7%; Pred. No. 4.7e-39;
Matches 87; Conservative 14; Mismatches 12; Indels 2; Gaps 1;

Qy 2 ESGGLVPSQTLSTCTVSGSGSIRSGYWSWRQPGKLEWIGNIYHSGNTYPSL 61
Db 24 ESGGLVPSQTLSTCTVSGSGSIRSGYWSWRQPGKLEWIGNIYHSGNTYPSL 83

Qy 62 KSRITMSVDTSKNHFSLRLTSVTADPAVYVCARSDGVT--TLDMWGQGLTVTVSS 114
Db 84 KSRITMSVDTSKNHFSLRLTSVTADPAVYVCARSDGVT--TLDMWGQGLTVTVSS 138

RESULT 5
095973 PRELIMINARY; PRT; 150 AA.
AC 095973;
DT 01-MAY-1999 (TREMBLrel. 10; Created)
DT 01-MAY-1999 (TREMBLrel. 10; Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26; Last annotation update)
DE VHA heavy chain variable region precursor (Fragment).
GN Name=IGH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103795; AAC79084.1; -.
DR PIR; S31673; S31673.
DR PIR; S78056; S78056.
DR HSP; P01820; IGI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG-V.
DR SMART; SM00406; IGV. 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 >150 VHA heavy chain variable region.
FT NON TER 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;

Query Match 75.9%; Score 466; DB 2; Length 150;
Best Local Similarity 76.1%; Pred. No. 3.4e-39;
Matches 86; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

Qy 2 ESGGLVPSQTLSTCTVSGSGSIRSGYWSWRQPGKLEWIGNIYHSGNTYPSL 61
Db 24 ESGGLVPSQTLSTCTVSGSGSIRSGYWSWRQPGKLEWIGNIYHSGNTYPSL 83
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Db 25 ESGGLVPSQTLSTCTVSGSGSIRSGYWSWRQPGKLEWIGNIYHSGNTYPSL 84
Qy 62 KSRITMSVDTSKNHFSLRLTSVTADPAVYVCARSDGVT--TLDMWGQGLTVTVSS 114
Db 85 KSRITMSVDTSKNHFSLRLTSVTADPAVYVCARSDGVT--TLDMWGQGLTVTVSS 137

RESULT 6
096KX8 PRELIMINARY; PRT; 496 AA.
AC 096KX8;
DT 01-DEC-2001 (TREMBLrel. 19; Created)
DT 01-DEC-2001 (TREMBLrel. 19; Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26; Last annotation update)
DE MGC27165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22386257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshlyak S., Carrincci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bogak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smaluk D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strauberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016369; AAH16369.1; -.
DR HSP; P01876; IOM0.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-V.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00406; IGV. 1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG-MHC; UNKNOWN_1.
SQ SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;

Query Match 75.9%; Score 466; DB 2; Length 496;
Best Local Similarity 74.2%; Pred. No. 1.2e-38;
Matches 89; Conservative 10; Mismatches 13; Indels 8; Gaps 2;

Qy 2 ESGGLVPSQTLSTCTVSGSGSIRSGYWSWRQPGKLEWIGNIYHSGNTYPSL 61
Db 25 ESGGLVPSQTLSTCTVSGSGSIRSGYWSWRQPGKLEWIGNIYHSGNTYPSL 84

Qy 62 KSRITMSVDTSKNHFSLRLTSVTADPAVYVCARSDGVT--TLDMWGQGLTVTVSS 114
Db 85 KSRITMSVDTSKNHFSLRLTSVTADPAVYVCARSDGVT--TLDMWGQGLTVTVSS 143
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RESULT 7
Q9UL73 PRELIMINARY; PRT; 119 AA.
ID Q9UL73
AC Q9UL73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22386257; PubMed=9614934; DOI=10.1006/clin.1998.4531;
   Wu X., Liu B., Van der Merwe P.L., Kalle N.N., Berney S.M.,
   RA Young D.C.;
   RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   RT fetus.";
   RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AAD56277.1; -.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BD86B6420EAOBE CRC64;

Query Match 75.5%; Score 463.5; DB 2; Length 119;
Best Local Similarity 77.6%; Pred. No. 4.8e-39;
Matches 90; Conservative 9; Mismatches 12; Indels 5; Gaps 2;

Qy 2 ESGGGLVKKPQTLSTLTCTVSGSGSIRSGGYMSWRQPGKGLWIGNIGYHSGNTYNPSTL 61
Db 6 ESGGGLVKKPSETLSTLTCTVSGSGSIS--YMSWRQPGKGLWIGYIGYHSGNTYNPSTL 63

Qy 62 KSRITMSVDTSKNPSLRITSVTAADTAIVYCARSDG--YTLDNWGGGTLVTYSS 114
Db 64 KSRVTISVDTSKNSQPSLRITSLTAADTAIVYCARLSNMGPIYFDWGGGTLVTYSS 119

RESULT 8
Q6GMX7 PRELIMINARY; PRT; 477 AA.
ID Q6GMX7
AC Q6GMX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
   RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
   RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
   RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
   RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
   RA Stadleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
   RA Brownstein M.J., Uedini T.B., Toshnyuki S., Carninci P., Prange C.,
   RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
   RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
   RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
   RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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   RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
   RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
   RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
   RA Rodriguez A.C., Grimwood J., Myers R.M., Butterfield Y.S.,
   RA Krzywinski M.I., Skaleja U., Smalhus D.E., Schercher A., Schein J.E.,
   RA Jones S.J., Marra M.A.;
   RT "Generation and initial analysis of more than 15,000 full-length human
   RT and mouse cDNA sequences.";
   RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RA Straubeberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073765; AAH73765.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-sect; 2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGc1; 3.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFE85 CRC64;

Query Match 74.4%; Score 457; DB 2; Length 477;
Best Local Similarity 77.4%; Pred. No. 9.7e-38;
Matches 89; Conservative 7; Mismatches 15; Indels 4; Gaps 2;

Qy 2 ESGGGLVKKPQTLSTLTCTVSGSGSIRSGGYMSWRQPGKGLWIGNIGYHSGNTYNPSTL 61
Db 25 ESGGGLVKKPSETLSTLTCTVSGSGSIS--YMSWRQPGKGLWIGYIGYHSGNTYNPSTL 82

Qy 62 KSRITMSVDTSKNPSLRITSVTAADTAIVYCARSDG--YTLDNWGGGTLVTYSS 114
Db 83 KSRVTISVDTSKNSQPSLRITSLTAADTAIVYCARLSNMGPIYFDWGGGTLVTYSS 137

RESULT 9
Q96EY0 PRELIMINARY; PRT; 620 AA.
ID Q96EY0
AC Q96EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
   RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
   RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
   RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
   RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
   RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
   RA Stadleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
   RA Brownstein M.J., Uedini T.B., Toshnyuki S., Carninci P., Prange C.,
   RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
   RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
   RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
   RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
   RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
   RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strauberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011857; AAH11857.2; -.
 DR PIR; S15590; S15590.
 DR HSSP; P01820; 1G7J.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-sec; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00407; IGV; 4.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
 SQ SEQUENCE 620 AA; 68125 MW; 990A1A4AE8FF27B CRC64;

Query Match 74.4%; Score 457; DB 2; Length 620;
 Best Local Similarity 78.0%; Pred. No. 1.3e-37;
 Matches 92; Conservative 7; Mismatches 11; Indels 8; Gaps 3;

Oy 2 ESGGLVPSQTLSTCTVSGSIRSGGYWVRQPGKLEWIGNITGSGNTYNSL 61
 Db 32 ESGGLVPSQTLSTCTVSGSIRSGGYWVRQPGKLEWIGNITGSGNTYNSL 89
 Oy 62 KSRITMSYDTSKMFSLRLTSTVTAADTAIVYVCASDGYTLDN-----WGQGLTVTVSS 114
 Db 90 KSRITMSYDTSKMFSLRLTSTVTAADTAIVYVCASDGYTLDN-----WGQGLTVTVSS 146

RESULT 10
 Q6P418 PRELIMINARY; PRT; 576 AA.
 ID Q6P418; PRT; 576 AA.
 AC Q6P418;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE IGH protein.
 GN Name=IGHD;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA MEDLINE=22288257; PubMed=12477932; DOI=10.1073/pnae.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stabileton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uscid T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Mizny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shechenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,

RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strauberg R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC063384; AAH63384.1; -.
 DR HSSP; P01820; 1A7N.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-sec; 2.
 DR SMART; SM00407; IG; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IGV; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 SQ SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;

Query Match 73.5%; Score 451; DB 2; Length 576;
 Best Local Similarity 76.7%; Pred. No. 4.8e-37;
 Matches 89; Conservative 7; Mismatches 16; Indels 4; Gaps 2;

Oy 2 ESGGLVPSQTLSTCTVSGSIRSGGYWVRQPGKLEWIGNITGSGNTYNSL 61
 Db 32 ESGGLVPSQTLSTCTVSGSIRSGGYWVRQPGKLEWIGNITGSGNTYNSL 90
 Oy 62 KSRITMSYDTSKMFSLRLTSTVTAADTAIVYVCASDGYTLDN-----YTLDNMGGLTVTVSS 114
 Db 91 KSRITMSYDTSKMFSLRLTSTVTAADTAIVYVCASDGYTLDN-----YTLDNMGGLTVTVSS 146

RESULT 11
 HYZF_HUMAN STANDARD; PRT; 129 AA.
 ID HYZF_HUMAN
 AC P01824;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V-II region WH1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=8222235; PubMed=6806818;
 RA Takahashi N., Terauchi D., Debutre B., Lin L.-C., Putnam F.W.;
 RT "Complete amino acid sequence of the delta heavy chain of human
 RT immunoglobulin D.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
 CC -I- MISCELLANEOUS: This chain was isolated from an Igd myeloma
 CC protein.
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02099; D2HUMA.
 DR HSSP; P01820; 1G7J.
 DR GlycoSiteDB; P01824; -.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 113 Ig-like.

RC TISSUE=Lymph;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.2; -.
DR PIR; G34964; G34964.
DR HSP; P01861; IADO.
DR Pfam; PF07654; Cl-sec; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 595 AA; 65290 MW; 0D4B5076545714E CRC64;

Query Match 69.5%; Score 426.5; DB 2; Length 595;
Best Local Similarity 70.0%; Pred. No. 1.5e-34;
Matches 84; Conservative 10; Mismatches 15; Indels 11; Gaps 3;

Qy 4 GPGVKSQTLSTCTVSGSIRSGYVSWRPPGKLEWIGNIYHSGNTYNNPSLKS 63
Db 34 GAGLLKPSSETLSTCGVYGSF--SGYVSWIRPPGKLEWIGNIYHSGNTYNNPSLKS 91
Qy 64 RITMSVDTSKNHFSLRTSVTAADTAVYYCAR-----SDG-YTLDNMGGTLVTVSS 114
Db 92 RVTISVDTSKKQLSLKLSVNAADTAVYYCARVITRASPGTDGRYGMVWGQITVTVSS 151

RESULT 15
Q6GMX5 PRELIMINARY; PRT; 597 AA.
ID Q6GMX5
AC Q6GMX5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
CX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosnak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.F.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073767; AAH73767.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003597; IG_cl.

DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-sec; 4.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;

Query Match 69.5%; Score 426.5; DB 2; Length 597;
Best Local Similarity 70.0%; Pred. No. 1.5e-34;
Matches 84; Conservative 10; Mismatches 15; Indels 11; Gaps 3;

Qy 4 GPGVKSQTLSTCTVSGSIRSGYVSWRPPGKLEWIGNIYHSGNTYNNPSLKS 63
Db 27 GAGLLKPSSETLSTCGVYGSF--SGYVSWIRPPGKLEWIGNIYHSGNTYNNPSLKS 84
Qy 64 RITMSVDTSKNHFSLRTSVTAADTAVYYCAR-----SDG-YTLDNMGGTLVTVSS 114
Db 85 RVTISVDTSKKQLSLKLSVNAADTAVYYCARVITRASPGTDGRYGMVWGQITVTVSS 144

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Job time : 72.6818 secs

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OM protein - protein search, using sw model

Run on: July 26, 2005, 08:50:20 ; Search time 85.3273 Seconds
(without alignments)
516.724 Million cell updates/sec

Title: US-10-027-725A-8
Perfect score: 614
Sequence: 1 IESGPGIVKPSQTLSTLCTV.....RSDGYTLDMWGQGLTVVSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	614	100.0	114	5	ABG30446 Human IGE
2	608	99.0	114	5	ABG30447 Human IGE
3	546	88.9	114	5	ABG30445 Human IGE
4	511	83.2	128	8	ADP22124 Human ant
5	511	83.2	128	8	ADP22104 Human ant
6	511	83.2	128	8	ADP22096 Human ant
7	510.5	83.1	121	7	ADP03982 Murine-ex
8	510	83.1	118	7	ADP03968 Murine-ex
9	509.5	83.0	123	7	ADP03870 Murine-ex
10	507.5	82.7	125	7	ADP03871 Murine-ex
11	507	82.6	120	7	ADP03974 Murine-ex
12	507	82.6	120	7	ADP03873 Murine-ex
13	507	82.6	122	7	ADP03977 Murine-ex
14	507	82.6	473	4	AAB36206 Human imm
15	506	82.4	221	7	ADJ32126 Human int
16	505.5	82.3	121	7	ADP03981 Murine-ex
17	505	82.2	128	8	ADP22120 Human ant
18	504.5	82.2	117	7	ADCC99784 Anti-huma
19	504.5	82.2	117	7	ADDO5388 Anti-MUC1
20	504.5	82.2	117	7	ADFO9826 Human ant
21	503.5	82.0	119	2	ADP03970 Murine-ex
22	502.5	81.8	123	2	AAW78433 Antibody
23	502.5	81.8	123	5	ABB97976 Heavy cha
24	502.5	81.8	123	7	ADG88414 anti-Ob-R
25	502.5	81.8	123	7	ADP03872 Murine-ex

26	502	81.8	124	7	ADP03935	Adp03935 Murine-ex
27	501	81.6	252	5	ABP45318	Adp45318 Human Bly
28	501	81.6	252	7	ADG96145	Adg96145 Single ch
29	500.5	81.5	127	4	AAg80217	AAg80217 Human aut
30	500	81.4	120	7	ADP03958	Adp03958 Murine-ex
31	500	81.4	120	7	ADP03969	Adp03969 Murine-ex
32	500	81.4	121	7	ADJ80377	Adj80377 Antibody
33	500	81.4	126	3	AAB30584	Aab30584 A human v
34	500	81.4	126	5	ABP54970	Abp54970 Anti-idio
35	500	81.4	251	5	ABG80712	ABG80712 Amyloid P
36	500	81.4	254	5	ABG80713	ABG80713 Amyloid P
37	500	81.4	263	5	ABG80714	ABG80714 Human Igg
38	499.5	81.4	120	4	AAB62775	Aab62775 Human HIV
39	499.5	81.4	123	7	AAy42965	AAy42965 Kabat Id
40	499.5	81.4	135	7	AAy42974	AAy42974 Kabat Id
41	499	81.3	116	7	ADP03957	Adp03957 Murine-ex
42	498.5	81.2	125	7	ADP03868	Adp03868 Murine-ex
43	498.5	81.2	125	7	ADP03876	Adp03876 Murine-ex
44	498	81.1	123	4	AAB62745	Aab62745 Human HIV
45	497.5	81.0	119	7	ADP03961	Adp03961 Murine-ex

ALIGNMENTS

RESULT 1	
ABG30446	
ID	ABG30446 standard; protein: 114 AA.
XX	
AC	ABG30446;
DT	21-OCT-2002 (first entry)
XX	
DE	Human IGE Fab clone 60 heavy chain protein.
XX	
KW	Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;
KM	timothy grass pollen allergen; passive immunotherapy.
XX	
OS	Homo sapiens.
XX	
FN	
FT	Key
FT	Region
FT	Location/Qualifiers
FT	/note= "FRI region"
FT	27..33
FT	Region
FT	/note= "CDR1 region"
FT	34..47
FT	Region
FT	/note= "FR2 region"
FT	48..63
FT	Region
FT	/note= "CDR2 protein"
FT	64..95
FT	Region
FT	/note= "FR3 region"
FT	96..103
FT	Region
FT	/note= "CDR2 region"
FT	104..114
FT	Region
FT	/note= "FR4 region"
XX	
PN	WO200253595-A1.
XX	
PD	11-JUL-2002.
XX	
PP	27-DEC-2001; 2001WO-SE002908.
XX	
XX	29-DEC-2000; 2000SE-00004892.
PR	
XX	
XX	(PNA) PHARMACIA DIAGNOSTICS AB.
PA	
XX	
XX	Flicker S, Steinberger P, Kraft D, Valenta R;
PI	
XX	WPI: 2002-583604/62.
DR	
DR	N-PSDB; ABK89638.
XX	
PT	Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT	variable region of group 2 allergen specific-human IGE Fabs, useful for

PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
XX
PS Disclosure; Page 37; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE
CC antibodies to Phi P 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific Fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The Fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific Fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergen patients
CC IgE antibodies to Phi P 2. The present sequence represents the human IgG
CC Fab, clone 60 heavy chain protein of the invention
CC
XX Sequence 114 AA;
SQ
Query Match 100.0%; Score 614; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.9e-45;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LBSGPGLVKPSQTLSTCTVSGGSIRSGYVSWVROPFGKLEWIGNIYHSGNTYVNS 60
1 LBSGPGLVKPSQTLSTCTVSGGSIRSGYVSWVROPFGKLEWIGNIYHSGNTYVNS 60
Db 1 LBSGPGLVKPSQTLSTCTVSGGSIRSGYVSWVROPFGKLEWIGNIYHSGNTYVNS 60
QY 61 LKSRITMSVDTSKNHFSLRLTSTVADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
61 LKSRITMSVDTSKNHFSLRLTSTVADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
Db 61 LKSRITMSVDTSKNHFSLRLTSTVADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
RESULT 2
ABG30447 ID ABG30447 standard; protein; 114 AA.
XX
AC ABG30447;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human IgE Fab clone 100 heavy chain protein.
XX
KM Human; Fab; antiallergic; vaccine; grass pollen; Phi P 2;
KM timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Region 1..26
FT /note= "FR1 region"
FT Region 27..33
FT /note= "CDR1 region"
FT Region 34..47
FT /note= "FR2 region"
FT Region 48..63
FT /note= "CDR2 protein"
FT Region 64..95
FT /note= "FR3 region"
FT Region 96..103
FT /note= "CDR2 region"
FT Region 104..114
FT /note= "FR4 region"
XX
XX WO200253595-A1.
XX
XX 11-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-SB002908.
XX

PR 29-DEC-2000; 2000SE-00004892.
XX
XX (PHAA) PHARMACIA DIAGNOSTICS AB.
XX
XX Flicker S, Steindberger P, Kraft D, Valenta R;
PI WPI; 2002-583604/62.
XX
XX N-PSDB; ABK89639.
DR
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
XX Disclosure; Page 38; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE
CC antibodies to Phi P 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific Fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The Fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific Fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergen patients
CC IgE antibodies to Phi P 2. The present sequence represents the human IgG
CC Fab, clone 100 heavy chain protein of the invention
CC
XX Sequence 114 AA;
SQ
Query Match 99.0%; Score 608; DB 5; Length 114;
Best Local Similarity 97.4%; Pred. No. 3.2e-44;
Matches 111; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 LBSGPGLVKPSQTLSTCTVSGGSIRSGYVSWVROPFGKLEWIGNIYHSGNTYVNS 60
1 LBSGPGLVKPSQTLSTCTVSGGSIRSGYVSWVROPFGKLEWIGNIYHSGNTYVNS 60
Db 1 LBSGPGLVKPSQTLSTCTVSGGSIRSGYVSWVROPFGKLEWIGNIYHSGNTYVNS 60
QY 61 LKSRITMSVDTSKNHFSLRLTSTVADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
61 LKSRITMSVDTSKNHFSLRLTSTVADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
Db 61 LKSRITMSVDTSKNHFSLRLTSTVADTAVYYCARSDGYTLDMWGQGLTVTVSS 114
RESULT 3
ABG30445 ID ABG30445 standard; protein; 114 AA.
XX
AC ABG30445;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human IgE Fab clone 94 heavy chain protein.
XX
KM Human; Fab; antiallergic; vaccine; grass pollen; Phi P 2;
KM timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Region 1..26
FT /note= "FR1 region"
FT Region 27..33
FT /note= "CDR1 region"
FT Region 34..47
FT /note= "FR2 region"
FT Region 48..63
FT /note= "CDR2 protein"
FT Region 64..95
FT /note= "FR3 region"
FT
FT Region

FT	Region	96..103
FT	/note= "CDR2 region"	
FT	Region	104..114
XX	/note= "FR4 region"	
PN	MO200253595-A1.	
XX		
PD	11-JUL-2002.	
XX		
PF	27-DEC-2001; 2001WO-SE002908.	
PR	29-DEC-2000; 2000SE-00004892.	
XX	(PHAA) PHARMACIA DIAGNOSTICS AB.	
PA	Flicker S, Steinberger P, Kraft D, Valenta R;	
PI	WPI : 2002-583604/62.	
DR	N-PADB; ABR89637.	
XX		
PT	Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising	
PT	variable region of group 2 allergen specific-human Igr Fabs, useful for	
PT	diagnosing or passive immunotherapy of type I allergy, for environmental	
PT	allergen detection.	
XX		
PS	Disclosure; Page 36; 45pp; English.	
XX		
CC	This invention relates to the DNA and protein sequences of group 2	
CC	allergen-specific human Ige Fabs and methods for their use. The proteins	
CC	of the invention may have antiallergic activities and may be used as a	
CC	vaccine or an inhibitor of binding of grass pollen allergic patient's Ige	
CC	antibodies to Phi p 2 (a major timothy grass pollen allergen). The group	
CC	2 allergen-specific fabs of the invention may be useful for environmental	
CC	allergen detection and for standardisation of allergen extracts. The fabs	
CC	- or a vaccine againts a type I allergy is useful for passive	
CC	immunotherapy of type I allergy, it is also useful for diagnosing a type	
CC	I allergy. The allergen-specific fabs of the invention are useful for	
CC	inter alia, diagnosis, therapy and prevention of type I allergy. They are	
CC	also useful for identification of group 2 allergen-containing pollen and	
CC	may be used for blocking the binding of grass pollen allergic patients	
CC	Ige antibodies to Phi p 2. The present sequence represents the human Ige	
CC	fab, clone 94 heavy chain protein of the invention	
XX		
SQ	Sequence 114 AA;	
	Query Match 88.9%; Score 546; DB 5; Length 114;	
	Best Local Similarity 89.5%; Pred. No. 6.1e-39;	
	Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0	
OY	1 LESGGGLVKKPSSQLTCTSVSGSIRSGGYVSWVRQPKGLEWIGNIYHSGNTYYNS 60	
DB	1 LESGGGLVKRPQTLSLSCAVSGSIRSGGYVSWVRQHPKGLIEWIGIYIHSGNTYYNS 60	
OY	61 LKSRTWSVDTSKNHPSLRISLTVAADRAVYYCARSDGTLDLWNQGTLVTYSS 114	
DB	61 LKSRFMSVDITSENKFSRLINSLVTAADRAVYYCARLDGDTLDIWCGGLTVYSS 114	
RESULT 4		
ADP22124	ID ADP22124 standard; protein; 128 AA.	
XX	ADP22124;	
AC	ADP22124;	
DT	09-SEP-2004 (first entry)	
XX		
DE	Human anti-TNFa antibody heavy chain variable region SEQ ID NO:30.	
XX		
KW	human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;	
KW	anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;	
KW	antibacterial; antiinflammatory; antipsoriatic; antirheumatic;	
KW	eating-disorder; immunomodulator; immunosuppressive; nephrotoxic;	
KW	neuroprotective; vasculotopic; antiboprotic; TNFa antagonist;	

OS TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KW prostate cancer; immuno-mediated inflammatory disease;
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 KW septic shock; cachexia; anorexia; multiple sclerosis.
 XX
 OS Homo sapiens.
 XX
 XX MO2004050683-A2.
 XX
 XX 17-JUN-2004.
 XX
 XX 02-DEC-2003; 2003WO-US038281.
 XX
 XX 02-DEC-2002; 2002US-0430729P.
 XX
 XX (ABGE-) ABGENIX INC.
 XX
 XX Babcock JS, Kang JS, Poord O, Green L, Peng X, Klakamp S,
 P1 Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R,
 P1 Manchenlenko K, Faggioni R, Senaldi G, Gaojuan JS;
 P1
 XX WPI: 2004-480601/45.
 DR N-PSDB; ADP22123.
 XX
 XX
 XX New recombinant human monoclonal antibody that specifically binds to
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.
 PT
 PS Example 10; SEQ ID NO 30; 213pp; English.
 XX
 CC The present invention describes a human monoclonal antibody (I) that
 CC specifically binds to tumour necrosis factor-alpha (TNFα) and comprises:
 CC (a) a heavy chain complementarily determining region 1 (CDRI) having the
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDRI having the two fully defined 11 amino acid
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
 CC (M1) the level of TNFα in a patient sample, comprising contacting with
 CC (I), and detecting the level of binding between the antibody and TNFα in
 CC the sample; (2) a composition comprising the antibody or its functional
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFα induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNFα induced apoptosis by administering the human monoclonal antibody of
 CC (I). (I) has antibody, antiatherosclerotic, antiarthritic,
 CC antibacterial, antiinflammatory, antiproliferative, antinephritic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNFα antagonist. The antibody (I) is useful in the preparation of
 CC medication for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNFα
 CC antibody heavy chain variable region, which is used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 128 AA;
 XX
 XX Query Match 83.2%; Score 511; DB 8; Length 128;
 XX Best Local Similarity 78.9%; Pred. No. 6.5e-36;
 XX Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;

Db 6 ESRGLVKEPQTLSTCTVSGGSISSGGYWSWVRQPGKLEWIGNIYYSGTYNPSL 65
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSDG-----YTIIDNNQGGTLVY 111
 Db 66 KSRVITISVDTSKQFSLKLSVTAADTAAYVYCARSDNQYWNDEVDYGLDVMGQGITVT 125
 QY 112 VSS 114
 Db 126 VSS 128
 Db 126 VSS 128
 RESULT 5
 ADP22104
 ID ADP22104 standard; protein; 128 AA.
 AC ADP22104;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human anti-TNFa antibody heavy chain variable region SEQ ID NO:10.
 XX
 KW human, monoclonal antibody; tumour necrosis factor-alpha; TNFa;
 KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KW prostate cancer; immun-mediated inflammatory disease;
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 KW septic shock; cachexia; anorexia; multiple sclerosis.
 KW
 OS Homo sapiens.
 XX
 PN WO2004050683-A2.
 PD 17-JUN-2004.
 XX
 PF 02-DEC-2003; 2003WO-US038281.
 XX
 PR 02-DEC-2002; 2002US-0430729P.
 XX
 PA (ABGE-) ABGENIX INC.
 PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
 PI Haak-Frendscho M, Rathnaswami P, Pigott C, Liang ML, Lee R;
 PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan US;
 DR WPI; 2004-480601/45.
 XX N-PSDB; ADP22103.
 XX
 PT New recombinant human monoclonal antibody that specifically binds to
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.
 XX
 PS Example 10; SEQ ID NO 10; 213pp; English.
 XX
 CC The present invention describes a human monoclonal antibody (I) that
 CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
 CC (M1) the level of TNFa in a patient sample, comprising contacting with
 CC (1), and detecting the level of binding between the antibody and TNFa in
 CC the sample; (2) a composition comprising the antibody or its functional
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced

CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNFa induced apoptosis by administering the human monoclonal antibody of
 CC (1). (1) has anabolic, antiarteriosclerotic, antiarthritic,
 CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
 CC disorder, immunomodulator, immunosuppressive, nephrotropic,
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNFa antagonist. The antibody (I) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis, Crohn's
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNFa
 CC antibody heavy chain variable region, which is used in the
 CC exemplification of the present invention.
 CC
 SQ Sequence 128 AA;
 Query Match 83.2%; Score 511; DB 8; Length 128;
 Best Local Similarity 78.9%; Pred. No. 6.5e-36;
 Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;
 QY 2 ESRGLVKEPQTLSTCTVSGGSISSGGYWSWVRQPGKLEWIGNIYYSGTYNPSL 61
 Db 6 ESRGLVKEPQTLSTCTVSGGSISSGGYWSWVRQPGKLEWIGNIYYSGTYNPSL 65
 QY 62 KSRITMSVDTSKNHFSLRLTSVTAADTAAYVYCARSDG-----YTIIDNNQGGTLVY 111
 Db 66 KSRVITISVDTSKQFSLKLSVTAADTAAYVYCARSDNQYWNDEVDYGLDVMGQGITVT 125
 QY 112 VSS 114
 Db 126 VSS 128
 Db 126 VSS 128
 RESULT 6
 ADP22096
 ID ADP22096 standard; protein; 128 AA.
 XX
 AC ADP22096;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human anti-TNFa antibody heavy chain variable region SEQ ID NO:2.
 XX
 KW human, monoclonal antibody; tumour necrosis factor-alpha; TNFa;
 KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
 KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
 KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KW prostate cancer; immuno-mediated inflammatory disease;
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 KW septic shock; cachexia; anorexia; multiple sclerosis.
 KW
 OS Homo sapiens.
 XX
 PN WO2004050683-A2.
 PD 17-JUN-2004.
 XX
 PF 02-DEC-2003; 2003WO-US038281.
 XX
 PR 02-DEC-2002; 2002US-0430729P.
 XX
 PA (ABGE-) ABGENIX INC.
 PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;

PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
PI Manchulenchu K, Faggioni R, Senaldi G, Qiaojuan JS;
PI WPI; 2004-480601/45.
DR N-PSDB; ADP22095.
XX
PT New recombinant human monoclonal antibody that specifically binds to
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT arthritis.
XX
PS Example 10; SEQ ID NO 2; 213pp; English.
XX
CC The present invention describes a human monoclonal antibody (I) that
CC specifically binds to tumor necrosis factor-alpha (TNF) and comprises:
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC (M1) the level of TNF in a patient sample, comprising contacting with
CC (1), and detecting the level of binding between the antibody and TNF in
CC the sample; (2) a composition comprising the antibody or its functional
CC fragment and a carrier; (3) treating (M2) an animal suffering from a
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC animal in need of treatment for the disease by administering the human
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNF induced
CC apoptosis in an animal by selecting an animal in need of treatment for
CC TNF induced apoptosis by administering the human monoclonal antibody of
CC (I). (I) has anabolic, antiarteriosclerotic, antirheumatic,
CC antibacterial, antiinflammatory, antiproliferative, antihemetic, eating-
CC disorder, immunomodulator, immunosuppressive, nephrotoxic,
CC neuroprotective, vasotropic and antiproliferative activities, and can be used
CC as a TNF antagonist. The antibody (I) is useful in the preparation of a
CC medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-most reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence represents a human anti-TNFa
CC antibody heavy chain variable region, which is used in the
CC exemplification of the present invention.
XX
XX Sequence 128 AA;
SQ
Query Match 83.2%; Score 511; DB 8; Length 128;
Best Local Similarity 78.9%; Pred. No. 6.5e-36;
Matches 97; Conservative 7; Mismatches 9; Indels 10; Gaps 1;
QY 2 ESGGGLVKEPQTLSTLTCTVSGGSIIRSGGYWVWVOPPGKLEWIGNIYHSGNTYVPSL 61
DB 6 ESGGGLVKEPQTLSTLTCTVSGGSIIRSGGYWVWVOPPGKLEWIGNIYHSGNTYVPSL 65
QY 62 KSRITMSVDTSKNHFSLRLTSTVTAADTAIVVYCARSDG-----YTLDMWCGTLYVT 111
DB 66 KSRITISVDTSKNHFSLRLTSTVTAADTAIVVYCARSDG-----YTLDMWCGTLYVT 125
QY 112 VSS 114
DB 126 VSS 128
RESULT 7
ADP03982 ID ADP03982 standard; protein, 121 AA.
XX
AC ADP03982;
XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 152.
XX

KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW cytosolic; colorectal neoplasm; renal cell carcinoma;
KW cervical intraepithelial squamous neoplasia;
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KW gene therapy; murine; mouse; human; heavy chain variable domain.
XX
OS Unidentified.
XX
PN WO2003048328-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038550.
XX
PR 03-DEC-2001; 2001US-0337275P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudae J, Foltz I, Handa M, Gallo M;
XX
DR WPI; 2003-523295/49.
XX
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.;
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS Example 2; SEQ ID NO 152; 89pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytosolic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
XX Sequence 121 AA;
SQ
Query Match 83.1%; Score 510.5; DB 7; Length 121;
Best Local Similarity 82.8%; Pred. No. 6.8e-36;
Matches 96; Conservative 8; Mismatches 9; Indels 3; Gaps 1;
QY 2 ESGGGLVKEPQTLSTLTCTVSGGSIIRSGGYWVWVOPPGKLEWIGNIYHSGNTYVPSL 61
DB 6 ESGGGLVKEPQTLSTLTCTVSGGSIIRSGGYWVWVOPPGKLEWIGNIYHSGNTYVPSL 65
QY 62 KSRITMSVDTSKNHFSLRLTSTVTAADTAIVVYCARSDG-----GYTLDMWCGTLYVTSS 114
DB 66 KSRITISVDTSKNHFSLRLTSTVTAADTAIVVYCARSDG-----GYTLDMWCGTLYVTSS 121
RESULT 8
ADP03968 ID ADP03968 standard; protein, 118 AA.
XX
AC ADP03968;
XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 138.
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW cytosolic; colorectal neoplasm; renal cell carcinoma;
KW cervical intraepithelial squamous neoplasia;
KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KW gene therapy; murine; mouse; human; heavy chain variable domain.
XX

OS Unidentified.
 XX WO2003048328-A2.
 PN
 XX
 XX 12-JUN-2003.
 PD
 XX
 XX 02-DEC-2002; 2002WO-US038550.
 PF
 XX
 XX 03-DEC-2001; 2001US-0337275P.
 PR
 XX
 XX (ABGE-) ABGENIX INC.
 PA
 XX Gudae J, Foltz I, Handa M, Gallo M;
 PI WPI; 2003-523295/49.
 DR
 XX
 XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
 XX
 XX Example 2; SEQ ID NO 138; 89pp; English.
 PS
 XX The invention relates to a novel isolated monoclonal antibody (mAb)
 CC comprising a heavy chain polypeptide and light chain polypeptide having a
 CC sequence chosen from one of 53 fully defined amino acid sequences given
 CC in the specification, where the antibody specifically binds carbonic
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
 CC demonstrates cytosstatic activity and may be useful for treating a tumour,
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
 CC tumour or breast cancer, possibly via gene therapy. The current sequence
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
 CC (heavy chain variable domain) protein of the invention. The protein was
 CC generated via the introduction of the human CA IX protein into a
 CC transgenic mouse strain.
 CC
 SQ Sequence 118 AA;
 Query Match 83.1%; Score 510; DB 7; Length 118;
 Best Local Similarity 85.0%; Pred. No. 7.3e-36;
 Matches 96; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
 QY 2 ESGPGLVKEPQTLSTCTVSGGSRGGYMSWVRQPGKGLWIGNIHSGNTYNPSTL 61
 DB 6 ESGPGLVKEPQTLSTCTVSGGSRGGYMSWVRQPGKGLWIGNIHSGNTYNPSTL 65
 QY 62 KSRITMSVDFSKNHFSLRLTSVTAADTAAYVYCARSDGYTLDMWGQGLVTVSS 114
 DB 66 KSRVITISVDTSKQFSLKLSSTVTAADTAAYVYCARVYSGSDGYWGQGLVTVSS 118
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 10.
 XX
 XX monoclonaal antibody; carbonic anhydrase IX; CA IX tumour antigen;
 KW cytosstatic; colorectal neoplasm; renal cell carcinoma;
 KW cervical intraepithelial squamous neoplasia;
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
 KW gene therapy; murine; mouse; human; heavy chain variable domain.
 XX
 OS Unidentified.
 XX
 XX WO2003048328-A2.
 PN
 XX
 XX 12-JUN-2003.
 PD
 XX

PF 02-DEC-2002; 2002WO-US038550.
 XX
 XX 03-DEC-2001; 2001US-0337275P.
 XX
 XX (ABGE-) ABGENIX INC.
 PA
 XX Gudae J, Foltz I, Handa M, Gallo M;
 PI WPI; 2003-523295/49.
 DR
 XX
 XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
 XX
 XX Claim 1; SEQ ID NO 10; 89pp; English.
 PS
 XX The invention relates to a novel isolated monoclonal antibody (mAb)
 CC comprising a heavy chain polypeptide and light chain polypeptide having a
 CC sequence chosen from one of 53 fully defined amino acid sequences given
 CC in the specification, where the antibody specifically binds carbonic
 CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
 CC demonstrates cytosstatic activity and may be useful for treating a tumour,
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
 CC tumour or breast cancer, possibly via gene therapy. The current sequence
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
 CC (heavy chain variable domain) protein of the invention. The protein was
 CC generated via the introduction of the human CA IX protein into a
 CC transgenic mouse strain.
 CC
 SQ Sequence 123 AA;
 Query Match 83.0%; Score 509.5; DB 7; Length 123;
 Best Local Similarity 82.2%; Pred. No. 8.4e-36;
 Matches 97; Conservative 8; Mismatches 8; Indels 5; Gaps 1;
 QY 2 ESGPGLVKEPQTLSTCTVSGGSRGGYMSWVRQPGKGLWIGNIHSGNTYNPSTL 61
 DB 6 ESGPGLVKEPQTLSTCTVSGGSRGGYMSWVRQPGKGLWIGNIHSGNTYNPSTL 65
 QY 62 KSRITMSVDFSKNHFSLRLTSVTAADTAAYVYCARSDGYTLDMWGQGLVTVSS 114
 DB 66 KSRVITISVDTSKQFSLKLSSTVTAADTAAYVYCARVYSGSDGYWGQGLVTVSS 123
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 11.
 XX
 XX monoclonaal antibody; carbonic anhydrase IX; CA IX tumour antigen;
 KW cytosstatic; colorectal neoplasm; renal cell carcinoma;
 KW cervical intraepithelial squamous neoplasia;
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
 KW gene therapy; murine; mouse; human; heavy chain variable domain.
 XX
 OS Unidentified.
 XX
 XX WO2003048328-A2.
 PN
 XX
 XX 12-JUN-2003.
 PD
 XX
 XX 02-DEC-2002; 2002WO-US038550.
 PF
 XX
 XX 03-DEC-2001; 2001US-0337275P.
 PR
 XX
 XX (ABGE-) ABGENIX INC.
 PA
 XX

PI Gudas J, Foltz I, Handa M, Gallo M;
 XX WPI; 2003-523295/49.
 XX
 PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
 XX
 PS Claim 1; SEQ ID NO 11; 89pp; English.
 XX
 CC The invention relates to a novel isolated monoclonal antibody (mab)
 CC comprising a heavy chain polypeptide and light chain polypeptide having a
 CC sequence chosen from one of 53 fully defined amino acid sequences given
 CC in the specification, where the antibody specifically binds carbonic
 CC anhydrase IX (CA IX) tumor antigen. The antibody of the invention
 CC demonstrates cyrostatic activity and may be useful for treating a tumor,
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
 CC tumour or breast cancer, possibly via gene therapy. The current sequence
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
 CC (heavy chain variable domain) protein of the invention. The protein was
 CC generated via the introduction of the human CA IX protein into a
 CC transgenic mouse strain.
 CC
 CC Sequence 125 AA;
 XX
 SQ
 Query Match 82.7%; Score 507.5; DB 7; Length 125;
 Best Local Similarity 81.7%; Pred. No. 1.3e-35;
 Matches 98; Conservative 7; Mismatches 8; Indels 7; Gaps 2;
 QY 2 ESGPGLVKEPQTLSTCTVSGSIRSGYWSWVROPKGKLEWIGNIYHSGNTYNSL 61
 DB 6 ESGPGLVKEPQTLSTCTVSGSIRSGYWSWVROPKGKLEWIGNIYHSGNTYNSL 65
 QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAIVYYCARSDGVT--LDNMCGTLVTYSS 114
 DB 66 KSRITISVDTSKNHFSLRTSVTAADTAIVYYCARSDGVT--LDNMCGTLVTYSS 125
 DB
 QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAIVYYCARSDGVT--LDNMCGTLVTYSS 114
 DB 66 KSRITISVDTSKNHFSLRTSVTAADTAIVYYCARSDGVT--LDNMCGTLVTYSS 125
 DB
 RESULT 11
 ADP03974
 ID ADP03974 standard; protein; 120 AA.
 XX
 AC ADP03974;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.
 XX
 KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
 KW cyrostatic; colorectal neoplasm; renal cell carcinoma;
 KW cervical intraepithelial squamous neoplasia;
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
 KW gene therapy; murine; mouse; human; heavy chain variable domain.
 XX
 OS Unidentified.
 OS
 PN WO2003048328-A2.
 PN
 PD 12-JUN-2003.
 PD
 PF 02-DEC-2002; 2002W0-US038550.
 PF
 PR 03-DEC-2001; 2001US-0337275P.
 PR
 PA (ABGE-) ABGENIX INC.
 PA
 PI Gudas J, Foltz I, Handa M, Gallo M;
 XX WPI; 2003-523295/49.
 XX
 PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical

PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
 XX
 PS Example 2; SEQ ID NO 144; 89pp; English.
 XX
 CC The invention relates to a novel isolated monoclonal antibody (mab)
 CC comprising a heavy chain polypeptide and light chain polypeptide having a
 CC sequence chosen from one of 53 fully defined amino acid sequences given
 CC in the specification, where the antibody specifically binds carbonic
 CC anhydrase IX (CA IX) tumor antigen. The antibody of the invention
 CC demonstrates cyrostatic activity and may be useful for treating a tumor,
 CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
 CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
 CC tumour or breast cancer, possibly via gene therapy. The current sequence
 CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
 CC (heavy chain variable domain) protein of the invention. The protein was
 CC generated via the introduction of the human CA IX protein into a
 CC transgenic mouse strain.
 CC
 CC Sequence 120 AA;
 XX
 SQ
 Query Match 82.6%; Score 507; DB 7; Length 120;
 Best Local Similarity 83.6%; Pred. No. 1.3e-35;
 Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;
 QY 2 ESGPGLVKEPQTLSTCTVSGSIRSGYWSWVROPKGKLEWIGNIYHSGNTYNSL 61
 DB 6 ESGPGLVKEPQTLSTCTVSGSIRSGYWSWVROPKGKLEWIGNIYHSGNTYNSL 65
 QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAIVYYCARSDGVT--LDNMCGTLVTYSS 114
 DB 66 KSRITISVDTSKNHFSLRTSVTAADTAIVYYCARSDGVT--LDNMCGTLVTYSS 120
 DB
 QY 62 KSRITMSVDTSKNHFSLRTSVTAADTAIVYYCARSDGVT--LDNMCGTLVTYSS 114
 DB 66 KSRITISVDTSKNHFSLRTSVTAADTAIVYYCARSDGVT--LDNMCGTLVTYSS 120
 DB
 RESULT 12
 ADP03873
 ID ADP03873 standard; protein; 120 AA.
 XX
 AC ADP03873;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.
 XX
 KW monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
 KW cyrostatic; colorectal neoplasm; renal cell carcinoma;
 KW cervical intraepithelial squamous neoplasia;
 KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
 KW gene therapy; murine; mouse; human; heavy chain variable domain.
 XX
 OS Unidentified.
 OS
 PN WO2003048328-A2.
 PN
 PD 12-JUN-2003.
 PD
 PF 02-DEC-2002; 2002W0-US038550.
 PF
 PR 03-DEC-2001; 2001US-0337275P.
 PR
 PA (ABGE-) ABGENIX INC.
 PA
 PI Gudas J, Foltz I, Handa M, Gallo M;
 XX WPI; 2003-523295/49.
 XX
 PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
 PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
 PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
 XX
 PS Claim 1; SEQ ID NO 13; 89pp; English.
 PS
 CC The invention relates to a novel isolated monoclonal antibody (mab)
 CC comprising a heavy chain polypeptide and light chain polypeptide having a

CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumor antigen. The antibody of the invention
CC demonstrates cytoskeletal activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.

SO Sequence 120 AA:

Query Match 82.6%; Score 507; DB 7; Length 120;
Best Local Similarity 83.6%; Pred. No. 1.3e-35;
Matches 97; Conservative 8; Mismatches 7; Indels 4; Gaps 2;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWROPKGLKLEWIGNIYHSGNTYVPSL 61
Db 6 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWIRQHPKGLKLEWIGIYVSGSTYVPSL 65

Qy 62 KSRITMSVDTSKNHFSLRTSVTAADTAVYYCARSDGYT---LDNMGQGLTVVSS 114
Db 66 KSRVITISVDTSKNQFSLKLSVTAAADTAVYYCAR-DEQNTWYFPLWGRGLTVVSS 120

RESULT 13
ADP03977
ID ADP03977 standard; protein; 122 AA.
XX
AC ADP03977;
DT 29-JUL-2004 (first entry)
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.
XX
XX Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.
XX
KM monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM cytoskeletal; colorectal neoplasm; renal cell carcinoma;
KM cervical intraepithelial squamous neoplasia;
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM gene therapy; murine; mouse; human; heavy chain variable domain.
XX
OS Unidentified.
PN WO2003048328-A2.
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002MO-US038550.
XX
PR 03-DEC-2001; 2001US-0337275P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Foltz I, Handa M, Gallo M;
XX WPI; 2003-523295/49.
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Example 2; SEQ ID NO 147; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumor antigen. The antibody of the invention
CC demonstrates cytoskeletal activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal

CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.

SO Sequence 122 AA:

Query Match 82.6%; Score 507; DB 7; Length 122;
Best Local Similarity 82.1%; Pred. No. 1.4e-35;
Matches 96; Conservative 8; Mismatches 9; Indels 4; Gaps 1;

Qy 2 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWROPKGLKLEWIGNIYHSGNTYVPSL 61
Db 6 ESGPGLVKPSQTLSTCTVSGGSIKSGGYWVWIRQHPKGLKLEWIGIYVSGSTYVPSL 65

Qy 62 KSRITMSVDTSKNHFSLRTSVTAADTAVYYCAR---SPGYTLDMNGQGLTVVSS 114
Db 66 KSRVITISVDTSKNQFSLKLSVTAAADTAVYYCARYDILTYGMDWVGQGLTVVSS 122

RESULT 14
AAB36206
ID AAB36206 standard; protein; 473 AA.
XX
AC AAB36206;
DT 15-FEB-2001 (first entry)
DE Human immune system associated protein HISAP-4.
XX
XX Human immune system associated protein; HISAP-4; immune disorder;
KM Human; immune system associated protein; HISAP-4; immune disorder;
KM infection; autoimmune disease; cancer.
XX
OS Homo sapiens.
PN US6135941-A.
PD 24-OCT-2000.
XX
PF 27-MAR-1998; 98US-00049672.
XX
PR 27-MAR-1998; 98US-00049672.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
PI Hillman JL, Au-Young J;
XX WPI; 2001-030926/04.
XX
DR N-FSDB; AAC66522.
XX
XX New human immune system associated proteins (HISAP) and polynucleotides
PT encoding the HISAP, useful for diagnosing, treating or preventing immune
PT or cell proliferative disorders or infections.
XX
XX Claim 1; Col 53-56; 54pp; English.
XX
XX The present invention provides the coding and protein sequences for a
CC number of human immune system associated proteins (HISAPs). These can be
CC used in the diagnosis and treatment of various autoimmune disorders,
CC infections and cell proliferation diseases. The diseases include AIDS,
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, arteriosclerosis, cirrhosis and cancer

SO Sequence 473 AA:

Query Match 82.6%; Score 507; DB 4; Length 473;
Best Local Similarity 79.8%; Pred. No. 5.7e-35;
Matches 95; Conservative 9; Mismatches 9; Indels 6; Gaps 1;

[illegible]

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A;Residues: 13-111 <HAW>
A;Cross-references: EMBL:X54437
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-13/Domain: signal sequence (fragment) #status predicted <SIG>
F;14-15/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;27-111/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 476.5; DB 2; Length 135;
Best Local Similarity 76.3%; Pred. No. 1.5e-37;
Matches 90; Conservative 13; Mismatches 10; Indels 5; Gaps 2;

QY 2 ESGGGLVPAQQTSLSCAVSGSIRSGGYWMTIRQHPGKLEWIGYIHSGNTYNPSTL 61
D 18 ESGGGLVPAQQTSLSCAVSGSIRSGGYWMTIRQHPGKLEWIGYIHSGNTYNPSTL 77
QY 62 KSRIVSVDTSENKFSRLNSVTADTAAYVYCARL--DGYTL--DIWGQTLVTYSS 114
D 78 KSRIVSVDTSENKFSRLNSVTADTAAYVYCARLGPDDYTLDDGMDVWGQTLVTYSS 135

RESULT 3

IG heavy chain - human
S31514
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31514
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A;Reference number: S31509
A;Accession: S31514
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <CHA>
A;Cross-references: EMBL:X69862; NID:G33086; PIDN:CAA49496.1; PID:G33087
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;22-106/Domain: immunoglobulin homology <IMM>

Query Match 78.1%; Score 475.5; DB 2; Length 128;
Best Local Similarity 76.7%; Pred. No. 1.8e-37;
Matches 89; Conservative 10; Mismatches 14; Indels 3; Gaps 1;

QY 2 ESGGGLVPAQQTSLSCAVSGSIRSGGYWMTIRQHPGKLEWIGYIHSGNTYNPSTL 61
D 13 ESGGGLVPAQQTSLSCAVSGSIRSGGYWMTIRQHPGKLEWIGYIHSGNTYNPSTL 72
QY 62 KSRIVSVDTSENKFSRLNSVTADTAAYVYCARL--DGYTL--DIWGQTLVTYSS 114
D 73 KSRIVSVDTSENKFSRLNSVTADTAAYVYCARLIGYVFGFDPWGQTLVTYSS 128

RESULT 4

S69912
IG V-D-J region (ND) - human
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69912
R;Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A;Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi
A;Reference number: S69909; MUID:94335315; PMID:8057663
A;Accession: S69912
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-122 <SAH>
A;Cross-references: EMBL:Z33398; NID:G871347; PIDN:CAA83849.1; PID:G887460
A;Note: the sequence of residues 108-122 and the corresponding nucleic acid sequence are
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 465; DB 2; Length 122;

Best Local Similarity 75.2%; Pred. No. 1.6e-36;
Matches 88; Conservative 14; Mismatches 11; Indels 4; Gaps 1;

QY 2 ESGGGLVPAQQTSLSCAVSGSIRSGGYWMTIRQHPGKLEWIGYIHSGNTYNPSTL 61
D 6 ESGGGLVPAQQTSLSCAVSGSIRSGGYWMTIRQHPGKLEWIGYIHSGNTYNPSTL 65
QY 62 KSRIVSVDTSENKFSRLNSVTADTAAYVYCAR--LDGYTL--DIWGQTLVTYSS 114
D 66 KSRIVSVDTSENKFSRLNSVTADTAAYVYCARLGPDDYTLDDGMDVWGQTLVTYSS 122

RESULT 5

IG heavy chain V region precursor - human
S13519
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S13519
R;Mortari, F.; Ochs, H.D.; Wedgwood, R.U.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A;Reference number: S13519; MUID:9187691; PMID:2011536
A;Accession: S13519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <MOR>
A;Cross-references: EMBL:X56158; NID:G37724; PIDN:CAA9626.1; PID:G37725
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 464.5; DB 2; Length 147;
Best Local Similarity 75.9%; Pred. No. 2.2e-36;
Matches 88; Conservative 11; Mismatches 14; Indels 3; Gaps 1;

QY 2 ESGGGLVPAQQTSLSCAVSGSIRSGGYWMTIRQHPGKLEWIGYIHSGNTYNPSTL 61
D 32 ESGGGLVPAQQTSLSCAVSGSIRSGGYWMTIRQHPGKLEWIGYIHSGNTYNPSTL 91
QY 62 KSRIVSVDTSENKFSRLNSVTADTAAYVYCAR--LDGYTL--DIWGQTLVTYSS 114
D 92 KSRIVSVDTSENKFSRLNSVTADTAAYVYCARPLMFELPDYWGQTLVTYSS 147

RESULT 6

S30534
IG heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30534
R;Martelet, X.
submitted to the EMBL Data Library, October 1992
A;Reference number: S30520
A;Accession: S30534
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <MAR>
A;Cross-references: EMBL:Z18320
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;13-99/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 460; DB 2; Length 130;
Best Local Similarity 72.8%; Pred. No. 5.1e-36;
Matches 91; Conservative 10; Mismatches 12; Indels 12; Gaps 2;

QY 2 ESGGGLVPAQQTSLSCAVSGSIRSGGYWMTIRQHPGKLEWIGYIHSGNTYNPSTL 61
D 6 ESGGGLVPAQQTSLSCAVSGSIRSGGYWMTIRQHPGKLEWIGYIHSGNTYNPSTL 65
QY 62 KSRIVSVDTSENKFSRLNSVTADTAAYVYCARLGG-----YTL-----LDIWGQTL 109
D 66 KSRIVSVDTSENKFSRLNSVTADTAAYVYCARLGGKGFWSGYITRNSRAAFDIWGQTL 125

RESULT 11

S31690
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31690
R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tommelle, C.
Submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31690
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-130 <CUI>
A/Cross-references: EMBL:Z14199; NID:G30984; PIDN:CAA78568.1; PID:G30985
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;20-102/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 451.5; DB 2; Length 130;
Best Local Similarity 72.1%; Pred. No. 3.2e-35;
Matches 88; Conservative 11; Mismatches 12; Indels 11; Gaps 2;

QY 2 ESGGGLVKKPAQOTLSLCAVSGSIRSGYWSWIRQHPGKLEWIGYIYHSGNTYNPSTL 61
Db 11 ESGGGLVKKPSETLSLTCTVSGGSISS--YWSWSRQPPGKLEWIGYIYHSGNTYNPSTL 68
QY 62 KSRIAMSVDTSENKFSRLNSVTADTAAYVYCARLDG-----YTLDIWGQGLTVTV 112
Db 69 KSRVTISVDTSENKQFSLKLSVTADTAAYVYCARGGSVLWFGRLVYFPDVGQGLTVTV 128

QY 113 SS 114
Db 129 SS 130

RESULT 12

S19668
Ig heavy chain V region (VH4DUH6) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 20-Jun-2000
C/Accession: S19668; S24445
R/Markes, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage.
A/Reference number: S19663; MUID:92085276; PMID:1748994
A/Accession: S19668
A/Molecule type: mRNA
A/Residues: 1-127 <MAR>
A/Cross-references: EMBL:X61648
R/Jones, P.T.
Submitted to the EMBL Data Library, October 1991
A/Reference number: S24442
A/Accession: S24445
A/Molecule type: mRNA
A/Residues: 1-118, 'E', 120-121, 'T', 123-126, 'F', <TON>
A/Cross-references: EMBL:X61648; NID:G37722; PIDN:CAA43829.1; PID:G1335380
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 450.5; DB 2; Length 127;
Best Local Similarity 69.7%; Pred. No. 3.9e-35;
Matches 85; Conservative 15; Mismatches 13; Indels 9; Gaps 1;

QY 2 ESGGGLVKKPAQOTLSLCAVSGSIRSGYWSWIRQHPGKLEWIGYIYHSGNTYNPSTL 61
Db 6 QSGGGLVKKPQOTLSLTCTVSGGSISS--YWSWSRQPPGKLEWIGYIYHSGNTYNPSTL 65
QY 62 KSRIAMSVDTSENKFSRLNSVTADTAAYVYCARLDG-----YTLDIWGQGLTVTV 112
Db 66 KSRVTISVDTSENKQFSLKLSVTADTAAYVYCARGGSVLWFGRLVYFPDVGQGLTVTV 125

QY 113 SS 114
Db 126 SS 127

RESULT 13

S09711
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C/Accession: S09711
R/Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A/Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of
A/Reference number: S09710; MUID:90262535; PMID:2111699
A/Accession: S09711
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-146 <HUG>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;34-118/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 450.5; DB 2; Length 146;
Best Local Similarity 68.0%; Pred. No. 4.5e-35;
Matches 83; Conservative 17; Mismatches 13; Indels 9; Gaps 1;

QY 2 ESGGGLVKKPAQOTLSLCAVSGSIRSGYWSWIRQHPGKLEWIGYIYHSGNTYNPSTL 61
Db 25 ESGGGLVKKPSETLSLTCTVSGGSVSSGGLYWSWIRQHPGKLEWIGYIYHSGNTYNPSTL 84
QY 62 KSRIAMSVDTSENKFSRLNSVTADTAAYVYCARLDG-----DGYTLDIWGQGLTVTV 112
Db 85 RSRVTISVDTSENKQFSLKLSVTADTAAYVYCARVLSRFSISQSYMDVWGQGLTVTV 144

QY 113 SS 114
Db 145 SS 146

RESULT 14

S31511
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C/Accession: S31511
R/Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A/Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto-
A/Reference number: S31509
A/Accession: S31511
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-155 <CHA>
A/Cross-references: EMBL:X69866; NID:G33094; PIDN:CAA49500.1; PID:G33095
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 73.8%; Score 449.5; DB 2; Length 155;
Best Local Similarity 70.8%; Pred. No. 5.9e-35;
Matches 85; Conservative 15; Mismatches 11; Indels 9; Gaps 2;

QY 2 ESGGGLVKKPAQOTLSLCAVSGSIRSGYWSWIRQHPGKLEWIGYIYHSGNTYNPSTL 61
Db 38 ESGGGLVKKPSETLSLTCTVSGGSISS--YWSWSRQPPGKLEWIGYIYHSGNTYNPSTL 95
QY 62 KSRIAMSVDTSENKFSRLNSVTADTAAYVYCARLDG-----LDGYTLDIWGQGLTVTV 114
Db 96 KSRVTISVDTSENKQFSLKLSVTADTAAYVYCARGGSVLWFGRLVYFPDVGQGLTVTV 155

RESULT 15

```

S31512
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31512
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
Submitted to the EMBL Data Library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autoC
A:Reference number: S31509
A:Accession: S31512
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <CRA>
A:Cross-references: EMBL:X69860; NID:G33082; PIDN:CAA49494.1; PID:G33083
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterodimer; immunoglobulin
F:47-129/Domain: immunoglobulin homology <IMM>

Query Match      73.3%; Score 446.5; DB 2; Length 155;
Beet Local Similarity 70.0%; Pred. No. 1.le-34;
Matches 84; Conservative 16; Mismatches 11; Indels 9; Gaps 2;

Oy      2  ESGGGLVPAQTLISCAVSGSIRSGGYMSWIRQHPKGLGEMIGVYHSGNTYVPSL 61
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      38  ESGGGLVPESTLISLTCTVSGSGISS--YVMSWIRQPPKGLGEMIGVYHSGATNPPI 95

Oy      62  KSRIAMSVDTSENKFSRLNSVTADTAAYVYCARLDG-----YTLDDIMGGTLTVSS 114
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      96  KSRVTVISVDTSKQPSLKVSSVTADTAIVYICAKGGGSISSMYVYVGMDDVWQGGITTVVSS 155

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Search completed: July 26, 2005, 09:27:48
Job time : 15.6818 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: July 26, 2005, 08:52:21 ; Search time 71.6818 Seconds
(without alignments)
814.391 Million cell updates/sec

Title: US-10-027-725A-7

Perfect score: 609
Sequence: 1 LESGPGLVKEPQTLISLCAV.....RLDGYTLIDWGGTLVTSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	483.5	79.4	476 2	OG6MX1
2	473	77.7	478 2	O72379
3	451	74.1	150 2	O95973
4	449	73.7	477 2	OG6MX7
5	446.5	73.3	119 2	O9UL73
6	444	72.9	465 2	OG6MX6
7	440	72.2	576 2	O6P418
8	432	70.9	496 2	O96KX8
9	430.2	70.7	492 2	O72374
10	430	70.6	620 2	O96EY0
11	419.5	68.9	129 1	HV2P_HUMAN
12	412.5	67.7	478 2	OG6NY3
13	409.5	67.2	595 2	O8MX4
14	409.5	67.2	597 2	OG6MX5
15	409.5	67.2	597 2	O9BUT0
16	409.5	67.2	625 2	O96AA6
17	408	67.0	139 2	O86SX2
18	405.5	66.6	597 2	O9BOB8
19	405	66.6	130 2	O81ZD7
20	405	66.5	146 1	HV2I_HUMAN
21	388	63.7	473 2	O8TC63
22	383	62.9	136 2	O6LBO5
23	377.5	62.0	479 2	O99M22
24	374.5	61.5	137 1	HV46_MOUSE
25	374	61.4	116 2	O6Z3Y6
26	370.5	60.8	262 2	O65Z11
27	369.5	60.7	117 1	HV2G_HUMAN
28	362	59.4	122 2	O9UL75
29	361.5	59.4	113 1	HV47_MOUSE
30	357.5	58.7	476 2	O6MZK7
31	342.5	56.2	116 1	HV61_MOUSE

32	341.5	56.1	116 1	HV60_MOUSE	P18531 mus musculu
33	334	54.8	117 1	HV62_MOUSE	P18533 mus musculu
34	326	53.5	118 2	O81I05	O81I05 mus musculu
35	323	53.0	121 2	O99NG4	O99NG4 mus musculu
36	321.5	52.8	144 1	HV43_MOUSE	P01819 mus musculu
37	316.5	52.0	121 2	O9US6	O9US6 mus musculu
38	315	51.7	482 2	O91X92	O91X92 mus musculu
39	312.5	51.3	118 2	O9UL74	O9UL74 mus musculu
40	304.5	50.0	466 2	O6IN78	O6IN78 mus musculu
41	304	49.9	135 1	HV02_XENLA	P20957 xenopus lae
42	304	49.9	473 2	O6MZ77	O6MZ77 mus musculu
43	302.5	49.7	240 2	O65ZC9	O65ZC9 mus musculu
44	301	49.4	606 2	O6GM72	O6GM72 mus musculu
45	300	49.3	120 1	HV2B_HUMAN	P01815 mus musculu

ALIGNMENTS

RESULT 1
OG6MX1 PRELIMINARY; PRT; 476 AA.
ID OG6MX1
AC OG6MX1
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX MEDLINE=22388257; Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rudin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshitsugu S., Carrincci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Matok J.A., Gunaratne P.H.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Gale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kravinsky M.I., Skalska U., Smallos D.E., Schermer A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX Strausberg R.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_1.
DR InterPro; IPR003066; IG_1c.
DR InterPro; IPR003596; IG_1c.
DR Pfam; PF07654; CI-sect; 3.
DR Pfam; PF00647; IG_4.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IG_3.
DR SMART; SM00406; IG_1.
DR PROSITE; PS50835; IG_1like; 4.
DR PROSITE; PS00290; IG_1c; UNKNOWN_2.

KM Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
Query Match 79.4%; Score 483.5; DB 2; Length 476;
Best Local Similarity 72.6%; Pred. No. 8,76-43;
Matches 90; Conservative 16; Mismatches 5; Indels 13; Gaps 2;
QY 2 ESGPGLVKPAQTLSTLSCAVSGSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYVPSL 61
DB 25 ESGPGLVKPQTLSTLTCTVSGSGSISSDYYWMIROHPGKLEWIGYIYVSGSYVPSL 84
QY 62 KSRIVMSVDTSENKFSRLNSVTADTAIVYCARLDGTY-----LGGYTLDIWGQGLTV 110
DB 85 KSRVTLISDTSKQFSLRMSVTADTAIVYFCARAGWGSFRWALDGF--NIWGQGLTV 142
QY 111 TVSS 114
DB 143 TVSS 146
RESULT 2
QY 072379 PRELIMINARY; PRT; 478 AA.
AC 072379;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686K04218 (Fragment).
GN Name=DKFZp686K04218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Human rectum tumor;
RC Bioecker H., Boecker M., Mewes H.W., Weill B., Amlid C., Oeanger A.,
RA Podo G., Han M., Wiemann S.,
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX58066; CAD97996.1; -.
DR HSSP; P01820; I67J.
DR InterPro; IPR007110; Iq-1like.
DR InterPro; IPR003597; Iq-cl.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR003596; Iq_v.
DR Pfam; PF07654; C1-sec; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; Iq_LIKE; 4.
DR PROSITE; PS00290; Iq_MHC; UNKNOWN_2.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;
Query Match 77.7%; Score 473; DB 2; Length 478;
Best Local Similarity 75.7%; Pred. No. 1,1e-41;
Matches 87; Conservative 17; Mismatches 9; Indels 2; Gaps 1;
QY 2 ESGPGLVKPAQTLSTLSCAVSGSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYVPSL 61
DB 24 ESGPGLVKPQTLSTLTCTVSGSGSISDYYWMIROHPGKLEWIGYIYVSGSYVPSL 83
QY 62 KSRIVMSVDTSENKFSRLNSVTADTAIVYCARLDGTY-----LGGYTLDIWGQGLTV 114
DB 84 ESRVTLISDTSKQFSLRMSVTADTAIVYFCARAGWGSFRWALDGF--NIWGQGLTV 138
RESULT 3
QY 095973 PRELIMINARY; PRT; 150 AA.
AC 095973;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE Vh4 heavy chain variable region precursor (Fragment).
GN Name=IGM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sub C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103795; AAC79084.1; -.
DR PIR; S31673; S31673.
DR PIR; S78056; S78056.
DR HSSP; P01820; I67J.
DR InterPro; IPR007110; Iq-1like.
DR InterPro; IPR003596; Iq_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; Iq_LIKE; 1.
KM Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 >150 Vh4 heavy chain variable region.
FT NON TER 150
SQ SEQUENCE 150 AA; 16315 MW; 85664E04938AA7C9 CRC64;
Query Match 74.1%; Score 451; DB 2; Length 150;
Best Local Similarity 74.3%; Pred. No. 7e-40;
Matches 84; Conservative 12; Mismatches 17; Indels 0; Gaps 0;
QY 2 ESGPGLVKPAQTLSTLSCAVSGSGSIRSGGYWMIROHPGKLEWIGYIYHSGNTYVPSL 61
DB 25 ESGPGLVKPQTLSTLTCTVSGSGSISDYYWMIROHPGKLEWIGYIYVSGSYVPSL 84
QY 62 KSRIVMSVDTSENKFSRLNSVTADTAIVYCARLDGTY-----LGGYTLDIWGQGLTV 114
DB 85 KSRVTLISDTSKQFSLRMSVTADTAIVYFCARAGWGSFRWALDGF--NIWGQGLTV 137
RESULT 4
QY 06GMX7 PRELIMINARY; PRT; 477 AA.
AC 06GMX7;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udell T.B., Toshikiyuki S., Cantanici P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalak U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)."


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RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073765; AAH73765.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CF85 CRC64;

Query Match 73.7%; Score 449; DB 2; Length 477;
Best Local Similarity 75.7%; Pred. No. 4.1e-39;
Matches 87; Conservative 10; Mismatches 14; Indels 4; Gaps 2;

Qy 2 ESGGLVAPQATLSLSCAVSGSIRSGGYWMIROHKGKLEWIGYIYHSGNTYVPSL 61
Db 25 ESGGLVAPSETLSLCTVSGSIS--YVWSWIRQIRKGLKLEWIGIYHSGNTYVPSL 82

Qy 62 KSRIAMVDTSNENKFSRLNSVTADTAIVYCCARLDG--YTLDIMOGGLTVTVSS 114
Db 83 KSRVTLSDTSKQPSLRINSVTADTAIVYCCARLDG--YTLDIMOGGLTVTVSS 137

RESULT 5
Q9UL73 PRELIMINARY; PRT; 119 AA.
ID Q9UL73
AC Q9UL73;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TREMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Betney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035041; AADS6277.1; -.
DR PIR; PH0876; PH0876.
DR PIR; S12416; S12416.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13219 MW; 1BDB86B6420EAOBE CRC64;

Query Match 73.3%; Score 446.5; DB 2; Length 119;
Best Local Similarity 74.1%; Pred. No. 1.6e-39;
Matches 86; Conservative 12; Mismatches 13; Indels 5; Gaps 2;

Qy 2 ESGGLVAPQATLSLSCAVSGSIRSGGYWMIROHKGKLEWIGYIYHSGNTYVPSL 61
Db 25 ESGGLVAPSETLSLCTVSGSIS--YVWSWIRQIRKGLKLEWIGIYHSGNTYVPSL 82
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Db 6 ESGGLVAPSETLSLCTVSGSIS--YVWSWIRQIRKGLKLEWIGYIYHSGNTYVPSL 63
Qy 62 KSRIAMVDTSNENKFSRLNSVTADTAIVYCCARLDG--YTLDIMOGGLTVTVSS 114
Db 64 KSRVTLSDTSKQPSLRINSVTADTAIVYCCARLDG--YTLDIMOGGLTVTVSS 119

RESULT 6
Q6GMX6 PRELIMINARY; PRT; 465 AA.
ID Q6GMX6
AC Q6GMX6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heist F.,
RA Datchenko L., Marins K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386B CRC64;

Query Match 72.9%; Score 444; DB 2; Length 465;
Best Local Similarity 77.0%; Pred. No. 1.3e-38;
Matches 87; Conservative 9; Mismatches 15; Indels 2; Gaps 1;

Qy 2 ESGGLVAPQATLSLSCAVSGSIRSGGYWMIROHKGKLEWIGYIYHSGNTYVPSL 61
Db 25 ESGGLVAPSETLSLCTVSGSIS--YVWSWIRQIRKGLKLEWIGIYHSGNTYVPSL 82

Qy 62 KSRIAMVDTSNENKFSRLNSVTADTAIVYCCARLDG--YTLDIMOGGLTVTVSS 114
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DB 83 KSRVTSVDSKQFSLKLSVTAADTAAYYCAGRFTFDYWGQGLTVTVSS 135

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RESULT 7
ID 06P418 PRELIMINARY; PRT; 576 AA.
AC 06P418;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGHG protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshitsuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -.
DR HSSP; P01820; 1A7N.
DR InterPro; IPR003599; IG_1like.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_1like.
DR InterPro; IPR003006; IG_1like.
DR InterPro; IPR003596; IG_1like.
DR Pfam; PF07654; C1-sev; 2.
DR SMART; SM00409; IG_1.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IG1; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 576 AA; 63363 MM; FBB97C949D720F1B CRC64;

Query Match 72.2%; Score 440; DB 2; Length 576;
Best Local Similarity 73.3%; Pred. No. 4.5e-38;
Matches 85; Conservative 13; Mismatches 14; Indels 4; Gaps 2;

QY 2 EESGGLVLPKQOTLSLCAVSGSIRSGGYWMIROHPGKLEWIGITYHSGNTYNPSTL 61
DB 32 EESGGLVLPKQOTLSLCAVSGSIRSGGYWMIROHPGKLEWIGITYHSGNTYNPSTL 90
QY 62 KSRVTSVDSKQFSLKLSVTAADTAAYYCAGRFTFDYWGQGLTVTVSS 114
DB 91 KSRVTSVDSKQFSLKLSVTAADTAAYYCAGRFTFDYWGQGLTVTVSS 146

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RESULT 8
ID 096KX8 PRELIMINARY; PRT; 496 AA.
AC 096KX8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE MCC27165 protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshitsuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016369; AAH16369.1; -.
DR HSSP; P01876; 10M0.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_1like.
DR InterPro; IPR003006; IG_1like.
DR InterPro; IPR003596; IG_1like.
DR Pfam; PF07654; C1-sev; 2.
DR SMART; SM00406; IG1; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 496 AA; 53391 MM; D3f6929849040D69 CRC64;

Query Match 70.3%; Score 432; DB 2; Length 496;
Best Local Similarity 69.2%; Pred. No. 2.7e-37;
Matches 83; Conservative 13; Mismatches 16; Indels 8; Gaps 2;

QY 2 EESGGLVLPKQOTLSLCAVSGSIRSGGYWMIROHPGKLEWIGITYHSGNTYNPSTL 61
DB 25 EESGGLVLPKQOTLSLCAVSGSIRSGGYWMIROHPGKLEWIGITYHSGNTYNPSTL 84
QY 62 KSRVTSVDSKQFSLKLSVTAADTAAYYCAGRFTFDYWGQGLTVTVSS 114
DB 85 KSRVTSVDSKQFSLKLSVTAADTAAYYCAGRFTFDYWGQGLTVTVSS 143

RESULT 9
ID 072374 PRELIMINARY; PRT; 492 AA.
AC 072374;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)

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DT 01-OCT-2003 (TrEMBLrel. 25, last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DT Hypothetical protein DKFZp686C02218 (Fragment).
 GN Name=DKFZp686C02218;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RA Bioecker H., Boecker W., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.,
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX538077; CAD98001.1;
 DR HSSP; P01820; IG7J.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG-LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 FT NCN TER 1 1
 SQ SEQUENCE 492 AA; 5376 MW; 1E7A15760F0CA74B CRC64;
 Query Match 70.7%; Score 430.5; DB 2; Length 492;
 Best Local Similarity 71.6%; Pred. No. 3.9e-37;
 Matches 83; Conservative 13; Mismatches 17; Indels 3; Gaps 2;
 QY 2 ESGGGLVKKPQNTLSGAVSGGSIIRSGGYWSWIRHPGKGLWIGYIHSGNTYNSPL 61
 DB 37 ESGGGLVKKPSETLSLTCTVSGGSVSNRYMGWIRPGKGLWIGYIHSGNTYNSPL 96
 QY 62 KSRIVMSVDTSEKFSRLNSVTADTAVYYCA--LTLDIMGCGTLVTSS 114
 DB 97 KSRITIVDTSKHFSRLNSVTADTAVYYCAVHVGSPYGMFDPKCGTLVTSS 152
 RESULT 10
 Q96EYO PRELIMINARY; PRT; 620 AA.
 AC Q96EYO;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE IGHM protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Krausberg R.L., Collins E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,
 RA Blakeau R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallov D.E., Scherch A., Schein J.E.,

RA Jones S.J., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC01857; AAH1857.2;
 DR PIR; S15590; S15590.
 DR HSSP; P01820; IG7J.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 4.
 DR SMART; SM00407; IGV; 1.
 DR SMART; SM00409; IGV; 2.
 DR SMART; SM00407; IGV; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG-LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Hypothetical protein.
 FT NCN TER 1 1
 SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6B8FF27B CRC64;
 Query Match 70.6%; Score 430; DB 2; Length 620;
 Best Local Similarity 74.4%; Pred. No. 5.7e-37;
 Matches 87; Conservative 9; Mismatches 15; Indels 6; Gaps 2;
 QY 2 ESGGGLVKKPQNTLSGAVSGGSIIRSGGYWSWIRHPGKGLWIGYIHSGNTYNSPL 61
 DB 32 ESGGGLVKKPSETLSLTCTVSGGSISS--YVSWIRPGKGLWIGYIHSGNTYNSPL 89
 QY 62 KSRIVMSVDTSEKFSRLNSVTADTAVYYCA---RLDGYLIDIMGCGTLVTSS 114
 DB 90 KSRIVMSVDTSEKFSRLNSVTADTAVYYCA--PWLPTVGLFVWGGTLVTSS 146
 RESULT 11
 HV2P_HUMAN STANDARD; PRT; 129 AA.
 ID HV2P_HUMAN
 AC P01824;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, last sequence update)
 DT 05-JUL-2004 (Rel. 44, last annotation update)
 DE Ig heavy chain V-II region WH.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=8222235; PubMed=6806818;
 RA Takahashi N., Tetaert D., Deubrie B., Lin L.-C., Putnam F.W.,
 RT "Complete amino acid sequence of the delta heavy chain of human
 RT immunoglobulin D."
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
 CC -1- MISCELLANEOUS: This chain was isolated from an Igd myeloma
 CC protein.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PIR; A02099; D2HUMA.
 DR HSSP; P01820; IG7J.
 DR GlycoSiteDB; P01824;
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG-LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 113
 Ig-like.

FT NON TER 129 129 D5D53D47ABE51319 CRC64;
SQ SEQUENCE 129 AA, 14117 MW, 14117 MW;
Query Match 68.9%; Score 419.5; DB 1; Length 129;
Best Local Similarity 62.7%; Pred. No. 1.3e-36;
Matches 79; Conservative 16; Mismatches 16; Indels 15; Gaps 2;
QY 2 ESGPGLVKPAQTLISLCAVSGGSIRSGYYWSMIRHPGKLEWIGIYTHSGNTYNPSTL 61
DB 6 ESGPGLVKPSETLSTLCISVSGGPRRRRGYYGWMIRDPGKLEWIGVYTYGSIYNPSTL 65
QY 62 KSRFMSVDTSEKFEELRLNSVTAAADTAIYCAR-----LDGVTLDIMWGQT 108
DB 66 RGVVTSVDTSKQFSLNLSMSGADTAIYCARGNPPYYDITGSDDG-IDVMGQGT 123
QY 109 LVTWSS 114
DB 124 TVHWSS 129
RESULT 12
Q6NTH3
ID Q6NTH3 PRELIMINARY; PRT; 478 AA.
AC Q6NTH3;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M., Ustin T.B., Toshitsuki S., Carninci P., Prange C.,
Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszinski M.I., Skalka U., Smallus D.E., Scherch A., Schein J.E.,
Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
RL EMBL; BC066594; AAH6554.1; -;
DR HSSP; P01820; 1A7N.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 4.
DR PROSITE; PSS0835; IG-LIKE; 4.

DR PROSITE; PSS0290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA, 51856 MW, 5F8B98F60F077256 CRC64;
Query Match 67.7%; Score 412.5; DB 2; Length 478;
Best Local Similarity 66.9%; Pred. No. 3.1e-35;
Matches 79; Conservative 17; Mismatches 13; Indels 9; Gaps 3;
QY 2 ESGPGLVKPAQTLISLCAVSGGSIRSGYYWSMIRHPGKLEWIGIYTHSGNTYNPSTL 61
DB 25 ESGPGLVKPSETLSTLCISVSGDSIAS--YWSWIRKSPQCGMGIYIFHSGLTYNPSTL 82
QY 62 KSRFMSVDTSEKFEELRLNSVTAAADTAIYCAR-----TLIMQGTLTWSS 114
DB 83 ESRVTSVDTSKQFSLNLSMSGADTAIYCAR--GYGKSRYPFLMGKGVPTWSS 138
RESULT 13
Q6WUX4
ID Q6WUX4 PRELIMINARY; PRT; 595 AA.
AC Q6WUX4;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M., Ustin T.B., Toshitsuki S., Carninci P., Prange C.,
Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszinski M.I., Skalka U., Smallus D.E., Scherch A., Schein J.E.,
Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.2; -;
DR PIR; G34964; G34964.
DR HSSP; P01861; 1ADQ.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 5.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 595 AA, 65290 MW, 0D4B50776545714E CRC64;
Query Match 67.2%; Score 409.5; DB 2; Length 595;
Best Local Similarity 66.7%; Pred. No. 8.3e-35;
Matches 80; Conservative 14; Mismatches 15; Indels 11; Gaps 3;

QY 4 GPGVLVKAQQTLSLSCAVSGGSTRSGGYWSWIRHPHGKLEWIGYIHSGNTYNPISLKS 63
 Db 34 GAGLKLKRETSLSLTCGYGGSF--SGYWSWIRHPHGKLEWIGIEINHGSSGNTYNPISLKS 91
 QY 64 RIANSVDTSENKFSLRINSVTAADTVAYYCARL-----DG-YTLIDWQGLTVYSS 114
 Db 92 RVTISVDTSKQSLSTLKSSVNAADTVAYYCARVITRAPFGTDGRYGMWVGQFTTVYSS 151
 RESULT 14
 Q6GMX5 PRELIMINARY; PRT; 597 AA.
 AC O6GMX5;
 DT 05-JUN-2004 (TREMBLrel. 27, Created)
 DT 05-JUN-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUN-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RX MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheeter C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stadleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueirin T.B., Toshynki S., Carrini P., Prange S.J.,
 RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
 RA Krzyzanski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Mariz M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC073767; AAH73767.1; ..
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-1like.
 DR InterPro: IPR003597; IG-cl.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF07654; CI-set; 4.
 DR Pfam: PF00047; Ig; 4.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IG; 4.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 5.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;

[illegible]

Thu Jul 28 05:42:30 2005

us-10-027-725a-7.rup

Page 8

Search completed: July 26, 2005, 09:26:17
Job time : 73.6818 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 26, 2005, 08:50:20 ; Search time 85.3273 Seconds
(without alignments)
516.724 Million cell updates/sec

Title: US-10-027-725A-7
Perfect score: 609
Sequence: 1 LKSGPLVKAQTLISCAV.....RLDGYTLDMGQGLTVTSS 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	609	100.0	114	5	ABg30445 Human IGE
2	547	89.8	114	5	ABg30447 Human IGE
3	546	89.7	114	5	ABg30446 Human IGE
4	519	85.2	122	7	ADP03877 Murine-ex
5	518.5	85.1	121	7	ADP03882 Murine-ex
6	517.5	85.0	125	7	ADP03871 Murine-ex
7	514.5	84.5	121	7	ADP03981 Murine-ex
8	512	84.1	118	7	ADP03968 Murine-ex
9	512	84.1	120	7	ADP03874 Murine-ex
10	512	84.1	120	7	ADP03873 Murine-ex
11	509.5	83.7	123	7	ADP03872 Murine-ex
12	508.5	83.5	123	7	ADP03870 Murine-ex
13	508.5	83.5	123	7	ADP03879 Murine-ex
14	508.5	83.5	123	7	ADP03878 Murine-ex
15	508.5	83.5	125	7	ADP03868 Murine-ex
16	508.5	83.5	125	7	ADP03876 Murine-ex
17	506.5	83.2	119	7	ADP03961 Murine-ex
18	506.5	83.2	123	5	AAW78433 Antinody
19	506.5	83.2	123	5	ABB97976 Heavy cha
20	505.5	83.2	123	7	ADG88414 anti-Op-R
21	505.5	83.0	119	7	ADP03970 Murine-ex
22	505	82.9	252	5	ADP45983 Human Bly
23	505	82.9	252	5	ADG96810 Single ch
24	504.5	82.8	125	7	ADP03983 Murine-ex
25	504	82.8	120	7	ADP03969 Murine-ex

26	503.5	82.7	127	7	ADP03874
27	503	82.6	124	7	ADP03935
28	502	82.4	123	4	AAB62745
29	501.5	82.3	117	7	ADG99784
30	501.5	82.3	117	7	ADDO5388
31	501.5	82.3	117	7	ADP09826
32	500.5	82.2	251	6	ABJ19829
33	500.5	82.2	251	8	ADH13871
34	499.5	82.0	120	4	AAB62775
35	499	81.9	473	4	AAB36206
36	498.5	81.9	253	5	ABP45608
37	498.5	81.9	253	7	ADG96435
38	497	81.6	110	7	ADP03934
39	497	81.6	121	7	ADJ80377
40	497	81.6	128	8	ADP22124
41	497	81.6	128	8	ADP22104
42	497	81.6	128	8	ADP22096
43	496.5	81.5	123	7	ADP03877
44	496.5	81.5	446	8	ADK52356
45	496	81.4	172	3	AAV93713

ALIGNMENTS

RESULT 1					
ID	ABG30445	standard; protein, 114 AA.			
XX	AC	ABG30445;			
XX	XX	21-OCT-2002 (first entry)			
DT	XX	Human IGE Fab clone 94 heavy chain protein.			
XX	DE	Human, fab; antiallergic; vaccine; grass pollen; Phi p 2.			
XX	KW	timothy grass pollen allergen; passive immunotherapy.			
XX	OS	Homo sapiens.			
XX	XX	Location/Qualifiers			
FT	Key	1..26			
FT	Region	/note= "FR1 region"			
FT	Region	27..33			
FT	Region	/note= "CDR1 region"			
FT	Region	34..47			
FT	Region	/note= "FR2 region"			
FT	Region	48..63			
FT	Region	/note= "CDR2 protein"			
FT	Region	64..95			
FT	Region	/note= "FR3 region"			
FT	Region	96..103			
FT	Region	/note= "CDR2 region"			
FT	Region	104..114			
FT	Region	/note= "FR4 region"			
XX	XX	WO200253595-A1.			
XX	XX	11-JUL-2002.			
XX	PD	27-DEC-2001; 2001WO-SE002908.			
XX	PF	29-DEC-2000; 2000SE-00004892.			
XX	PR	(PHAA) PHARMACIA DIAGNOSTICS AB.			
XX	PA	Flicker S, Steinberger P, Kraft D, Valenta R;			
XX	XX	WPL; 2002-583604/62.			
XX	DR	N-PSDB; ABK83637.			
XX	XX	Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising			
PT	PT	variable region of group 2 allergen specific-human Igs Fabs, useful for			

ADP03874	Murine-ex
ADP03935	Murine-ex
AAB62745	Human HIV
ADG99784	Anti-huma
ADDO5388	Anti-WC1
ADP09826	Human ant
ABJ19829	Human VEG
ADH13871	Human vas
AAB62775	Human HIV
AAB36206	Human Imm
ABP45608	Human Bly
ADG96435	Single ch
ADP03934	Murine-ex
ADJ80377	Antinody
ADP22124	Human ant
ADP22104	Human ant
ADP22096	Human ant
ADP03877	Murine-ex
ADK52356	Human ant
AAV93713	The heavy

PT diagnosing or passive immunotherapy of type I allergy, for environmental
XX allergen detection.
XX
PS Disclosure; Page 36; 45pp; English.
XX
CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergen patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific Fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The Fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific Fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergen patients
CC IgE antibodies to Phi p 2. The present sequence represents the human IgG
CC Fab, clone 94 heavy chain protein of the invention
CC
XX Sequence 114 AA;
SQ

Query Match 100.0%; Score 609; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.1e-48; Mismatches 0; Gaps 0;
Matches 114; Conservative 0; Indels 0; Gaps 0;

QY 1 LESGPGLVKPAQTLISLCAVSGSIRSGYVMSWIRQHPGKLEWIGYIYHSGNTYVNS 60
1 LESGPGLVKPAQTLISLCAVSGSIRSGYVMSWIRQHPGKLEWIGYIYHSGNTYVNS 60
Db 1 LESGPGLVKPAQTLISLCAVSGSIRSGYVMSWIRQHPGKLEWIGYIYHSGNTYVNS 60
QY 61 LKSRIMSVDTSEKFSRLNSVTAAADTAVYYCARLDGYTLDMWGQGLTVTVSS 114
61 LKSRIMSVDTSEKFSRLNSVTAAADTAVYYCARLDGYTLDMWGQGLTVTVSS 114
Db 61 LKSRIMSVDTSEKFSRLNSVTAAADTAVYYCARLDGYTLDMWGQGLTVTVSS 114

RESULT 2
ABG30447 standard; protein, 114 AA.
XX
AC ABG30447;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human IgE Fab clone 100 heavy chain protein.
XX
KM Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;
KM timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Region 1..26
FT /note= "FR1 region"
FT Region 27..33
FT /note= "CDR1 region"
FT Region 34..47
FT /note= "FR2 region"
FT Region 48..63
FT /note= "CDR2 protein"
FT Region 64..95
FT /note= "FR3 region"
FT Region 96..103
FT /note= "CDR2 region"
FT Region 104..114
FT /note= "FR4 region"
XX
FN WO200253595-A1.
XX
PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-SE002908.
XX

PR 29-DEC-2000; 2000SE-00004892.
XX
XX (PHAA) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
XX WPI, 2002-583604/62.
DR N-PSDB; ABK89639.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs; useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
XX Disclosure; Page 38; 45pp; English.
XX
PS This invention relates to the DNA and protein sequences of group 2
XX allergen-specific human IgE Fabs and methods for their use. The proteins
XX of the invention may have antiallergic activities and may be used as a
XX vaccine or an inhibitor of binding of grass pollen allergen patient's IgE
XX antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
XX 2 allergen-specific Fabs of the invention may be useful for environmental
XX allergen detection and for standardisation of allergen extracts. The Fabs
XX - or a vaccine against a type I allergy is useful for passive
XX immunotherapy of type I allergy, it is also useful for diagnosing a type
XX I allergy. The allergen-specific Fabs of the invention are useful for
XX inter alia, diagnosis, therapy and prevention of type I allergy. They are
XX also useful for identification of group 2 allergen-containing pollen and
XX may be used for blocking the binding of grass pollen allergen patients
XX IgE antibodies to Phi p 2. The present sequence represents the human IgG
XX Fab, clone 100 heavy chain protein of the invention
XX
SQ Sequence 114 AA;
SQ

Query Match 89.8%; Score 547; DB 5; Length 114;
Best Local Similarity 89.8%; Pred. No. 1.5e-42; Mismatches 7; Indels 0; Gaps 0;
Matches 102; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 LESGPGLVKPAQTLISLCAVSGSIRSGYVMSWIRQHPGKLEWIGYIYHSGNTYVNS 60
1 LESGPGLVKPAQTLISLCAVSGSIRSGYVMSWIRQHPGKLEWIGYIYHSGNTYVNS 60
Db 1 LESGPGLVKPAQTLISLCAVSGSIRSGYVMSWIRQHPGKLEWIGYIYHSGNTYVNS 60
QY 61 LKSRIMSVDTSEKFSRLNSVTAAADTAVYYCARLDGYTLDMWGQGLTVTVSS 114
61 LKSRIMSVDTSEKFSRLNSVTAAADTAVYYCARLDGYTLDMWGQGLTVTVSS 114
Db 61 LKSRIMSVDTSEKFSRLNSVTAAADTAVYYCARLDGYTLDMWGQGLTVTVSS 114

RESULT 3
ABG30446
ID ABG30446 standard; protein, 114 AA.
XX
AC ABG30446;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human IgE Fab clone 60 heavy chain protein.
XX
KM Human; fab; antiallergic; vaccine; grass pollen; Phi p 2;
KM timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Region 1..26
FT /note= "FR1 region"
FT Region 27..33
FT /note= "CDR1 region"
FT Region 34..47
FT /note= "FR2 region"
FT Region 48..63
FT /note= "CDR2 protein"
FT Region 64..95
FT /note= "FR3 region"
FT Region 96..103
FT /note= "CDR2 region"
FT Region 104..114
FT /note= "FR4 region"
FT Region 105..114
FT /note= "FR4 region"
FT

FT	Region	96..103
FT	/note= "CDR2 region"	
FT	Region	104..114
FT	/note= "FRA region"	
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XX	MO200253595-A1.	
XX		
PD	11-JUL-2002.	
XX		
PF	27-DEC-2001; 200IWO-SE002908.	
XX		
PR	29-DEC-2000; 2000SE-00004892.	
XX		
PA	(PHAA) PHARMACIA DIAGNOSTICS AB.	
XX		
P1	Flicker S, Steimberger P, Kraft D, Valenta R;	
XX		
DR	WPI; 2002-583604/62.	
XX	N-PsDB; ABR9638.	
PT		
PT	Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising	
PT	variable region of group 2 allergen specific-human IgE Fabs, useful for	
PT	diagnosing or passive immunotherapy of type I allergy, for environmental	
PT	allergen detection.	
XX		
XX	Disclosure; Page 37; 45pp; English.	
XX		
CC	This invention relates to the DNA and protein sequences of group 2	
CC	allergen-specific human IgE Fabs and methods for their use. The proteins	
CC	of the invention may have antiallergic activities and may be used as a	
CC	vaccine or an inhibitor of binding of grass pollen allergic patient's IgE	
CC	antibodies to Phi P 2 (a major Timothy grass pollen allergen). The group	
CC	2 allergen-specific fabs of the invention may be useful for environmental	
CC	allergen detection and for standardisation of allergen extracts. The fabs	
CC	- or a vaccine against a type I allergy is useful for passive	
CC	immunotherapy of type I allergy, it is also useful for diagnosing a type	
CC	I allergy. The allergen-specific fabs of the invention are useful for	
CC	inher alia, diagnosis, therapy and prevention of type I allergy. They are	
CC	also useful for identification of group 2 allergen-containing pollen and	
CC	may be used for blocking the binding of grass pollen allergic patients	
CC	IgE antibodies to Phi P 2. The present sequence represents the human IgG	
CC	fab, clone 60 heavy chain protein of the invention	
SQ		
XQ	Sequence 114 AA;	
	Query Match 89.7%; Score 546; DB 5; Length 114;	
	Best Local Similarity 89.5%; Pred. No.1.9e-42;	
	Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0	
DY	1 LESGGVLVKAQTSLSCAVSGSIRSGGYMSWIROHFGKLEWIGYIHSGNTYYNS 60	
Db	1 LESGGVLVKSQTSLTCTVSGGSIRSGGYMSWRQPGRGLEWIGNIYHSGNITYNS 60	
DY	61 LKSRITMSVDTSSENKFSTRINSVTADTAIVYCAALDGTTLIDWGCGTLTVSS 114	
Db	61 LKSRITMSVDTSKNMFSRLRTSVTAADTAIVYCAASDDGYTLIDNWCGTLTVSS 114	
RESULT 4		
ID	ADP03977 standard; protein; 122 AA.	
XX	ADP03977;	
XX		
DT	29-JUL-2004 (first entry)	
XX		
DE	Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 147.	
XX		
KW	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;	
KW	cytostatic; colorectal neoplasm; renal cell carcinoma;	
KW	cervical intraepithelial squamous neoplasia;	
KW	cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;	
KW	gene therapy; murine; mouse; human; heavy chain variable domain.	

[illegible]

XX	02-DEC-2002; 2002WO-US038550.
PF	
XX	
PR	03-DEC-2001; 2001US-0337275P.
XX	
PA	(ABGE-) ABGENIX INC.
XX	
PI	Gudas J, Foltz I, Handa M, Gallo M,
XX	
DR	WPI, 2003-523295/49.
XX	
XX	
PT	New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT	colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT	intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX	
PS	Example 2; SEQ ID NO 152; 89pp; English.
XX	
CC	The invention relates to a novel isolated monoclonal antibody (mab)
CC	comprising a heavy chain polypeptide and light chain polypeptide having a
CC	sequence chosen from one of 53 fully defined amino acid sequences given
CC	in the specification, where the antibody specifically binds carbonic
CC	anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC	demonstrates cytostatic activity and may be useful for treating a tumour,
CC	such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC	cervical intraepithelial squamous and glandular neoplasia, esophageal
CC	tumour or breast cancer, possibly via gene therapy. The current sequence
CC	is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC	(heavy chain variable domain) protein of the invention. The protein was
CC	generated via the introduction of the human CA IX protein into a
CC	transgenic mouse strain.
XX	
SO	Sequence 121 AA;
	Query Match 85.1%; Score 518.5; DB 7; Length 121;
	Best Local Similarity 81.9%; Pred. No. 6.7e-40;
	Matches 95; Conservative 11; Mismatches 7; Indels 3; Gaps 11
QY	2 ESGPGLVPAQTLSTSCAVSGSIRSGYYSWIRQHPKGLWITGYIHSGNTYYNPSL 61
DB	6 ESGPGLVPRSQTLSTLCTVSGSISGGYYMSWIRQHPKGLWIGIYYSSTYYNPSL 65
QY	62 KSRIMSVDTSENKRSRLRNSTADTAVYVYCARLD---GYLDTWGGTLYTVSS 114
DB	66 KSRVITSVDTSNQPSLKLSSVTADTAVYVYCAYYDIILGVAFDIDWGGTWTVSS 121
	RESULT 6
	ADP03871
ID	ADP03871 standard; protein; 125 AA.
XX	
AC	ADP03871;
XX	
DT	29-JUL-2004 (first entry)
DE	
XX	Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 11.
XX	
KW	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW	cytostatic; colorectal neoplasm; renal cell carcinoma;
KW	cervical intraepithelial squamous neoplasia;
KW	cervical intraepithelial glandular neoplasia; esophageal; breast cancer;
KW	gene therapy; murine; mouse; human; heavy chain variable domain.
XX	
OS	Unidentified.
XX	
PN	WO2003048328-A2.
XX	
PD	12-JUN-2003.
XX	
PF	02-DEC-2002; 2002WO-US038550.
XX	
PR	03-DEC-2001; 2001US-0337275P.
XX	
PA	(ABGE-) ABGENIX INC.

XX	Gudas J, Foltz I, Handa M, Gallo M,
PI	WPI, 2003-523295/49.
DR	
XX	
XX	New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT	colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT	intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX	
PS	Claim 1; SEQ ID NO 11; 89pp; English.
XX	
CC	The invention relates to a novel isolated monoclonal antibody (mab)
CC	comprising a heavy chain polypeptide and light chain polypeptide having a
CC	sequence chosen from one of 53 fully defined amino acid sequences given
CC	in the specification, where the antibody specifically binds carbonic
CC	anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC	demonstrates cytosstatic activity and may be useful for treating a tumour,
CC	such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC	cervical intraepithelial squamous and glandular neoplasia, esophageal
CC	tumour or breast cancer, possibly via gene therapy. The current sequence
CC	is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC	(heavy chain variable domain) protein of the invention. The protein was
CC	generated via the introduction of the human CA IX protein into a
CC	transgenic mouse strain.
XX	
SQ	Sequence 125 AA;
Query Match	85.0%; Score 517.5; DB 7; Length 125;
Best Local Similarity	81.7%; Pred. No. 8.6e-40;
Matches	98; Conservative 9; Mismatches 6; Indels 7; Gaps 2
OY	2 ESGPGLVPAQTLSLSCAVSGSIRSGGYMSWIROHPGKLEWIGIYHSGNTYYNPSL 61
DB	6 ESGPGLVPAQSOTLSLTCTVSSGGSISSGGYWMSWIRHPGKLEWIGIYISGNTYYNPSL 65
OY	62 KSRIAMSVDTSENKRSLRNSTADTAADVYYCAR-----LDGY--TLDIWGCGTLVTSS 114
DB	66 KSRITISVDTSKNQPSLKLSISTATADTAADVYYCARTYYDFLTGYPDPAFDIWGGTMTVASS 125
RESULT 7	
ADP03981	
ID	ADP03981 standard; protein; 121 AA.
XX	
AC	ADP03981;
XX	
DT	29-JUN-2004 (first entry)
XX	
DE	Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 151.
XX	
KM	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KW	cytostatic; colorectal neoplasm; renal cell carcinoma;
KX	cervical intraepithelial squamous neoplasia;
KW	cervical intraepithelial glandular neoplasia; esophageal; breast cancer;
KX	gene therapy; murine; mouse; human; heavy chain variable domain.
XX	
OS	Unidentified.
XX	
PN	WO2003048328-A2.
XX	
PD	12-JUN-2003.
XX	
PJ	02-DEC-2002; 2002WO-US038550.
XX	
PR	03-DEC-2001; 2001US-0337275F.
XX	
PA	(ABGE-) ABGENIX INC.
XX	
PI	Gudas J, Foltz I, Handa M, Gallo M;
XX	
DR	WPI, 2003-523295/49.
XX	
PT	New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,

CC	comprising a heavy chain polypeptide and light chain polypeptide having a
CC	sequence chosen from one of 53 fully defined amino acid sequences given
CC	in the specification, where the antibody specifically binds carbonic
CC	anhydratase IX (CA IX) tumour antigen. The antibody of the invention
CC	demonstrates cytoskeletal activity and may be useful for treating a tumour,
CC	such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC	cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC	tumour or breast cancer, possibly via gene therapy. The current sequence
CC	is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC	(heavy chain variable domain) protein of the invention. The protein was
CC	generated via the introduction of the human CA IX protein into a
CC	transgenic mouse strain.
XX	
XX	Sequence 118 AA:
XX	
XX	Query Match 84.1%; Score 512; DB 7; Length 118;
XX	Best Local Similarity 83.2%; Pred. No. 2.6e-39;
XX	Matches 94; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
Qy	2 ESGPGLVPAQTLISLSCAVSGGSIIRSGGYTWSMIRQHPKGLIEWIGIYHSGNTYTNPSL 61
Db	6 ESGGGLVMPQSQTLSLTCTVSGSGSISGGGYMSWIRQHPKGLIEWIGIYHSGNTYTNPSL 65
Qy	62 KSRITAMSDTSENKFSLELNSTADTAADTAIVVYCARLDTLTIWGCGTLVTWSS 114
Db	66 KSRITISVDTSKNPFSLKLTSSVTADTAIVVYCARYSGSGSDIWGGGTLVTWSS 118
XX	
XX	RESULT 9
XX	ADP03974
XX	ID ADP03974 standard; protein; 120 AA.
XX	
XX	ADP03974;
XX	
XX	29-JUN-2004 (first entry)
XX	
XX	Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 144.
XX	
XX	monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX	cytostatic; colorectal neoplasm; renal cell carcinoma;
XX	cervical intraepithelial squamous neoplasia;
XX	cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX	gene therapy; murine; mouse; human; heavy chain variable domain.
XX	
XX	Unidentified.
XX	
XX	WO2003048328-A2.
XX	
XX	12-JUN-2003.
XX	
XX	02-DEC-2002; 2002WO-US038550.
XX	
XX	03-DEC-2001; 2001US-0337275P.
XX	
XX	(ABGE-) ABGENIX INC.
XX	
XX	Gudas J, Foltz I, Handa M, Gallo M;
XX	
XX	WPI, 2003-523295/49.
XX	
XX	New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
XX	colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX	intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX	
XX	Example 2, SEQ ID NO 144; 89pp; English.
XX	
XX	The invention relates to a novel isolated monoclonal antibody (mAb)
XX	comprising a heavy chain polypeptide and light chain polypeptide having a
XX	sequence chosen from one of 53 fully defined amino acid sequences given
XX	in the specification, where the antibody specifically binds carbonic
XX	anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX	demonstrates cytoskeletal activity and may be useful for treating a tumour,
XX	such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX	cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX	tumour or breast cancer, possibly via gene therapy. The current sequence
XX	is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX	(heavy chain variable domain) protein of the invention. The protein was
XX	generated via the introduction of the human CA IX protein into a
XX	transgenic mouse strain.

CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
SQ Sequence 120 AA;
Query Match 84.1%; Score 512; DB 7; Length 120;
Best Local Similarity 81.9%; Pred. No. 2,6e-39;
Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;
QY 2 ESGPGLVKAQTLTSLSCAVSGGSIIRSGGYWMIWRHKGKLEWIGYIYHSGNTYNPSTL 61
DB 6 ESGPGLVKAQTLTSLTCTVSGGSIIRSGGYWMIWRHKGKLEWIGYIYHSGNTYNPSTL 65
QY 62 KSRVAMSVDTSSENFSLRLNSVTAAADTAAYVYCARLDGT--LDIMOGTLYTVSS 114
DB 66 KSRVTVISVDTSKQFSLKLSSTVAADTAAYVYCAR-DGYNWYFPLMGRTLYTVSS 120
RESULT 10
ADP03873
ID ADP03873 standard; protein; 120 AA.
XX
AC ADP03873;
XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 13.
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM cytosstatic; colorectal neoplasm; renal cell carcinoma;
KM cervical intraepithelial squamous neoplasia;
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM gene therapy; murine; mouse; human; heavy chain variable domain.
XX
OS Unidentified.
XX
PN WO2003048328-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038550.
XX
PR 03-DEC-2001; 2001US-0337275P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Foltz I, Handa M, Gallo M;
XX
DR WPI; 2003-523295/49.
XX
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS Claim 1; SEQ ID NO 13; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mab)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX demonstrates cytosstatic activity and may be useful for treating a tumour,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX tumour or breast cancer, possibly via gene therapy. The current sequence
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX (heavy chain variable domain) protein of the invention. The protein was
XX generated via the introduction of the human CA IX protein into a
XX transgenic mouse strain.

XX
SQ Sequence 120 AA;
Query Match 84.1%; Score 512; DB 7; Length 120;
Best Local Similarity 81.9%; Pred. No. 2,6e-39;
Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;
QY 2 ESGPGLVKAQTLTSLSCAVSGGSIIRSGGYWMIWRHKGKLEWIGYIYHSGNTYNPSTL 61
DB 6 ESGPGLVKAQTLTSLTCTVSGGSIIRSGGYWMIWRHKGKLEWIGYIYHSGNTYNPSTL 65
QY 62 KSRVAMSVDTSSENFSLRLNSVTAAADTAAYVYCARLDGT--LDIMOGTLYTVSS 114
DB 66 KSRVTVISVDTSKQFSLKLSSTVAADTAAYVYCAR-DGYNWYFPLMGRTLYTVSS 120
RESULT 11
ADP03872
ID ADP03872 standard; protein; 123 AA.
XX
AC ADP03872;
XX
DT 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 12.
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM cytosstatic; colorectal neoplasm; renal cell carcinoma;
KM cervical intraepithelial squamous neoplasia;
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM gene therapy; murine; mouse; human; heavy chain variable domain.
XX
OS Unidentified.
XX
PN WO2003048328-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038550.
XX
PR 03-DEC-2001; 2001US-0337275P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Foltz I, Handa M, Gallo M;
XX
DR WPI; 2003-523295/49.
XX
PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
PS Claim 1; SEQ ID NO 12; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mab)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX demonstrates cytosstatic activity and may be useful for treating a tumour,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX tumour or breast cancer, possibly via gene therapy. The current sequence
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX (heavy chain variable domain) protein of the invention. The protein was
XX generated via the introduction of the human CA IX protein into a
XX transgenic mouse strain.
SQ Sequence 123 AA;
Query Match 83.7%; Score 509.5; DB 7; Length 123;
Best Local Similarity 78.8%; Pred. No. 4,6e-39;
Matches 93; Conservative 13; Mismatches 7; Indels 5; Gaps 1;

[illegible]

RESULT 12
ADP03870
ID ADP03870 standard; protein; 123 AA

DT	29-JUL-2004	(first entry)	CA	IX	monoclonal antibody VH protein -SEQ 10
XX					Murine-expressed anti-human
XX					
KM					monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM					cervical; colorectal neoplasm; renal cell carcinoma;
KM					cervical intraepithelial squamous neoplasia;
KM					cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM					gene therapy; murine; mouse; human; heavy chain variable domain.
XX					
XX					Unidentified.
XX					

PN	WO2003048328-A2.
XX	
XX	
PD	12-JUN-2003.
XX	
XX	
PF	02-DEC-2002; 2002WO-US038550
XX	
XX	
PR	03-DEC-2001; 2001US-0337275P

PA (ABGE-) ABGENIX INC.
XX
XX Gudäs J, Foltz I, Handa M, Gallo M,
PI
XX
DR WPI; 2003-523295/49.

PT Intreepithelial squamous and glandular neoplasia or esophageal tumors
XX Claim 1; SEQ ID NO 10; 89pp; English.
PS

CC The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.

Query Match	83.5%	Score 508.5	DB 7	Length 123
Best Local Similarity	80.5%	Pred. No. 5.6e-39		
Matches 95; Conservative	10;	Mismatches 8;	Indels 5;	Gaps 1;

Oy 2 ESGPGLVPAQ^{TLS}LSCAVSGGS.RSGGYWMSWRQH^PGKLEWIGYIYHSGNTYYNPSL 61
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 ESGPGLVKPQT^{SLT}CTIVSGGGSSGGGYWMSWRQH^PGKCLEWIGYIYHSGSTYYNPSL 65

QY 62 KSRIAMSVDTS ENKESLR LNSVTADTAVYYCARL-----DGYTLDIWGQTLTVSS 114

Db

66 KSRVTISVDTSKNQFSIKLSSVTADTAVYICARAGKYGGSSYLDYWGCGTILVTSS 123

RESULT 13
ADP03879
ID ADP03879 standard; protein; 123 AA

DT 29-JUL-2004 (first entry)

DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 19.

KM monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen
KM cytostatic; colorectal neoplasm; renal cell carcinoma;

KW cervical intraepithelial glandular neoplasia; oesophageal; breast cancer
KW gene therapy; murine; mouse; human; heavy chain variable domain.

OS Unidentified

PN WO2003048328-A2.

PD 12-JUN-2003.

PF 02-DEC-2002; 2002WO-US038550.

PR 03-DEC-2001; 2001US-0337275P.

PA (ABGE-) ABGENIX INC

PI Gudas J, Foltz I, Handa M, Gallo M,

DR WPI; 2003-523295/49

PT New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors

PS Claim 1; SEQ ID NO 19; 89pp; English

The invention relates to a novel isolated monoclonal antibody (mab) comprising a heavy chain polypeptide and light chain polypeptide having a sequence chosen from one of 53 fully defined amino acid sequences given in the specification, where the antibody specifically binds carbonic anhydrase IX (CA IX) tumour antigen. The antibody of the invention demonstrates cytostatic activity and may be useful for treating a tumour, such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma, cervical intraepithelial squamous and glandular neoplasia, oesophageal tumour or breast cancer, possibly via gene therapy. The current sequence is that of a murine-expressed anti-human CA IX monoclonal antibody VH (heavy chain variable domain) protein of the invention. The protein was generated via the introduction of the human CA IX protein into a transgenic mouse strain.

Query Match	83.5%	Score 508.5	DB 7	Length 123
Best Local Similarity	80.5%	Pred. No. 5.66-39		
Matches 95; Conservative	10;	Mismatches 8;		Indels 5; Gaps 1.

[illegible]

Db 66 KSRVVISVDTSNQSLKLSVTADTAIVVYCARERVTDYVYVGLDVGQGTIVTSS 123

RESULT 14
ADP03878

```
ID ADP03878 standard; protein: 123 AA.
AC
XX ADP03878;
XX
XX 29-JUL-2004 (first entry)
XX
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 18.
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM cytosolic; colorectal neoplasm; renal cell carcinoma;
KM cervical intraepithelial squamous neoplasia;
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX Unidentified.
OS
XX WO2003048328-A2.
XX
XX 12-JUN-2003.
XX
XX 02-DEC-2002; 2002WO-US038550.
XX
XX 03-DEC-2001; 2001US-0337275P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudas J, Foltz I, Handa M, Gallo M;
XX
XX WPI; 2003-523295/49.
XX
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Claim 1; SEQ ID NO 18; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytosolic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
XX Sequence 123 AA;
SQ
Query Match 83.5%; Score 508.5; DB 7; Length 123;
Best Local Similarity 80.5%; Pred. No. 5.6e-39;
Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;
QY 2 ESGPGLVPAQTLSLSCAVSGSIRSGGYWMTIRHFGKGLWIGYIYHSGNTYVNSL 61
D6 ESGPGLVPAQTLSLSCAVSGSIRSGGYWMTIRHFGKGLWIGYIYHSGNTYVNSL 65
QY 62 KSRVAVDVTSENKFSRLNSVTADTAIVYCAR----LDGYTLDIWGQGLTVVSS 114
D6 KSRVAVDVTSENKFSRLNSVTADTAIVYCARERVTDYDYYGGLDWGQGLTVVSS 123
```

RESULT 15

ID ADP03868 standard; protein: 125 AA.

XX ADP03868;

XX 29-JUL-2004 (first entry)

```
DE Murine-expressed anti-human CA IX monoclonal antibody VH protein -SEQ 8.
XX
XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
KM cytosolic; colorectal neoplasm; renal cell carcinoma;
KM cervical intraepithelial squamous neoplasia;
KM cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
KM gene therapy; murine; mouse; human; heavy chain variable domain.
XX
XX Unidentified.
OS
XX WO2003048328-A2.
XX
XX 12-JUN-2003.
XX
XX 02-DEC-2002; 2002WO-US038550.
XX
XX 03-DEC-2001; 2001US-0337275P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudas J, Foltz I, Handa M, Gallo M;
XX
XX WPI; 2003-523295/49.
XX
XX
XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.,
PT colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
PT intraepithelial squamous and glandular neoplasia or esophageal tumors.
XX
XX Claim 1; SEQ ID NO 8; 89pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody (mAb)
CC comprising a heavy chain polypeptide and light chain polypeptide having a
CC sequence chosen from one of 53 fully defined amino acid sequences given
CC in the specification, where the antibody specifically binds carbonic
CC anhydrase IX (CA IX) tumour antigen. The antibody of the invention
CC demonstrates cytosolic activity and may be useful for treating a tumour,
CC such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
CC cervical intraepithelial squamous and glandular neoplasia, oesophageal
CC tumour or breast cancer, possibly via gene therapy. The current sequence
CC is that of a murine-expressed anti-human CA IX monoclonal antibody VH
CC (heavy chain variable domain) protein of the invention. The protein was
CC generated via the introduction of the human CA IX protein into a
CC transgenic mouse strain.
XX
XX Sequence 125 AA;
SQ
Query Match 83.5%; Score 508.5; DB 7; Length 125;
Best Local Similarity 79.2%; Pred. No. 5.7e-39;
Matches 95; Conservative 12; Mismatches 6; Indels 7; Gaps 2;
QY 2 ESGPGLVPAQTLSLSCAVSGSIRSGGYWMTIRHFGKGLWIGYIYHSGNTYVNSL 61
D6 ESGPGLVPAQTLSLSCAVSGSIRSGGYWMTIRHFGKGLWIGYIYHSGNTYVNSL 65
QY 62 KSRVAVDVTSENKFSRLNSVTADTAIVYCAR----LDGY--TLDIWGQGLTVVSS 114
D6 KSRVAVDVTSENKFSRLNSVTADTAIVYCARFYDIIYGVDPADIWGQGLTVVSS 125
```

Search completed: July 26, 2005, 09:19:17
Job time : 87.3273 secs

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OM protein - protein search, using sw model

Run on: July 26, 2005, 09:26:32 ; Search time 72.5455 Seconds

(without alignments)
611.274 Million cell updates/sec

Title: US-10-027-725A-7

Perfect score: 609
Sequence: 1 LESGGLVXPAQTLSLSCAV.....RLDGYTLDIWQGLTVVSS 114Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

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Database : Published Applications MA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	609	100.0	114	US-10-027-725A-7	Sequence 7, Appl1
2	556	91.3	114	US-10-027-725A-9	Sequence 9, Appl1
3	546	89.7	114	US-10-027-725A-8	Sequence 8, Appl1
4	519	85.2	122	US-10-309-762-147	Sequence 147, App
5	518.5	85.1	121	US-10-309-762-152	Sequence 152, App
6	517.5	85.0	125	US-10-309-762-11	Sequence 11, Appl
7	514.5	84.5	121	US-10-309-762-151	Sequence 151, App
8	512	84.1	118	US-10-309-762-138	Sequence 138, App
9	512	84.1	120	US-10-309-762-13	Sequence 13, Appl
10	512	84.1	120	US-10-309-762-144	Sequence 144, App
11	509.5	83.7	123	US-10-309-762-12	Sequence 12, Appl

12	508.5	83.5	123	US-10-309-762-10	Sequence 10, Appl
13	508.5	83.5	123	US-10-309-762-18	Sequence 18, Appl
14	508.5	83.5	123	US-10-309-762-19	Sequence 19, Appl
15	508.5	83.5	125	US-10-309-762-8	Sequence 8, Appl1
16	508.5	83.5	125	US-10-309-762-16	Sequence 16, Appl
17	508.5	83.5	144	US-10-893-576-35	Sequence 35, Appl
18	506.5	83.2	119	US-10-309-762-131	Sequence 131, App
19	505.5	83.0	119	US-10-309-762-140	Sequence 140, App
20	505	82.9	252	US-09-880-748-11994	Sequence 1994, Ap
21	505	82.9	252	US-10-293-418-1994	Sequence 1994, Ap
22	504.5	82.8	125	US-10-309-762-153	Sequence 153, App
23	504.5	82.8	480	US-10-910-901-6	Sequence 6, Appl1
24	504	82.8	120	US-10-309-762-139	Sequence 139, App
25	503.5	82.7	127	US-10-309-762-14	Sequence 14, Appl
26	503	82.6	124	US-10-309-762-75	Sequence 75, Appl
27	503	82.6	143	US-10-309-762-96	Sequence 96, Appl
28	501.5	82.3	117	US-10-330-613-13	Sequence 13, Appl
29	501.5	82.3	117	US-10-330-530-13	Sequence 13, Appl
30	501.5	82.3	117	US-10-660-357-13	Sequence 13, Appl
31	501	82.3	149	US-10-910-901-22	Sequence 22, Appl
32	500.5	82.2	123	US-10-893-576-190	Sequence 190, App
33	500.5	82.2	251	US-10-120-414-75	Sequence 75, Appl
34	500	82.1	125	US-10-805-177-53	Sequence 53, Appl
35	498.5	81.9	253	US-09-880-748-1619	Sequence 1619, Ap
36	498.5	81.9	253	US-10-293-418-1619	Sequence 1619, Ap
37	497.5	81.7	148	US-10-893-576-31	Sequence 31, Appl
38	497	81.6	110	US-10-309-762-74	Sequence 74, Appl
39	497	81.6	121	US-10-453-698-137	Sequence 137, App
40	497	81.6	121	US-10-727-155-2	Sequence 137, App
41	497	81.6	128	US-10-727-155-10	Sequence 2, Appl1
42	497	81.6	128	US-10-727-155-30	Sequence 10, Appl
43	497	81.6	123	US-10-309-762-17	Sequence 30, Appl
44	496.5	81.5	123	US-10-309-762-17	Sequence 17, Appl
45	496.5	81.5	446	US-10-644-277-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-10-027-725A-7
; Sequence 7, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027.725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-027-725A-7

Query Match 100.0%; Score 609; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 5.7e-49;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESGGLVXPAQTLSLSCAVSGGSIKSGGYWIRQHPGKGLWIGIYHSQNTYNS 60
DB 1 LESGGLVXPAQTLSLSCAVSGGSIKSGGYWIRQHPGKGLWIGIYHSQNTYNS 60
QY 61 LKSRIVSVDSSEKFSRLNSVTAAADAVYYCARLDGYTLDIWQGLTVVSS 114
DB 61 LKSRIVSVDSSEKFSRLNSVTAAADAVYYCARLDGYTLDIWQGLTVVSS 114

RESULT 2

```
US-10-027-725A-9
; Sequence 9, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-9
```

```
Query Match          91.3%; Score 556; DB 14; Length 114;
Best Local Similarity 90.4%; Pred. No. 4,8e-44;
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy 1 EESGPGLVKPAQTSLSCAVSGSIRSGGYWMTROHPGKLEWIGIYHSGNTYNP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EESGPGLVKPSQTLSTCTVSGGSIRSGGYWMTROPPGKLEWIGIYHSGNTYNP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 LKSRIAMSVDTSENKFSRLNSVTAAADTAAYVYCARLDYTDIMWOGTLVT 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LKSRIAMSVDTSENKFSRLNSVTAAADTAAYVYCARLDYTDIMWOGTLVT 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 3
US-10-027-725A-8
; Sequence 8, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-027-725A-8
```

```
Query Match          89.7%; Score 546; DB 14; Length 114;
Best Local Similarity 89.5%; Pred. No. 4,1e-43;
Matches 102; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
```

```
Qy 1 EESGPGLVKPAQTSLSCAVSGSIRSGGYWMTROHPGKLEWIGIYHSGNTYNP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EESGPGLVKPSQTLSTCTVSGGSIRSGGYWMTROPPGKLEWIGIYHSGNTYNP 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 LKSRIAMSVDTSENKFSRLNSVTAAADTAAYVYCARLDYTDIMWOGTLVT 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LKSRIAMSVDTSENKFSRLNSVTAAADTAAYVYCARLDYTDIMWOGTLVT 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 4
US-10-309-762-147
; Sequence 147, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
```

```
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX, 027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-147
```

```
Query Match          85.2%; Score 519; DB 15; Length 122;
Best Local Similarity 81.2%; Pred. No. 1,4e-40;
Matches 95; Conservative 12; Mismatches 6; Indels 4; Gaps 1;
```

```
Qy 2 EESGPGLVKPAQTSLSCAVSGSIRSGGYWMTROHPGKLEWIGIYHSGNTYNP 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 EESGPGLVKPSQTLSTCTVSGGSIRSGGYWMTROHPGKLEWIGIYHSGNTYNP 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 62 KSRITAMSVDTSENKFSRLNSVTAAADTAAYVYCARLDYTDIMWOGTLVT 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRITAMSVDTSENKFSRLNSVTAAADTAAYVYCARLDYTDIMWOGTLVT 122
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 5
US-10-309-762-152
; Sequence 152, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX, 027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-152
```

```
Query Match          85.1%; Score 518.5; DB 15; Length 121;
Best Local Similarity 81.9%; Pred. No. 1,6e-40;
Matches 95; Conservative 11; Mismatches 7; Indels 3; Gaps 1;
```

```
Qy 2 EESGPGLVKPAQTSLSCAVSGSIRSGGYWMTROHPGKLEWIGIYHSGNTYNP 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 6 EESGPGLVKPSQTLSTCTVSGGSIRSGGYWMTROHPGKLEWIGIYHSGNTYNP 65
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 62 KSRITAMSVDTSENKFSRLNSVTAAADTAAYVYCARLDYTDIMWOGTLVT 114
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 66 KSRITAMSVDTSENKFSRLNSVTAAADTAAYVYCARLDYTDIMWOGTLVT 121
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
RESULT 6
US-10-309-762-11
; Sequence 11, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
```



```

; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-11
```

```

Query Match      85.0%; Score 517.5; DB 15; Length 125;
Best Local Similarity 81.7%; Pred. No. 2e-40;
Matches 98; Conservative 9; Mismatches 6; Indels 7; Gaps 2;
```

```

Qy      2  EESGGLVKAQTLTSLSCAVSGSIRSGGYWMTROHFGKLEWIGYIYHSGNTYVNSL 61
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      6  EESGGLVKAQTLTSLTCTVSGSISGGYWSWIRHFGKLEWIGYIYHSGNTYVNSL 65

Qy      62  KSRIVMSVDTSENKFSRLNSVTADTAIVYCAR----LDGY--TLDIMGGTLVTVSS 114
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      66  KSRITISVDTSKNQFSLKLSSTVTAADTAIVYCAITYDFTLGTGYPDADPDIMGGTLVTVSS 125
```

```

RESULT 7
US-10-309-762-151
```

```

; Sequence 151, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-151
```

```

Query Match      84.5%; Score 514.5; DB 15; Length 121;
Best Local Similarity 81.0%; Pred. No. 3.7e-40;
Matches 94; Conservative 13; Mismatches 6; Indels 3; Gaps 1;
```

```

Qy      2  EESGGLVKAQTLTSLSCAVSGSIRSGGYWMTROHFGKLEWIGYIYHSGNTYVNSL 61
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      6  EESGGLVKAQTLTSLTCTVSGSISGGYWSWIRHFGKLEWIGYIYHSGNTYVNSL 65

Qy      62  KSRIVMSVDTSENKFSRLNSVTADTAIVYCARL---DGYTLDIMGGTLVTVSS 114
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      66  KSRVITISVDTSKNQFSLKLSSTVTAADTAIVYCARLWFGYGMVDWGGTLVTVSS 121
```

```

RESULT 8
US-10-309-762-138
; Sequence 138, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
```

```

; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-138
```

```

Query Match      84.1%; Score 512; DB 15; Length 118;
Best Local Similarity 83.2%; Pred. No. 6.1e-40;
Matches 94; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
```

```

Qy      2  EESGGLVKAQTLTSLSCAVSGSIRSGGYWMTROHFGKLEWIGYIYHSGNTYVNSL 61
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      6  EESGGLVKAQTLTSLTCTVSGSISGGYWSWIRHFGKLEWIGYIYHSGNTYVNSL 65

Qy      62  KSRIVMSVDTSENKFSRLNSVTADTAIVYCARLDGYTLDIMGGTLVTVSS 114
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      66  KSRVITISVDTSKNQFSLKLSSTVTAADTAIVYCAITYSGSGSDWYMGGTLVTVSS 118
```

```

RESULT 9
```

```

US-10-309-762-13
; Sequence 13, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-13
```

```

Query Match      84.1%; Score 512; DB 15; Length 120;
Best Local Similarity 81.9%; Pred. No. 6.2e-40;
Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;
```

```

Qy      2  EESGGLVKAQTLTSLSCAVSGSIRSGGYWMTROHFGKLEWIGYIYHSGNTYVNSL 61
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      6  EESGGLVKAQTLTSLTCTVSGSISGGYWSWIRHFGKLEWIGYIYHSGNTYVNSL 65

Qy      62  KSRIVMSVDTSENKFSRLNSVTADTAIVYCARLDGYT--LDIMGGTLVTVSS 114
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      66  KSRVITISVDTSKNQFSLKLSSTVTAADTAIVYCAR--DGYNYWYFDIMGGTLVTVSS 120
```

```

RESULT 10
US-10-309-762-144
; Sequence 144, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-144
```

Query Match 84.1%; Score 512; DB 15; Length 120;

Best Local Similarity 81.9%; Pred. No. 6.2e-40;

Matches 95; Conservative 12; Mismatches 5; Indels 4; Gaps 2;

```

Qy 2 EESGGLVKKPAQTSLSCAVSGSIRSGGYWSWIRHDPKGLWIGIYHSNNTYNPSTL 61
Db 6 EESGGLVKKPAQTSLSCAVSGSIRSGGYWSWIRHDPKGLWIGIYHSNNTYNPSTL 65
Qy 62 KSRIAMVDTSSENKFSRLNSVTADTAAYVYCARLDTYTDLDIWGGTLVTYSS 114
Db 66 KSRVTISVDTSKQFSLKLSVTADTAAYVYCARLDGYNWYFDLWGRGLVTYSS 120
```

RESULT 11

US-10-309-762-12

; Sequence 12; Application US/10309762

; Publication No. US20040018198A1

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; APPLICANT: Foltz, Ian

; APPLICANT: Handa, Masahisa

; APPLICANT: Gallo, Michael

; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX

; FILE REFERENCE: AGENIX.027A

; CURRENT APPLICATION NUMBER: US/10/309,762

; CURRENT FILING DATE: 2002-12-02

; PRIOR APPLICATION NUMBER: 60/337275

; PRIOR FILING DATE: 2001-12-03

; NUMBER OF SEQ ID NOS: 246

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 123

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-309-762-12

Query Match 83.7%; Score 509.5; DB 15; Length 123;

Best Local Similarity 78.8%; Pred. No. 1.1e-39;

Matches 93; Conservative 13; Mismatches 7; Indels 5; Gaps 1;

```

Qy 2 EESGGLVKKPAQTSLSCAVSGSIRSGGYWSWIRHDPKGLWIGIYHSNNTYNPSTL 61
Db 6 EESGGLVKKPAQTSLSCAVSGSIRSGGYWSWIRHDPKGLWIGIYHSNNTYNPSTL 65
Qy 62 KSRIAMVDTSSENKFSRLNSVTADTAAYVYCARLDTYTDLDIWGGTLVTYSS 114
Db 66 KSRVTISVDTSKQFSLKLSVTADTAAYVYCARLDTYTDLDIWGGTLVTYSS 123
```

RESULT 12

US-10-309-762-10

; Sequence 10; Application US/10309762

; Publication No. US20040018198A1

```

; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-10
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Query Match 83.5%; Score 508.5; DB 15; Length 123;

Best Local Similarity 80.5%; Pred. No. 1.3e-39;

Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;

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Qy 2 EESGGLVKKPAQTSLSCAVSGSIRSGGYWSWIRHDPKGLWIGIYHSNNTYNPSTL 61
Db 6 EESGGLVKKPAQTSLSCAVSGSIRSGGYWSWIRHDPKGLWIGIYHSNNTYNPSTL 65
Qy 62 KSRIAMVDTSSENKFSRLNSVTADTAAYVYCARLDTYTDLDIWGGTLVTYSS 114
Db 66 KSRVTISVDTSKQFSLKLSVTADTAAYVYCARAGRTYSGSLDVGGGTLVTYSS 123
```

RESULT 13

US-10-309-762-18

; Sequence 18; Application US/10309762

; Publication No. US20040018198A1

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; APPLICANT: Foltz, Ian

; APPLICANT: Handa, Masahisa

; APPLICANT: Gallo, Michael

; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX

; FILE REFERENCE: AGENIX.027A

; CURRENT APPLICATION NUMBER: US/10/309,762

; CURRENT FILING DATE: 2002-12-02

; PRIOR APPLICATION NUMBER: 60/337275

; PRIOR FILING DATE: 2001-12-03

; NUMBER OF SEQ ID NOS: 246

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 18

; LENGTH: 123

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-309-762-18

Query Match 83.5%; Score 508.5; DB 15; Length 123;

Best Local Similarity 80.5%; Pred. No. 1.3e-39;

Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;

```

Qy 2 EESGGLVKKPAQTSLSCAVSGSIRSGGYWSWIRHDPKGLWIGIYHSNNTYNPSTL 61
Db 6 EESGGLVKKPAQTSLSCAVSGSIRSGGYWSWIRHDPKGLWIGIYHSNNTYNPSTL 65
Qy 62 KSRIAMVDTSSENKFSRLNSVTADTAAYVYCARLDTYTDLDIWGGTLVTYSS 114
Db 66 KSRVTISVDTSKQFSLKLSVTADTAAYVYCARERVTDYTYGGLDVWGGTLVTYSS 123
```

RESULT 14

US-10-309-762-19

; Sequence 19; Application US/10309762

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; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-19
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Query Match      83.5%; Score 508.5; DB 15; Length 123;
Best Local Similarity 80.5%; Pred. No. 1.3e-39;
Matches 95; Conservative 10; Mismatches 8; Indels 5; Gaps 1;
```

```
Qy      2  ESGPGLVPAQTLISCAVSGSIRSGYWSWIRHPKGLWIGYIYHSGNTYYNPSL 61
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      6  ESGPGLVPSQTLISLTCVSGSINSGGYWSWIRHPKGLWIGYIYSGSTYYNPSL 65
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      62 KSRVIAISVDTSQNSQSLKLSVTADTAIVYCAR-----LDGYTLDIWGQGLTVTVSS 114
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      66 KSRVIAISVDTSQNSQSLKLSVTADTAIVYCARERTDYDYGGIDVWGQGLTVTVSS 123
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 15
US-10-309-762-8
; Sequence 8, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-8
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Query Match      83.5%; Score 508.5; DB 15; Length 125;
Best Local Similarity 79.2%; Pred. No. 1.4e-39;
Matches 95; Conservative 12; Mismatches 6; Indels 7; Gaps 2;
```

```
Qy      2  ESGPGLVPAQTLISCAVSGSIRSGYWSWIRHPKGLWIGYIYHSGNTYYNPSL 61
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      6  ESGPGLVPSQTLISLTCVSGSINSGGYWSWIRHPKGLWIGYIYSGSTYYNPSL 65
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      62 KSRVIAISVDTSQNSQSLKLSVTADTAIVYCAR-----LDGY--TLDIWGQGLTVTVSS 114
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      66 KSRVIAISVDTSQNSQSLKLSVTADTAIVYCARITYDILITGYPDAFDIWGQGLTVTVSS 125
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Search completed: July 26, 2005, 10:05:18
Job time : 73.7121 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: July 27, 2005, 04:42:26 ; Search time 88.6545 Seconds

(without alignments)
5869.253 Million cell updates/sec

Title: US-10-027-725a-6

Perfect score: 318
Sequence: 1 gagctcagcagctctcctc.....ccaagtcggaatcaacga 318

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_NA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	291.4	91.6	974	4	US-09-859-053-29
2	291	91.5	388	3	US-09-042-353-358
3	291	91.5	388	3	US-08-758-417A-206
4	283.4	89.1	420	3	US-09-042-353-420
5	283.4	89.1	420	3	US-08-758-417A-220
6	283.4	89.1	3819	3	US-09-042-353-383
7	283.4	89.1	3819	3	US-08-758-417A-243
8	277	87.1	439	3	US-09-042-353-360
9	277	87.1	384	1	US-08-758-417A-208
10	275.4	86.6	384	1	US-08-259-372A-13
11	275.4	86.6	384	1	US-08-468-671-13
12	268.4	84.4	321	3	US-09-240-274-109
13	268.4	84.4	321	3	US-09-240-274-109
14	263.6	82.9	321	3	US-09-240-274-98
15	263.6	82.9	321	3	US-09-240-274-102
16	263.6	82.9	321	3	US-09-240-274-218
17	263.6	82.9	321	3	US-09-240-274-221
18	263.6	82.9	321	3	US-09-240-274-222
19	262	82.4	321	3	US-09-240-274-215
20	262	82.4	321	3	US-09-240-274-217
21	260.4	81.9	324	2	US-09-240-274-113
22	259.4	81.6	324	2	US-08-378-939-31
23	259.4	81.6	324	2	US-08-378-939-33
24	258.4	81.6	714	4	US-09-472-087-62
25	258.4	81.6	321	4	US-09-240-274-107
26	258.4	81.3	720	4	US-09-192-854-1
27	257.8	81.1	390	2	US-08-646-367-2

28	257.2	80.9	321	3	US-09-240-274-105	Sequence 105, App
29	257.2	80.9	321	3	US-09-240-274-216	Sequence 216, App
30	257	80.8	324	3	US-09-240-274-206	Sequence 206, App
31	256.2	80.6	324	2	US-08-378-939-23	Sequence 23, App1
32	255.6	80.4	321	3	US-09-240-274-104	Sequence 104, App
33	255.6	80.4	321	3	US-09-240-274-201	Sequence 201, App
34	255.6	80.4	321	3	US-09-240-274-211	Sequence 211, App
35	255.4	80.3	324	3	US-09-240-274-101	Sequence 101, App
36	255.4	80.3	324	3	US-09-240-274-112	Sequence 112, App
37	255.4	80.3	324	3	US-09-240-274-210	Sequence 210, App
38	254.6	80.1	324	2	US-08-378-939-17	Sequence 17, App1
39	254	79.9	321	2	US-09-240-274-207	Sequence 207, App
40	253	79.6	324	2	US-08-378-939-15	Sequence 15, App1
41	252.4	79.4	321	3	US-09-240-274-106	Sequence 106, App
42	252.2	79.3	324	3	US-09-240-274-224	Sequence 224, App
43	250.8	78.9	321	3	US-09-240-274-205	Sequence 205, App
44	250.6	78.8	324	3	US-09-240-274-110	Sequence 110, App
45	250.2	78.7	417	4	US-09-472-087-48	Sequence 48, App1

ALIGNMENTS

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RESULT 1
US-09-859-053-29
; Sequence 29, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Takashi
; APPLICANT: Tezuka, Katsunari
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ATL1M AND
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859, 053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(38)
; NAME/KEY: CDS
; LOCATION: (39)...(746)
; NAME/KEY: 3'UTR
; LOCATION: (750)...(974)
; NAME/KEY: sig_peptide
; LOCATION: (39)...(104)
US-09-859-053-29

Query Match          91.6%; Score 291.4; DB 4; Length 974;
Best Local Similarity 95.0%; Pred. No. 9.5e-92;
Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY      2 AGCTCAGCAGTCTTCATCTTCCGCTGTGATCTGTAGAGACAGATCCATTAATT 61
DB      112 AGATGACCCAGTCTTCATCTTCCGCTGTGATCTGTAGAGACAGATCCATTA 171
QY      62 GTCCGCGCAGTCAAGGATTTAGCAGTTGAGCTGATCAGCAGAAACAGGGAAG 121
DB      172 GTCCGCGCAGTCAAGGATTTAGCAGTTGAGCTGATCAGCAGAAACAGGGAAG 231
QY      122 CCCCTAACTCTGATCTATTTCTGATCAGTTGCAAGTGGGGTCCGTCAGATTCA 181
DB      232 CCCCTAACTCTGATCTATTTCTGATCAGTTGCAAGTGGGGTCCGTCAGATTCA 291
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QY 182 GCGGAGTGTATCTGGGACAGATTTCAGTCTCACCATCAGAGCCTGAGCCTGAAGATT 241
DB 292 GCGGAGTGTATCTGGGACAGATTTCAGTCTCACCATCAGAGCCTGAGCCTGAAGATT 351
QY 242 CTGCACTTACTATTTGTCACAGGCTAACATTTCCCTAACATTTTGGCCAGGGAGCA 301
DB 352 TTGCACTTACTATTTGTCACAGGCTAACATTTCCCTAACATTTTGGCCAGGGAGCA 411
QY 302 AGGTGAATCAACGA 318
DB 412 AGGTGAATCAACGA 428

RESULT 2
US-09-042-353-358
Sequence 358, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 358:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-358

Query Match 91.5%; Score 291; DB 3; Length 388;
Best Local Similarity 95.2%; Pred. No. 8.3e-92;
Matches 300; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2 AGCTCAGGCACTCTCCATCTTCCGTGCTGATCTGTAGAGAGAGAGTACCACTT 61
DB 74 AGATGACCCAGTCTCCATCTTCCGTGCTGATCTGTAGAGAGAGTACCACTT 133
QY 62 GTCCGGGAGTCAAGGATTTAGAGCTGTAGAGCTGTATCAGAGAAACAGGAAAG 121
DB 134 GTCCGGGAGTCAAGGATTTAGAGCTGTAGAGCTGTATCAGAGAAACAGGAAAG 193
QY 122 CCCCTAACTCTGATCTATTTGATCTCAGATCCAGTTTGGAAAGTGGGTCCTCAAGTTCA 181
DB 194 CCCCTAACTCTGATCTATGCTCATTCAGTTTGGAAAGTGGGTCCTCAAGTTCA 253
QY 182 GCGGAGTGTATCTGGGACAGATTTCAGTCTCAGATCAGAGAGCTGTGAAGATT 241
DB 254 GCGGAGTGTATCTGGGACAGATTTCAGTCTCAGATCAGAGAGCTGTGAAGATT 313
QY 242 CTGCACTTACTATTTGTCACAGGCTAACATTTCCGTAACATTTTGGCCAGGGAGCA 301
DB 314 TTGCACTTACTATTTGTCACAGGCTAACATTTCCGTAACATTTTGGCCAGGGAGCA 373
QY 302 AGGTGAATCAAC 316
DB 374 AGGTGAATCAAC 388

RESULT 3
US-08-758-417A-206
Sequence 206, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-08-758-417A-206

Query Match 91.5%; Score 291; DB 3; Length 388;
Best Local Similarity 95.2%; Pred. No. 8.3e-92;
Matches 300; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

2 AGCTACGCACTTCCATCTCCGCTGCTGCATCTGTAGAGAGACGATCCCAACTT 61
74 AGATGACCCAGCTTCATCTCCGCTGCTGCATCTGTAGAGAGACGATCCCAACTT 133
62 GTCCGCGCAGTCAAGGATTTAGCAGTTGCTAGCTGTATCAGAGAAACAGGGAAG 121
134 GTCCGCGCAGTCAAGGATTTAGCAGTTGCTAGCTGTATCAGAGAAACAGGGAAG 193
122 CCCCTAACTCTGATCTATTTGCTGCATCAGTTTGCAGAAAGTGGGGTCCCGTCAAGTTCA 181
194 CCCCTAACTCTGATCTATTTGCTGCATCAGTTTGCAGAAAGTGGGGTCCCGTCAAGTTCA 253
182 GCGGAGAGGATCTGCGACAGATTTCAGTTCACATCAGAGAGCTGAGAGCTGAAGATT 241
254 GCGGAGAGGATCTGCGACAGATTTCAGTTCACATCAGAGAGCTGAGAGCTGAAGATT 313
242 CTGCAGACTTACTATTGTCAACAGGCTAAAGTTTCCGTACACTTTTGGCCAGGGGACCA 301

DB 314 TTGCAACTTACTATTGTCAACAGGCTAAATGTTCCCGTACACTTTGGCCAGGGGACCA 373
CY 302 AGGTGAATCAAC 316
DB 374 AGCTGAGATCAAC 388

RESULT 4
US-09-042-353-420
Sequence 420, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 420:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-042-353-420

Query Match 89.1%; Score 283.4; DB 3; Length 420;
Best Local Similarity 93.4%; Pred. No. 4e-89;
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTTCCGTCTGATCTGTAGAGACAGATCCATTAATT 61
DB 80 AGATGACCCAGTCTCCATCTTCCGTCTGATCTGTAGAGACAGATCCATTAATT 139
QY 62 GTCCGGGAGTCTGAGGATTTAGAGTGTAGCTGTGATCAGCAAGCAAGGAAAG 121
DB 140 GTCCGGGAGTCTGAGGATTTAGAGTGTAGCTGTGATCAGCAAGCAAGGAAAG 199
QY 122 CCCCTAACTCTGATCTATTTGATCTGATCTGATCTGATCTGATCTGATCTGAT 181
DB 200 CACCTAAGCTCTGATCTATTTGATCTGATCTGATCTGATCTGATCTGATCTGAT 259
QY 182 GCGGAGTGTATCTGGGACAGATTTCAAGTCTGATCTGATCTGATCTGATCTGATCTGAT 241
DB 260 GCGGAGTGTATCTGGGACAGATTTCAAGTCTGATCTGATCTGATCTGATCTGATCTGAT 319
QY 242 CTGCACTTACTATTTGCAACAGGCTTAACAGTTTCCGTAACATTTTGGCCAGGGAGCA 301
DB 320 TTGCACTTACTATTTGCAACAGGCTTAACAGTTTCCGTAACATTTTGGTCAAGGGAACCA 379
QY 302 AGGTGAAATCAACGA 318
DB 380 AGCTGAGATCAACGA 396

RESULT 5

US-08-758-417A-220
Sequence 220, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lomberg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992

ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 220:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 220:
US-08-758-417A-220

Query Match 89.1%; Score 283.4; DB 3; Length 420;
Best Local Similarity 93.4%; Pred. No. 4e-89;
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTTCCGTCTGATCTGTAGAGACAGATCCATTAATT 61
DB 80 AGATGACCCAGTCTCCATCTTCCGTCTGATCTGTAGAGACAGATCCATTAATT 139
QY 62 GTCCGGGAGTCTGAGGATTTAGAGTGTAGCTGTGATCAGCAAGCAAGGAAAG 121
DB 140 GTCCGGGAGTCTGAGGATTTAGAGTGTAGCTGTGATCAGCAAGCAAGGAAAG 199
QY 122 CCCCTAACTCTGATCTATTTGATCTGATCTGATCTGATCTGATCTGATCTGAT 181
DB 200 CACCTAAGCTCTGATCTATTTGATCTGATCTGATCTGATCTGATCTGATCTGAT 259
QY 182 GCGGAGTGTATCTGGGACAGATTTCAAGTCTGATCTGATCTGATCTGATCTGATCTGAT 241
DB 260 GCGGAGTGTATCTGGGACAGATTTCAAGTCTGATCTGATCTGATCTGATCTGATCTGAT 319
QY 242 CTGCACTTACTATTTGCAACAGGCTTAACAGTTTCCGTAACATTTTGGCCAGGGAGCA 301
DB 320 TTGCACTTACTATTTGCAACAGGCTTAACAGTTTCCGTAACATTTTGGTCAAGGGAACCA 379
QY 302 AGGTGAAATCAACGA 318
DB 380 AGCTGAGATCAACGA 396


```

RESULT 6
US-09-042-353-393
; Sequence 393, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,353
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/16433
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,417
; FILING DATE: 02-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/21803

```

```

; FILING DATE: 01-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 014643-009040US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 393:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3819 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-042-353-393

Query Match      89.1%; Score 283.4; DB 3; Length 3819;
Beet Local Similarity 93.4%; Pred. No. 1.2e-88;
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY      2 AGCTCAGGCAAGTCTCCATCTTCGCTGCTGATCTGTAGAGAGAGAGTCAACATTAATT 61
DB      2513 AGATGACCAAGTCTCCATCTTCGCTGCTGATCTGTAGAGAGAGAGTCAACATCACTT 2572
QY      62 GTCCGGCGAGTCAAGGATATTAGCAGTTGTTAGCCTGTATCAGCAGAAACAGGAAAG 121
DB      2573 GTCCGGCGAGTCAAGGATATTAGCAGTTGTTAGCCTGTATCAGCAGAAACAGGTAAG 2632
QY      122 CCCCTAACTCTGATCTATTTCTGATTCAGTTTCCGTTGCAAAAGTGGGGTCCGTCAGAGTTCA 181
DB      2633 CACCTAAGCTCTGATCTATCTGATTCAGTTTCCGTTGCAAAAGTGGGGTCCGTCAGAGTTCA 2692
QY      182 GCGGCACTGATCTGCGACATTTTCAGTCTCACCATTAAGAGCCTGAGAGCTTGAAGTT 241
DB      2693 GCGGCACTGATCTGCGACATTTTCAGTCTCACCATTAAGAGCCTGAGAGCTTGAAGTT 2752
QY      242 CTGCACTTACTATTGTTCACAGGCTAACAGTTTCCGTTGCAAAAGTGGGGTCCGTCAGAGTTCA 301
DB      2753 TTGCACTTACTATTGTTCACAGGCTAACAGTTTCCGTTGCAAAAGTGGGGTCCGTCAGAGTTCA 2812
QY      302 AGGTGAAGTCAACGA 318
DB      2813 AGGTGAAGTCAACGA 2829

RESULT 7
US-08-758-417A-243
; Sequence 243, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 417
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,417A
; FILING DATE: 02-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <unknown>

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APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 243:
SEQUENCE CHARACTERISTICS:
LENGTH: 3819 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 243:
US-08-758-417A-243

Query Match 89.1%; Score 283.4; DB 3; Length 3819;
Best Local Similarity 93.4%; Pred. No. 1.2e-88;
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2 AGCTCAGGAGTCTCCGCTGCTGATCTGTAGAGACAGAGTCAACCACTT 61
DB 2513 AGATGACCCAGCTCTCCGCTGCTGATCTGTAGAGACAGAGTCAACCACTT 2512
QY 62 GTCCGGGAGTCAAGATTTAGAGTGGTTAGCTGGTATCAGCAGAAACAGGAAAG 121
DB 2573 GTCCGGGAGTCAAGATTTAGAGTGGTTAGCTGGTATCAGCAGAAACAGGTAAG 2632
QY 122 CCCCTAACTCTGATCTATTCTGCATCAGTTTGCAAAAGTGGGGTCCCGTCAAGTTCA 181
DB 2633 CACCTAAGCTCTGATCTATCTGCATCAGTTTGCAAAAGTGGTCCCATCAAGTTCA 2632
QY 182 GCGGAGTGTGAGTGGGAGAGATTTCACTCACCATCAGAGAGCTGAGGCTGAAGATT 241
DB 2693 GCGGAGTGTGAGTGGGAGAGATTTCACTCACCATCAGAGAGCTGAGGCTGAAGATT 2752
QY 242 CTGCACTTACTATTGTCAACAGGCTAACAGTTTCCCTAGACATTGTGGCCAGGGAGCA 301
DB 2753 TTGCACTTACTATTGTCAACAGGCTAACAGTTTCCCTAGACATTGTGGCCAGGGAGCA 2812
QY 302 AGGTGAAATCAACGA 318
DB 2813 AGCTGAGATCAACGA 2829

RESULT 8
US-09-042-353-360
Sequence 360, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.

TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 360:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 439 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-042-353-360

Query Match 87.1%; Score 277; DB 3; Length 439;
Best Local Similarity 92.1%; Pred. No. 7,1e-87;
Matches 292; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGCTCTCCATCTTCCGCTGTCATCTGTAGAGACAGAGTCAACCAATTAATT 61
DB 74 AGATGACCCAGTCTTCATCTCAGCTGTCATCTGTAGAGACAGAGTCAACCAATTAATT 133
QY 62 GTCCGGCGAGTCAAGGATTTAGCAAGTTGTTAGCCTGTATCAGCAGAAACAGGAAAG 121
DB 134 GTCCGGCGAGTCAAGGATTTAGCAAGTTGTTAGCCTGTATCAGCAGAAACAGGAAAG 193
QY 122 CCCCTAACTCTGATCTATTTCTGATCCAGTTTGCAAGTGGGTCCTCCGTCAGGTTCA 181
DB 194 CCCCTAACTCTGATCTATTTCTGATCCAGTTTGCAAGTGGGTCCTCCGTCAGGTTCA 253
QY 182 GCGGACGTGATCTGGGACAGATTTCACTCAGTCACAGAGCCTGAGCCTGAAGATT 241
DB 254 GCGGACGTGATCTGGGACAGATTTCACTCAGTCACAGAGCCTGAGCCTGAAGATT 313
QY 242 CTGCAACTTACTATTGTCAAGAGGCTTAACAGTTTCCGTACACTTTTGGCCAGGGAGCA 301
DB 314 TTGCAACTTATTATCGCAACAGATATGATTAACCCGTACACTTTTGGCCAGGGAGCA 373
QY 302 AGGTGAAATCAACGA 318
DB 374 AGCTGAGATCAACGA 390

RESULT 9

US-08-758-417A-208
; Sequence 208, Application US/08758417A
; Patent No. 6300129

GENERAL INFORMATION:

APPLICANT: Lonberg, Nils
; Kay, Robert M.

TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
; Producing Heterologous Antibodies

CORRESPONDENCE ADDRESS:

ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/758,417A
; FILING DATE: 02-Dec-1996
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995

APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: US 08/209,741

FILING DATE: 09-MAR-1994
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Serafini, Andrew T.
; REGISTRATION NUMBER: 41,303
; REFERENCE/DOCKET NUMBER: 014643-009030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 439 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-08-758-417A-208

Query Match 87.1%; Score 277; DB 3; Length 439;
Best Local Similarity 92.1%; Pred. No. 7,1e-87;
Matches 292; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGCTCTCCATCTTCCGCTGTCATCTGTAGAGACAGAGTCAACCAATTAATT 61
DB 74 AGATGACCCAGTCTTCATCTCAGCTGTCATCTGTAGAGACAGAGTCAACCAATTAATT 133
QY 62 GTCCGGCGAGTCAAGGATTTAGCAAGTTGTTAGCCTGTATCAGCAGAAACAGGAAAG 121
DB 134 GTCCGGCGAGTCAAGGATTTAGCAAGTTGTTAGCCTGTATCAGCAGAAACAGGAAAG 193
QY 122 CCCCTAACTCTGATCTATTTCTGATCCAGTTTGCAAGTGGGTCCTCCGTCAGGTTCA 181
DB 194 CCCCTAACTCTGATCTATTTCTGATCCAGTTTGCAAGTGGGTCCTCCGTCAGGTTCA 253
QY 182 GCGGACGTGATCTGGGACAGATTTCACTCAGTCACAGAGCCTGAGCCTGAAGATT 241
DB 254 GCGGACGTGATCTGGGACAGATTTCACTCAGTCACAGAGCCTGAGCCTGAAGATT 313
QY 242 CTGCAACTTACTATTGTCAAGAGGCTTAACAGTTTCCGTACACTTTTGGCCAGGGAGCA 301
DB 314 TTGCAACTTATTATCGCAACAGATATGATTAACCCGTACACTTTTGGCCAGGGAGCA 373
QY 302 AGGTGAAATCAACGA 318
DB 374 AGCTGAGATCAACGA 390

RESULT 10

US-08-259-372A-13
; Sequence 13, Application US/08259372A
; Patent No. 5563554

GENERAL INFORMATION:

APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
; ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN

CORRESPONDENCE ADDRESS:

ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,372A
FILING DATE: 14-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Hybridoma
CELL LINE: ZM1-2
FEATURE:
NAME/KEY: CDS
LOCATION: 1..384
US-08-259-372A-13

Query Match 86.6%; Score 275.4; DB 1; Length 384;
Best Local Similarity 91.8%; Pred. No. 2.4e-86;
Matches 291; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGCTTCATCTTCCGTCGATCTGTAGAGAGAGAGTCAACCTTAATTT 61
DB 68 AGATGACCCAGTCTCCATCTTCGTCGATCTGTGAGAGACAGAGTCAACCTTAATTT 127
QY 62 GTCCGGCAGTCAAGGATTTAGCAGTTGTTAGCCTGTGATCAGAGAAACAGGGAAG 121
DB 128 GTCCGGCAGTCAAGGATTTAGCAGTTGTTAGCCTGTGATCAGAGAAACAGGGAAG 187
QY 122 CCCCTAACTCTGATCTATTCTGATCAAGTTTGCAAGTGGGTCCTGCAAGTTCA 181
DB 188 CCCCTAACTCTGATCTATTCTGATCAAGTTTGCAAGTGGGTCCTGCAAGTTCA 247
QY 182 GCGGAGGTGATCTGGGACAGATTTCAAGTTCACATCAGAGCCTGAGAGCTGAAGATT 241
DB 248 TCGGAGGTGATCTGGGACAGATTTCAAGTTCACATCAGAGCCTGAGAGCTGAAGATT 307

QY 242 CTCGAATCTACTATTGTCAACAGGCTAACAGTTTCCGTCATCTTTGGCCAGGGACCA 301
DB 308 TTGCACTACTATTGTCAACAGGCTGACAGTCTCCCTTTACTTTGGCGGAGGACCA 367
QY 302 AGGTGAATCAACGCA 318
DB 368 AGGTGACTTCAACGCA 384

RESULT 11
US-08-468-671-13
Sequence 13, Application US/08468671
Patent No. 5648077
GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,671
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens

CELL TYPE: Hybridoma
CELL LINE: ZM1-2
FEATURE:
NAME/KEY: CDS
LOCATION: 1..384
US-08-468-671-13

Query Match 86.6%; Score 275.4; DB 1; Length 384;
Best Local Similarity 91.8%; Pred. No. 2.4e-86;
Matches 291; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTTCATCTCCGCTGCTGATCTGTAGAGACAGATCCATTAATT 61
DB 68 AGATGACCCAGCTTCATCTCCGCTGCTGATCTGTAGAGACAGATCCATTAATT 127
QY 62 GTCCGGCAGTCTGAGGATTTAGCAGTTAGCTGTATCAGAGAAACAGAGAAAG 121
DB 128 GTCCGGCAGTCTGAGGATTTAGCAGTTAGCTGTATCAGAGAAACAGAGAAAG 187
QY 122 CCCCTAACTCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 181
DB 188 CCCCTAACTCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 247
QY 182 GCGGAGTGTATCTGAGGACAGATTTCACTTCACCATCAGAGCTGAGCTGAAGTT 241
DB 248 TCGGAGTGTATCTGAGGACAGATTTCACTTCACCATCAGAGCTGAGCTGAAGTT 307
QY 242 CTGCACTTACTATTTGCAAGAGCTACAGTTCCCGTACCTTTGCGAGGAGGACA 301
DB 308 TTGCACTTACTATTTGCAAGAGCTACAGTTCCCGTACCTTTGCGAGGAGGACA 367
QY 302 AGGTGAATCAACGA 318
DB 368 AGGTGAGTCAACGA 384

RESULT 12

US-09-240-274-109
Sequence 109, Application US/09240274
Patent No. 6255455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 109
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 109
US-09-240-274-109

Query Match 84.4%; Score 268.4; DB 3; Length 321;
Best Local Similarity 90.3%; Pred. No. 6.3e-84;
Matches 287; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 GAGCTCAGCAGTCTTCATCTCCGCTGCTGATCTGTAGAGACAGATCCATTAATT 60
DB 4 GAGCTCAGCAGTCTTCATCTCCGCTGCTGATCTGTAGAGACAGATCCATTAATT 63
QY 61 TGTGGGAGTCTGAGGATTTAGCAGTTAGCTGTATCAGAGAAACAGAGAA 120
DB 64 TGTGGGAGTCTGAGGATTTAGCAGTTAGCTGTATCAGAGAAACAGAGAA 123

QY 121 GCCCTAACTCTGATCTATTTGATCCAGTTTGCAAGATGGGGTCCCGTCAAGTTTC 180
DB 124 GCCCTAACTCTGATCTATTTGATCCAGTTTGCAAGATGGGGTCCCGTCAAGTTTC 183
QY 181 AGCGCAGTGTATCTGGGACAGATTTAGTCTCAACATCAGACAGCTGACCTGAAGAT 240
DB 184 AGTGGCAGTGTATCTGGGACAGATTTAGTCTCAACATCAGACAGCTGACCTGAAGAT 243
QY 241 TCTGCACTTACTATTTGCAACAGCTTACAGTTTCCCGTACACTTTTGGCCAGGGACC 300
DB 244 TTTGCACTTACTATTTGCAACAGCTTAAATGTTACCGGTACACTTTTGGCCAGGGACC 303
QY 301 AAGGTGAATCAACGA 318
DB 304 AAGGTGAGATCAACGA 321

RESULT 13

US-09-240-274-199
Sequence 199, Application US/09240274
Patent No. 6255455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 199
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-199

Query Match 83.9%; Score 266.8; DB 3; Length 321;
Best Local Similarity 89.9%; Pred. No. 2.3e-83;
Matches 286; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 GAGCTCAGCAGTCTTCATCTCCGCTGCTGATCTGTAGAGACAGATCCATTAATT 60
DB 4 GAGCTCAGCAGTCTTCATCTCCGCTGCTGATCTGTAGAGACAGATCCATTAATT 63
QY 61 TGTGGGAGTCTGAGGATTTAGCAGTTAGCTGTATCAGAGAAACAGAGAA 120
DB 64 TGTGGGAGTCTGAGGATTTAGCAGTTAGCTGTATCAGAGAAACAGAGAA 123
QY 121 GCCCTAACTCTGATCTATTTGATCCAGTTTGGCAAGATGGGGTCCCGTCAAGTTTC 180
DB 124 GCCCTAACTCTGATCTATTTGATCCAGTTTGGCAAGATGGGGTCCCGTCAAGTTTC 183
QY 181 AGCGCAGTGTATCTGGGACAGATTTAGTCTCAACATCAGACAGCTGACCTGAAGAT 240
DB 184 AGTGGCAGTGTATCTGGGACAGATTTAGTCTCAACATCAGACAGCTGACCTGAAGAT 243
QY 241 TCTGCACTTACTATTTGCAACAGCTTACAGTTTCCCGTACACTTTTGGCCAGGGACC 300
DB 244 TTTGCACTTACTATTTGCAACAGCTTAAATGTTACCGGTACACTTTTGGCCAGGGACC 303
QY 301 AAGGTGAATCAACGA 318
DB 304 AAGGTGAGATCAACGA 321

RESULT 14

US-09-240-274-98

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; Sequence 98, Application US/09240274
; Patent No. 6253455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain F01
US-09-240-274-98
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Query March 82.9%; Score 263.6; DB 3; Length 321;
Best Local Similarity 89.3%; Pred. No. 3.1e-82;
Matches 284; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 GAGCTCAGCAGTCTCCATCTTCGTCATCTGTAGAGAGACAGATCCATACT 60
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DB 4 GAGCTCAGCAGTCTCCATCTTCGTCATCTGTAGAGAGACAGATCCATACT 63
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QY 61 TGTGGGCGAGTCAGGGTATTAGACGTTGTTAGCTGTATCAGCAGAAACCGAGGAAA 120
   |||||
DB 64 TGCCTGAGAGTCAGGGCTTTAGAAATGATTAGGCTGTATCAGCAGAAACCGAGGAAA 123
   |||||

QY 121 GCCCCTAACTCCGATCTATTTCGATCCAGTTTGCAGAGGGGTCGCCCTCAAGGTTTC 180
   |||||
DB 124 GCCCCTAAGCCGCTGATCTATGCTACATCCAGTTTGCAGAGGGGTCGCCCTCAAGGTTTC 183
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QY 181 AGCGCAGTGGATCTGGGACAGATTTCAGTCTCAACCATCAGAGCTCAGAGCTGAAGAT 240
   |||||
DB 184 AGCGCAGTGGATCTGGGACAGATTTCAGTCTCAACCATCAGAGCTCAGAGCTGAAGAT 243
   |||||

QY 241 TCTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCGTAACCTTTTGGCCAGGGGACC 300
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DB 244 TCTGCAACTTACTATTGTCTACAGCATATAGTTTCCGTAACCTTTTGGCCAGGGGACC 303
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QY 301 AAGGTGAAATCAACGA 318
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DB 304 AAGGTGAAATCAACGA 321
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RESULT 15
US-09-240-274-102
; Sequence 102, Application US/09240274
; Patent No. 6253455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I02
US-09-240-274-102

Query March 82.9%; Score 263.6; DB 3; Length 321;
Best Local Similarity 89.3%; Pred. No. 3.1e-82;
Matches 284; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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DB 4 GAGCTCAGCAGTCTCCATCTTCGTCATCTGTAGAGAGACAGATCCATACT 63
   |||||

QY 61 TGTGGGCGAGTCAGGGTATTAGACGTTGTTAGCTGTATCAGCAGAAACCGAGGAAA 120
   |||||
DB 64 TGCCTGAGAGTCAGGGCTTTAGAAATGATTAGGCTGTATCAGCAGAAACCGAGGAAA 123
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QY 121 GCCCCTAACTCCGATCTATTTCGATCCAGTTTGCAGAGGGGTCGCCCTCAAGGTTTC 180
   |||||
DB 124 GCCCCTAAGCCGCTGATCTATGCTACATCCAGTTTGCAGAGGGGTCGCCCTCAAGGTTTC 183
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QY 181 AGCGCAGTGGATCTGGGACAGATTTCAGTCTCAACCATCAGAGCTCAGAGCTGAAGAT 240
   |||||
DB 184 AGCGCAGTGGATCTGGGACAGATTTCAGTCTCAACCATCAGAGCTCAGAGCTGAAGAT 243
   |||||

QY 241 TCTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCGTAACCTTTTGGCCAGGGGACC 300
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DB 244 TCTGCAACTTACTATTGTCTACAGCATATAGTTTCCGTAACCTTTTGGCCAGGGGACC 303
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QY 301 AAGGTGAAATCAACGA 318
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DB 304 AAGGTGAAATCAACGA 321
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Search completed: July 27, 2005, 12:41:22
Job time : 88.6545 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:09:06 ; Search time 1819.51 Seconds

(without alignments)
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Title: US-10-027-725A-6

Perfect score: 318
Sequence: 1 gagctcagcagctctccatc.....ccaagtcggaatcaacga 318

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

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2: gb_hcg:*
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5: gb_ov:*
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14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	318	100.0	318	9	HS458381 Homo sapi
2	316.4	99.5	705	12	HS16KLC5
3	291.4	91.6	974	6	AX305000
4	291.4	91.6	974	6	AX306529
5	291.4	91.6	974	6	BD131246
6	291	91.5	388	6	AR161375
7	291	91.5	388	6	AR369968
8	291	91.5	388	6	BD096602
9	289.8	91.1	327	9	HS488657
10	289.4	91.0	322	9	AY043120
11	288.2	90.9	324	9	AF306360
12	288.2	90.6	324	9	AF146407
13	288.2	90.6	433	9	SS9162
14	288.2	90.6	812	9	AB064045
15	288.2	90.6	936	9	BC073764
16	287.4	90.4	310	9	HS4408418
17	287.4	90.4	318	9	AF103433
18	286.6	89.1	824	9	AY510107
19	286.6	89.9	324	9	AB095279

20	285.2	89.7	321	6	BD097622	BD097622 Antibody
21	285	89.6	330	9	AF240362	AF240362 Homo sapi
22	283.4	89.1	324	9	AB095282	AB095282 Homo sapi
23	283.4	89.1	420	6	AR161429	AR161429 Sequence
24	283.4	89.1	420	6	AR369974	AR369974 Sequence
25	283.4	89.1	420	6	BD096608	BD096608 Transgenic
26	283.4	89.1	3819	6	AR161402	AR161402 Sequence
27	283.4	89.1	3819	6	AR369997	AR369997 Sequence
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30	280.8	88.3	728	6	AX327729	AX327729 Sequence
31	280.4	88.2	321	6	AX365137	AX365137 Sequence
32	278.6	87.6	324	9	AB063969	AB063969 Homo sapi
33	278.6	87.6	326	9	AF103397	AF103397 Homo sapi
34	278.6	87.6	351	9	HSPBLIGVH	Z27177 H. sapiens r
35	277.6	87.3	330	9	HS16KLE1	X97555 H. sapiens m
36	277.6	87.3	716	6	AX327727	AX327727 Sequence
37	277	87.1	439	6	AR161377	AR161377 Sequence
38	277	87.1	439	6	AR369970	AR369970 Sequence
39	275.4	86.6	324	9	BD096604	BD096604 Transgenic
40	275.4	86.6	324	9	AB095289	AB095289 Homo sapi
41	275.4	86.6	384	6	I27685	I27685 Sequence 13
42	275.4	86.6	384	6	I55627	I55627 Sequence 13
43	275.2	86.5	312	9	HUMIGKAAA	L03678 Homo sapien
44	275.2	86.5	312	9	HSX98967	X98967 H. sapiens r
45	274.8	86.4	324	9	AB095284	AB095284 Homo sapi

ALIGNMENTS

RESULT 1
HSA458381
LOCUS HSA458381 318 bp mRNA linear PRI 30-APR-2002
DEFINITION Homo sapiens partial mRNA for immunoglobulin kappa light chain
ACCESSION AJ458381
VERSION AJ458381.1 GI:20387061
KEYWORDS IGRV gene; immunoglobulin kappa; light chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Flicker, S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y.,
Valent, P., Kraft, D. and Valenta, R.
TITLE Conversion of grass allergen-specific human IGH into a protective
IgG1 antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 318)
AUTHORS Flicker, S.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090
Vienna, AUSTRIA
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Best Local Similarity 100.0%; Pred. No. 3e-89;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCTACGAGATCTCCATCTTCGCTGCTGTCATCTGTAGAGACAGAGTACCATTAAT 60
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Qy 61 TGTGGGCGAGTCAAGGATATTAGACATTGTTAGCTGGTATACAGACAGAAACAGGAAA 120
Db 61 TGTGGGCGAGTCAAGGATATTAGACATTGTTAGCTGGTATACAGACAGAAACAGGAAA 120

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Qy 181 AGCGGAGTGGATCTGGGACAGATTTGAGTCTCAACATCAGACGCTGACCTGAAGAT 240
Db 181 AGCGGAGTGGATCTGGGACAGATTTGAGTCTCAACATCAGACGCTGACCTGAAGAT 240

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Db 241 TCTGCAACTTACTATTGTTCACAGAGGCTTACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300

Qy 301 AAGGTGAAATCAAAACA 318
Db 301 AAGGTGAAATCAAAACA 318

RESULT 2
HISGLCS 705 bp RNA linear SYN 29-MAR-2001
LOCUS DEFINITION Synthetic construct including Homo sapiens immunoglobulin kappa chain (clone: 5).

ACCESSION X95747
VERSION X95747.1 GI:1514580
KEYWORDS constant region; immunoglobulin; kappa light chain.
SOURCE Synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Steinberger, P., Kraft, D. and Valenta, R.
TITLE Construction of a combinatorial IGE library from an allergic patient. Isolation and characterization of human IGE Fabs with specificity for the major Timothy grass pollen allergen, Phl p 5
JOURNAL J. Biol. Chem. 271 (18), 10967-10972 (1996)
MEDLINE 96210038
PUBMED 8631916
REFERENCE 2 (bases 1 to 705)
AUTHORS Valenta, R. L. S.
TITLE Direct Submission
JOURNAL Submitted (19-FEB-1996) R. L. S. Valenta, Institute of General & Experimental Pathology, General Hospital, Waehringer Guertel 18-20, 1090 Vienna, AUSTRIA

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primer_bind 67..72
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ORIGIN

Query Match 99.5%; Score 316.4; DB 12; Length 705;
Best Local Similarity 99.7%; Pred. No. 8.7e-89;
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 187 GCCCCTAACTCTGATCTATTCGATCCAGTTTGCAAGTGGGGTCCGCTCAAGGTTTC 246

Qy 181 AGCGGAGTGGATCTGGGACAGATTTGAGTCTCAACATCAGACGCTGACCTGAAGAT 240
Db 247 AGCGGAGTGGATCTGGGACAGATTTGAGTCTCAACATCAGACGCTGACCTGAAGAT 306

Qy 241 TCTGCAACTTACTATTGTTCACAGAGGCTTACAGTTTCCCGTACACTTTTGGCCAGGGGACC 300
Db 307 TCTGCAACTTACTATTGTTCACAGAGGCTTACAGTTTCCCGTACACTTTTGGCCAGGGGACC 366

Qy 301 AAGGTGAAATCAAAACA 318
Db 367 AAGGTGAAATCAAAACA 384

RESULT 3
AX305000 974 bp DNA linear PAT 11-DEC-2001
LOCUS Sequence 29 from Patent EP1158004.
DEFINITION AX305000
ACCESSION AX305000.1 GI:17644678
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1
TITLE Takashi, T., Katsumari, T.P. and Nobuaki, H.
JOURNAL Human monoclonal antibody against a costimulatory signal
transduction molecule a11m and pharmaceutical use thereof
Patent: EP 1158004-A 29 28-NOV-2001;
Japan Tobacco Inc. (Jup)
FEATURES
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Location/Qualifiers
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FYPREAKVQMKVDNALOSGNSQSVTEQSDSDSYSLSTLTLSKADYEKKHYACEV
THQSLSPVTKSFNRGEC"
3'UTR
750..974
sig_peptide
39..104
ORIGIN
Query Match 91.6%; Score 291.4; DB 6; Length 974;
Best Local Similarity 95.0%; Pred. No. 6.9e-81;
Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 2 AGCTACGAGCTTCATCTTCGCTGCTGCATCTGTAGAGACAGATCAATTAATT 61
DB 112 AGATGACCCAGCTTCATCTTCGCTGCTGCATCTGTAGAGACAGATCAATTAATT 171
QY 62 GTCCGGGAGCTCAGGGATTAGCAGTTGGTAACTGATCAGCAAAACCAAGGAAAG 121
DB 172 GTCCGGGAGCTCAGGGATTAGCAGTTGGTAACTGATCAGCAAAACCAAGGAAAG 231
QY 122 CCCCTAACTCTGATCTATCTGATCAGATTTGGCAAGGGGTCCTCCGCAAGTTCA 181
DB 232 CCCCTAACTCTGATCTATCTGATCAGATTTGGCAAGGGGTCCTCCGCAAGTTCA 291
QY 182 GCGGACAGTATCTGGAGCAGATTTCACTCACCATCAGCAGCTGAGCTGAAGATT 241
DB 292 GCGGACAGTATCTGGAGCAGATTTCACTCACCATCAGCAGCTGAGCTGAAGATT 351
QY 242 CTGCACTTACTATTTGTCACAGGCTAAAGCTTTCCGTACACTTTTGCCAGGGAGCA 301
DB 352 TTGCACTTACTATTTGTCACAGGCTAAAGCTTTCCGTACACTTTTGCCAGGGAGCA 411
QY 302 AGGTGAATCAACGA 318
DB 412 AGGTGAATCAACGA 428
RESULT 4
AX306529 974 bp DNA linear PAT 11-DEC-2001
LOCUS Sequence 29 from Patent WO0187981.
DEFINITION AX306529
ACCESSION AX306529.1 GI:17645749
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1
TITLE Tsuji, T., Tezuka, K. and Hori, N.
JOURNAL Human monoclonal antibody against a costimulatory signal
transduction molecule a11m and pharmaceutical use thereof
Patent: WO 0187981-A 29 22-NOV-2001;
Japan Tobacco Inc. (Jup)
FEATURES
source
Location/Qualifiers
1..974
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
1..38
5'UTR
39..749
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD19048.1"
/translation="MDMRVPAQLGLLILMFPSGRCDIQMTQSPSSVSASVGRVITP
CRASQGISRLIAYTQKRGKAPKLLIYVASSLGVSRSRSGSGSDFTLTSLDP
EDFATYVCOQANSEPMTEGQGTKEIRTVAPSVFLPPEDEQLKSGTASVCLLN
FYPREAKVQMKVDNALOSGNSQSVTEQSDSDSYSLSTLTLSKADYEKKHYACEV
THQSLSPVTKSFNRGEC"
3'UTR
750..974
sig_peptide
39..104
ORIGIN
Query Match 91.6%; Score 291.4; DB 6; Length 974;
Best Local Similarity 95.0%; Pred. No. 6.9e-81;
Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 2 AGCTACGAGCTTCATCTTCGCTGCTGCATCTGTAGAGACAGATCAATTAATT 61
DB 112 AGATGACCCAGCTTCATCTTCGCTGCTGCATCTGTAGAGACAGATCAATTAATT 171
QY 62 GTCCGGGAGCTCAGGGATTAGCAGTTGGTAACTGATCAGCAAAACCAAGGAAAG 121
DB 172 GTCCGGGAGCTCAGGGATTAGCAGTTGGTAACTGATCAGCAAAACCAAGGAAAG 231
QY 122 CCCCTAACTCTGATCTATCTGATCAGATTTGGCAAGGGGTCCTCCGCAAGTTCA 181
DB 232 CCCCTAACTCTGATCTATCTGATCAGATTTGGCAAGGGGTCCTCCGCAAGTTCA 291
QY 182 GCGGACAGTATCTGGAGCAGATTTCACTCACCATCAGCAGCTGAGCTGAAGATT 241
DB 292 GCGGACAGTATCTGGAGCAGATTTCACTCACCATCAGCAGCTGAGCTGAAGATT 351
QY 242 CTGCACTTACTATTTGTCACAGGCTAAAGCTTTCCGTACACTTTTGCCAGGGAGCA 301
DB 352 TTGCACTTACTATTTGTCACAGGCTAAAGCTTTCCGTACACTTTTGCCAGGGAGCA 411
QY 302 AGGTGAATCAACGA 318
DB 412 AGGTGAATCAACGA 428
RESULT 5
BD131246 974 bp DNA linear PAT 18-SEP-2002
LOCUS Human monoclonal antibody against costimulation transducer
DEFINITION BD131246
ACCESSION BD131246
VERSION BD131246.1 GI:23226191
KEYWORDS Human monoclonal antibody against costimulation transducer
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1
TITLE Tsuji, T., Tezuka, K. and Hori, N.

TITLE Human monoclonal antibody against constitutiviation transducer
JOURNAL molecule AILIM and medicinal utilization thereof
Patent: JP 2002034581-A 28 05-FEB-2002;
COMMENT JAPAN TOBACCO INC
OS Homo sapiens (human)
PN JP 2002034581-A/28
PD 05-FEB-2002
PF 30-MAR-2001 JP 2001099508
PI TAKASHI TSUJI, KATSUNARI TEZUKA, NOBUAKI HORI
PC C12N15/09, A61K31/7088, A61K38/00, A61K39/395, A61K45/00, A61P37/08,
PC A61P43/00, A61P43/00, C07K16/28, C07K16/46, C07K19/00, C12N5/10, PC C12N15/02,
PC C12P21/08, G01N33/15, G01N33/50, G01N33/53, G01N33/566, G01N33/577// PC (C12P21/08, C12P1:91), C12N15/00, A61K37/02, C12N5/00, C12N15/00 CC Human monoclonal antibody against constitutiviation transducer CC
FEATURES
source CC and medicinal utilization thereof
FH Key Location/Qualifiers
FT 5'UTR (1) . . (38)
FT CDS (39) . . (749)
FT 3'UTR (750) . . (974)
FT sig_peptide (39) . . (104).
Location/Qualifiers
1. .974
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 91.6%; Score 291.4; DB 6; Length 974;
Best Local Similarity 95.0%; Pred. No. 6.9e-81;
Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 2 AGCTCAGCAGTCCATCTCCGTGTCGATCGTGTGAGAGAGTCCATTAATT 61
DB 112 AGATGACCCAGTCTCCATCTCCGTGTCGATCGTGTGAGAGAGTCCATTAATT 171
QY 62 GTCGGGCGAGTCAGGGATTATAGCAGTTGGTTCGCTGATCAGCAAAACAGGGAAG 121
DB 172 GTCGGGCGAGTCAGGGATTATAGCAGTTGGTTCGCTGATCAGCAAAACAGGGAAG 231
QY 122 CCCCTAACTCTGATCTATCTGATCAGTTGGCAAGTGGGGTCCGTCAGAGTTCA 181
DB 232 CCCCTAACTCTGATCTATCTGATCAGTTGGCAAGTGGGGTCCGTCAGAGTTCA 291
QY 182 GCGGCACTGATCTGGGACAGATTTCAGTCTCACCATCAGAGGCTGAGCTGAAGATT 241
DB 292 GCGGCACTGATCTGGGACAGATTTCAGTCTCACCATCAGAGGCTGAGCTGAAGATT 351
QY 242 CTGCACTTACTATTTGTCACAGGCTAACAGTTTCCGTCAGCTTTTGGCCAGGGAACA 301
DB 352 TTGCACTTACTATTTGTCACAGGCTAACAGTTTCCGTCAGCTTTTGGCCAGGGAACA 411
QY 302 AGGTGAATCAAAACA 318
DB 412 AGGTGAATCAAAACA 428
RESULT 6
LOCUS AR161375 388 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 358 from patent US 6255458.
ACCESSION AR161375
VERSION AR161375.1 GI:16227235
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 388)
AUTHORS Lonberg N and Kay R.M.
TITLES High affinity human antibodies and human antibodies against disoxin

JOURNAL Patent: US 6255458-A 358 03-JUL-2001;
FEATURES Location/Qualifiers
source 1. .388
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 91.5%; Score 291; DB 6; Length 388;
Best Local Similarity 95.2%; Pred. No. 1e-80;
Matches 300; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 2 AGCTCAGCAGTCCATCTCCGTGTCGATCGTGTGAGAGAGTCCATTAATT 61
DB 74 AGATGACCCAGTCTCCATCTCCGTGTCGATCGTGTGAGAGAGTCCATTAATT 133
QY 62 GTCGGGCGAGTCAGGGATTATAGCAGTTGGTTCGCTGATCAGCAAAACAGGGAAG 121
DB 134 GTCGGGCGAGTCAGGGATTATAGCAGTTGGTTCGCTGATCAGCAAAACAGGGAAG 193
QY 122 CCCCTAACTCTGATCTATCTGATCAGTTGGCAAGTGGGGTCCGTCAGAGTTCA 181
DB 194 CCCCTAACTCTGATCTATCTGATCAGTTGGCAAGTGGGGTCCGTCAGAGTTCA 253
QY 182 GCGGCACTGATCTGGGACAGATTTCAGTCTCACCATCAGAGGCTGAGCTGAAGATT 241
DB 254 GCGGCACTGATCTGGGACAGATTTCAGTCTCACCATCAGAGGCTGAGCTGAAGATT 313
QY 242 CTGCACTTACTATTTGTCACAGGCTAACAGTTTCCGTCAGCTTTTGGCCAGGGAACA 301
DB 314 TTGCACTTACTATTTGTCACAGGCTAACAGTTTCCGTCAGCTTTTGGCCAGGGAACA 373
QY 302 AGGTGAATCAAAACA 316
DB 374 AGGTGAATCAAAACA 388
RESULT 7
LOCUS AR369968 388 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 206 from patent US 6300129.
ACCESSION AR369968
VERSION AR369968.1 GI:34606408
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 388)
AUTHORS Lonberg N and Kay R.M.
TITLES Transgenic non-human animals for producing heterologous antibodies
JOURNAL Patent: US 6300129-A 206 09-OCT-2001;
FEATURES Location/Qualifiers
source 1. .388
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 91.5%; Score 291; DB 6; Length 388;
Best Local Similarity 95.2%; Pred. No. 1e-80;
Matches 300; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 2 AGCTCAGCAGTCCATCTCCGTGTCGATCGTGTGAGAGAGTCCATTAATT 61
DB 74 AGATGACCCAGTCTCCATCTCCGTGTCGATCGTGTGAGAGAGTCCATTAATT 133
QY 62 GTCGGGCGAGTCAGGGATTATAGCAGTTGGTTCGCTGATCAGCAAAACAGGGAAG 121
DB 134 GTCGGGCGAGTCAGGGATTATAGCAGTTGGTTCGCTGATCAGCAAAACAGGGAAG 193
QY 122 CCCCTAACTCTGATCTATCTGATCAGTTGGCAAGTGGGGTCCGTCAGAGTTCA 181
DB 194 CCCCTAACTCTGATCTATCTGATCAGTTGGCAAGTGGGGTCCGTCAGAGTTCA 253
QY 182 GCGGCACTGATCTGGGACAGATTTCAGTCTCACCATCAGAGGCTGAGCTGAAGATT 241

Db 254 GCGGAGATGATCTGGGACAGATTTCATCTCCACCATGACGCGCTGACGCTGAAGATT 313
Qy 242 CTGCAACTTACTATTGTCAACAGGCTAAACAGTTTCCGTACACTTTTGGCCAGGGGACCA 301
Db 314 TTGCAACTTACTATTGTCAACAGGCTAAAGTTTCCGTACACTTTTGGCCAGGGGACCA 373
Qy 302 AGGTGAATCAAC 316
Db 374 AGCTGAGATCAAC 388

RESULT 8
BD096602
LOCUS
DEFINITION Transgenic non-human animals capable of producing heterologous antibodies.
ACCESSION BD096602
VERSION BD096602.1 GI:22642190
KEYWORDS JP 2001527386-A/129.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 388)
AUTHORS Lomborg, N., and Kay, R.M.
TITLE Transgenic non-human animals capable of producing heterologous antibodies
JOURNAL Patent: JP 2001527386-A 129 25-DEC-2001;
COMMENT GENPHARM INTERNATIONAL
OS Unidentified
PN JP 2001527386-A/129
PD 25-DEC-2001
PF 01-DEC-1997 JP 1998525687
PR 02-DEC-1996 US 08/758417
PT NILS LOMBERG, ROBERT M KAY
PC C12N5/00, C12N5/28, C12N5/24, C12N5/10, C07K16/00, A61K39/00 CC
Strandedness: Single;
CC Topology: Linear;
CC Transgenic non-human animals capable of producing heterologous antibodies
CC producing heterologous antibodies
FH Key Location/Qualifiers
FT source 1..388
location/Qualifiers
1..388
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

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source location/Qualifiers
1..388
/organism="unidentified"

ORIGIN
Query Match 91.5%; Score 291; DB 6; Length 388;
Best Local Similarity 95.2%; Pred. No. 1e-80;
Matches 300; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 2 AGCTCAGCAGTCTCCATCTCCGCTGCTGATCTGTGAGAGACAGATCCATTAATT 61
Db 74 AGATGACCCAGTCTTCATCTCCGCTGCTGATCTGTGAGAGACAGATCCATTAATT 133
Qy 62 GTCCGGGAGATCAGAGGATTAAGCAGTTGGTAGCCTGTATCAGAGAAACAGAGAAAG 121
Db 134 GTCCGGGAGATCAGAGGATTAAGCAGTTGGTAGCCTGTATCAGAGAAACAGAGAAAG 193
Qy 122 CCCCTAACTCTGATCTATTCTGATCAGTTGGTGAAGTGGGGTCCGCTCAAGTTCA 181
Db 194 CCCCTAACTCTGATCTATTCTGATCAGTTGGTGAAGTGGGGTCCGCTCAAGTTCA 253
Qy 182 GCGGAGTGAATCTGGGACAGATTTCACTCAGTCACATCAGAGAGCTGAGCTGAAGATT 241
Db 254 GCGGAGTGAATCTGGGACAGATTTCACTCAGTCACATCAGAGAGCTGAGCTGAAGATT 313
Qy 242 CTGCAACTTACTATTGTCAACAGGCTAAACAGTTTCCGTACACTTTTGGCCAGGGGACCA 301

Db 314 TTGCAACTTACTATTGTCAACAGGCTAAAGTTTCCGTACACTTTTGGCCAGGGGACCA 373
Qy 302 AGGTGAATCAAC 316
Db 374 AGCTGAGATCAAC 388

RESULT 9
HSA388657
LOCUS
DEFINITION Homo sapiens partial mRNA for immunoglobulin kappa chain variable region (IGV gene), sample GN30.
ACCESSION AJ388657
VERSION AJ388657.1 GI:5578815
KEYWORDS IGV gene; immunoglobulin kappa chain; immunoglobulin light chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Capello, D., Fais, F., Vivenza, D., Migliaretti, G., Chiorazzi, N., Gardano, G., and Ferrarini, M.
TITLE Identification of three subgroups of B-cell chronic lymphocytic leukemia based upon mutations of BCL-6 and IGV genes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 327)
AUTHORS Fais, F.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-1999) Fais F., Clinical Immunology, Istituto Nazionale per la Ricerca sul Cancro, L.go R. Benzi 1, 16132, ITALY

FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="B-lymphocyte"
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/note="sample GN30"
1..327
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/function="immune response"
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/protein_id="CAB51308.1"
/db_xref="GI:5578815"
/translation="DIQMTQSPPSVSASVGRVTITCRASQGISMTAWYQOKPKAP KLIIYASSLSQGVPSRFSGSGSDPTLTITSLQPPDPATVYCOQANSFPRTRGGGT KVEIKRT"

ORIGIN
Query Match 91.1%; Score 289.8; DB 9; Length 327;
Best Local Similarity 94.6%; Pred. No. 2.6e-80;
Matches 300; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 2 AGCTCAGCAGTCTCCATCTTCCTGCTGCTGATCTGTGAGAGACAGATCCATTAATT 61
Db 8 AGATGACCCAGTCTTCATCTTCCTGCTGCTGATCTGTGAGAGACAGATCCATTAATT 67
Qy 62 GTCCGGGAGATCAGAGGATTAAGCAGTTGGTAGCCTGTATCAGAGAAACAGAGAAAG 121
Db 68 GTCCGGGAGATCAGAGGATTAAGCAGTTGGTAGCCTGTATCAGAGAAACAGAGAAAG 127
Qy 122 CCCCTAACTCTGATCTATTCTGATCAGTTGGTGAAGTGGGGTCCGCTCAAGTTCA 181
Db 128 CCCCTAACTCTGATCTATTCTGATCAGTTGGTGAAGTGGGGTCCGCTCAAGTTCA 187
Qy 182 GCGGAGTGAATCTGGGACAGATTTCACTCAGTCACATCAGAGAGCTGAGCTGAAGATT 241
Db 188 GCGGAGTGAATCTGGGACAGATTTCACTCAGTCACATCAGAGAGCTGAGCTGAAGATT 247

QY 242 CTGCACTTACTATGTGCAAGAGGTTCCTCCGTACACTTTTGGCCAGGGAGCA 301
|
Db 248 TTGGACTTACTATGTGCAAGAGGTTCCTCCGTACACTTTTGGCCAGGGAGCA 307
|
QY 302 AGGTGAAATCAACGA 318
|
Db 308 AGGTGAAATCAACGA 324
|
RESULT 10
AY043120 322 bp mRNA linear PRI 31-DEC-2001
LOCUS Homo sapiens MCLL047 immunoglobulin light chain variable region
DEFINITION mRNA, partial cds.
ACCESSION AY043120
VERSION AY043120.1 GI:18025629
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 322)
Ghiotto, F., Fais, F., Valetto, A., Albesiano, E., Allen, S.,
Schulman, P., Vinciguerra, V., Rai, K., Ferrarini, M. and Chiorazzi, N.
Ig VL gene repertoire in B cell type chronic lymphocytic leukemia
JOURNAL Unpublished
TITLE 2 (bases 1 to 322)
AUTHORS Ghiotto, F., Fais, F., Valetto, A., Albesiano, E., Allen, S.,
Schulman, P., Vinciguerra, V., Rai, K., Ferrarini, M. and Chiorazzi, N.
Direct Submission
JOURNAL Submitted (29-JUN-2001) North Shore-LIJ Research Institute, 350
Community Drive, Manhasset, NY 11030, USA
FEATURES
Source Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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lymphocytic leukemia (CLL)"
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/protein_id="AAK94824.1"
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ORIGIN
Query Match 91.0%; Score 289.4; DB 9; Length 322;
Best Local Similarity 94.9%; Pred. No. 3.4e-80;
Matches 299; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 2 AGCTCAGCAGTCCCATCTCCGNGTGCATCTGTGAGAGACAGATCCATTAATT 61
|
Db 8 AGATGACCCAGCTCCCATCTCCGNGTGCATCTGTGAGAGACAGATCCATTAATT 67
|
QY 62 GTCCGGCAGTCAAGGGATTAGCAGTTGTTAGCCTGGTATCAGAGAAACAGGGAAG 121
|
Db 68 GTCCGGCAGTCAAGGGATTAGCAGTTGTTAGCCTGGTATCAGAGAAACAGGGAAG 127
|
QY 122 CCCCTAACTCTGATCTATTCTGATCCAGTTTGCAAGTGGGGTCCGTCAGGTTCA 181
|
Db 128 CCCCTAACTCTGATCTATTCTGATCCAGTTTGCAAGTGGGGTCCGTCAGGTTCA 187
|
QY 182 GCGGCAAGTGAATCGGACAGATTTCAGTTCACATAGACAGCCTGAGGCTGAAGTT 241
|
Db 188 GCGGCAAGTGAATCGGACAGATTTCAGTTCACATAGACAGCCTGAGGCTGAAGTT 247
|
QY 242 CTGCACTTACTATGTGCAAGAGGTTCCTCCGTACACTTTTGGCCAGGGAGCA 301
|
Db 248 TTGCACTTACTATGTGCAAGAGGTTCCTCCGTACACTTTTGGCCAGGGAGCA 307
|

QY 302 AGGTGAAATCAAC 316
|
Db 308 AGGTGAAATCAAC 322
|
RESULT 11
AF306360 324 bp mRNA linear PRI 28-JUN-2001
LOCUS Homo sapiens clone TP2.4 immunoglobulin light chain variable region
DEFINITION mRNA, partial cds.
ACCESSION AF306360
VERSION AF306360.1 GI:14573216
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 324)
Pichurin, P., Guo, J., Yan, X., Rapoport, B. and McLachlan, S.M.
Human monoclonal autoantibodies to B-cell epitopes outside the
thyroid peroxidase autoantibody immunodominant region
JOURNAL Thyroid 11 (4), 301-313 (2001)
MEDLINE 21247463
PUBMED 11349828
REFERENCE 2 (bases 1 to 324)
AUTHORS McLachlan, S.M., Rapoport, B., Pichurin, P., Guo, J. and Yan, X.
Direct Submission
JOURNAL Submitted (18-SEP-2000) Medicine, Cedars-Sinai Medical Center, 8700
Beverly Blvd, B-131, Los Angeles, CA 90048, USA
FEATURES
Source Location/Qualifiers
1..324
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="TP2.4"
/cell_type="thyroid-infiltrating lymphocytes"
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/note="TP2.4 VL; thyroid peroxidase autoantibody; binds to
TPO non-immunodominant region"
/codon_start=1
/product="immunoglobulin light chain variable region"
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/db_xref="GI:14573217"
/translation="ELVMTQSPSSVSASVGDRAVITTCRASQGISWLAWYQQRGKAP
KLIIYAASLSQSGVPSRFSFGSGSDFTLTISLQPEDFATYYCQANSFPMFGQGT
KVEIK"

ORIGIN
Query Match 90.9%; Score 289.2; DB 9; Length 324;
Best Local Similarity 94.3%; Pred. No. 4e-80;
Matches 300; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 1 GAGCTCAGCAGTCCCATCTCCGNGTGCATCTGTGAGAGACAGATCCATTAATT 60
|
Db 7 GTGATGACCCAGCTCCCATCTCCGNGTGCATCTGTGAGAGACAGATCCATTAATT 66
|
QY 61 TGTGCGGCGAGTCAAGGGATTAGCAGTTGTTAGCCTGGTATCAGAGAAACAGGGAAG 120
|
Db 67 TGTGCGGCGAGTCAAGGGATTAGCAGTTGTTAGCCTGGTATCAGAGAAACAGGGAAG 126
|
QY 121 GCCCTTAACTCTGATCTATTCTGATCCAGTTTGCAAGTGGGGTCCGTCAGGTTTC 180
|
Db 127 GCCCTTAACTCTGATCTATTCTGATCCAGTTTGCAAGTGGGGTCCGTCAGGTTTC 186
|
QY 181 AGCGGCAAGTGAATCGGACAGATTTCAGTTCACATAGACAGCCTGAGGCTGAAGAT 240
|
Db 187 AGCGGCAAGTGAATCGGACAGATTTCAGTTCACATAGACAGCCTGAGGCTGAAGAT 246
|
QY 241 TGTGCACTTACTATGTGCAAGAGGTTCCTCCGTACACTTTTGGCCAGGGAGCA 300
|
Db 247 TTGCACTTACTATGTGCAAGAGGTTCCTCCGTACACTTTTGGCCAGGGAGCA 306
|

QY 301 AAGGTGGAATCAACGA 318
 Db 307 AAGGTGGAATCAACGA 324

RESULT 12

AF146407 324 bp mRNA linear PRI 01-FEB-2000
 LOCUS Homo sapiens antibody light chain variable region (EL-14) mRNA,
 DEFINITION partial cds.
 ACCESSION AF146407
 VERSION AF146407.1 GI:5081718
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 324)
 AUTHORS van Den Brink, E.N., Turenhout, E.A., Davies, J., Boveneschen, N.,
 Flijuvandraat, K., Ouweland, W.H., Peters, M. and Voorberg, J.
 Human antibodies with specificity for the C2 domain of factor VIII
 are derived from VH1 germ-line genes

JOURNAL Blood 95 (2), 558-563 (2000)

REFERENCE 2 (bases 1 to 324)
 MEDLINE 10627462
 PUBMED 20094679

AUTHORS van den Brink, E.N. and Voorberg, J.
 TITLE Direct Submission

JOURNAL Submitted (28-APR-1999) Blood Coagulation, CLB, Sanguin Blood
 Supply Foundation, Plesmanlaan 125, Amsterdam 1066 CX, The
 Netherlands

FEATURES

source Location/Qualifiers

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 /protein_id="AA039505.1"
 /db_xref="GI:5081718"
 /translation="DIVTQSPSSVSASVGDRTVITTCRASGSISSMTLAWYQKFKKAP
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 KVEIKR"

CDS

gene

ORIGIN

Query Match 90.6%; Score 288.2; DB 9; Length 324;
 Best Local Similarity 94.3%; Pred. No. 8.2e-80;
 Matches 299; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
 QY 1 GAGCTACGCGAGTCCATCTTCGTCGTCATCTGAGGAGACAGATCACCATACT 60
 Db 7 GTGTATGACCCAGTCTTCATCTTCGTCGTCATCTGAGGAGACAGATCACCATACT 66
 QY 61 TGTGCGGAGTCAAGGATTTAGAGATTGTTAGCTGTTATCAGACAGAAACAGGGGAA 120
 Db 67 TGTGCGGAGTCAAGGATTTAGAGATTGTTAGCTGTTATCAGACAGAAACAGGGGAA 126
 QY 121 GCCCTTAACTCTGATCTATTTGATCCAGTTTGCAAGTGGGGTCCGTCAGAGTTTC 180
 Db 127 GCCCTTAACTCTGATCTATGTCGATCCAGTTTGCAAGTGGGGTCCGTCAGAGTTTC 186
 QY 181 AGCGGAGTGTAGTGGGACAGATTTCAGTCCACCATCAGACAGCTGAGCTGAAGAT 240
 Db 187 AGCGGAGTGTAGTGGGACAGATTTCAGTCCACCATCAGACAGCTGAGCTGAAGAT 246
 QY 241 TCTGCACTTACTATTTGCAACAGGCTTAACAGTTTCCGTCACATTTTGGCAGGGGACC 300
 Db 247 TTTCGCACTTACTATTTGCAACAGGCTTAACAGTTTCCGTCACATTTTGGCAGGGGACC 306

QY 301 AAGGTGGAATCAACG 317
 Db 307 AAGGTGGAATCAACG 323

RESULT 13

SS9162 433 bp mRNA linear PRI 26-JUN-2000
 LOCUS Ig V kappa -anti-single/double-stranded DNA antibody NE-13 light
 DEFINITION chain variable region [human, B-cells, mRNA partial, 433 nt].
 ACCESSION SS9162
 VERSION SS9162.1 GI:299955
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 433)
 AUTHORS Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;
 Hirtabayashi, Y., Munakata, Y., Takai, O., Shibata, S., Sasaki, R. and
 Sano, H.

JOURNAL Human B-cell clones expressing lupus nephritis-associated anti-DNA
 MEDLINE 93248539
 PUBMED 8387226

REMARK GenBank staff at the National Library of Medicine created this
 entry [NCBI gisbgs 130630] from the original journal article.
 This sequence comes from Fig. 6.

FEATURES

source Location/Qualifiers

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 publication"
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CDS

gene

ORIGIN

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 Matches 299; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
 QY 2 AGCTACGCGAGTCTTCATCTTCGTCGTCATCTGAGGAGACAGATCACCATACT 61
 Db 74 AGATGACCCAGTCTTCATCTTCGTCGTCATCTGAGGAGACAGATCACCATACT 133
 QY 62 GTGCGGAGTCAAGGATTTAGAGATTGTTAGCTGTTATCAGACAGAAACAGGGGAA 121
 Db 134 GTGCGGAGTCAAGGATTTAGAGATTGTTAGCTGTTATCAGACAGAAACAGGGGAA 193
 QY 122 CCCCTTAACTCTGATCTATTTGATCCAGTTTGCAAGTGGGGTCCGTCAGAGTTTC 181
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 QY 182 GCGGCACTGTAGTGGGACAGATTTCAGTCCACCATCAGACAGCTGAGCTGAAGAT 241
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 QY 242 CTGCACTTACTATTTGCAACAGGCTTAACAGTTTCCGTCACATTTTGGCAGGGGACC 301

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Db 314 TTGCACTTACTATTGTCACAGGCTTAACAGCTTCCCTTACCCTTGGCGGAGGACCA 373
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LOCUS Homo sapiens IGH mRNA for immunoglobulin kappa light chain VLJ
DEFINITION region, partial cds, clone:K4.
ACCESSION AB064045
VERSION AB064045.1 GI:21669296
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hiroo, Y., Kakita, M.,
1 Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsun, H., Okada, J.,
Miyura, K. and Kurosawa, Y.
TITLE Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 812)
AUTHORS Kurosawa, Y.
JOURNAL Direct Submission
TITLE Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyosake 470-1192, Japan
COMMENT (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
URL: http://www.fujita-hu.ac.jp/immunity/.
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Matches 299; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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QY 302 AGGTGAATCAACGA 318
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Db 374 AGGTGAGATCAACGA 390
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LOCUS Homo sapiens cDNA clone MGC:88771 IMAGE:4576136, complete cds.
DEFINITION BC073764
ACCESSION BC073764.1 GI:49256424
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
1 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F.,
Diatchenko, L., Mansina, K., Parker, A.A., Rubin, G.M., Hong, L.,
Sapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schaefer, T.E., Brownstein, M.J., Ushed, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahney, J., Helton, E., Ketteman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shcherchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.E.,
Schmerch, A., Schein, J.E., Jones, S.V., and Marra, M.A.
TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
JOURNAL 2 (bases 1 to 936)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (23-JUN-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Louis Staudt
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (ULNI)
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>
Series: IRAL Plate: 58 Row: c Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction, similarity but not identity to protein.

Location/Qualifiers

FEATURES
source

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CDS

ORIGIN

Query Match 90.6%; Score 288.2; DB 9; Length 936;
Best local Similarity 94.3%; Pred. No. 7.2e-80;
Matches 299; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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QY 2 AGCTCAGCCAGTCCCATCTCCGCTGTCATCTGTAGAGACAGAGTCAACCACTT 61
Db 85 AGATGACCCAGTCTCCATCTCCGCTGTCATCTGTAGAGACAGAGTCAACCACTT 144
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QY 122 CCCCTAACTCTGATCTATCTGTCATCAGTTTGCAAAAGTGGGGTCCCGTCAAGTTCA 181
Db 205 CCCCTAACTCTGATCTATCTGTCATCAGTTTGCAAAAGTGGGGTCCCGTCAAGTTCA 264
QY 182 GCGGCACTGATCTGGGACAGATTTCACTTCACCATCAGCAGCCTGCAAGCTGAAGATT 241
Db 265 GCGGCACTGATCTGGGACAGATTTCACTTCACCATCAGCAGCCTGCAAGCTGAAGATT 324
QY 242 CTGCAACTTACTATTTGTCACAGGCTAACAGTTCCCGTACACTTTGGCCAGGGGACCA 301
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QY 302 AGGTGAATCAACGA 318
Db 385 AAGTGATATCAACGA 401
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
6179.670 Million cell updates/sec

Title: US-10-027-725A-6

Perfect score: 318

Sequence: 1 gagctcagcagctcctcctc.....ccaagtcgaaatcaacaga 318

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 6847908

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Listing first 45 summaries

EST:
1: gb_est1:
2: gb_est2:
3: gb_hc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gsa1:
9: gb_gsa2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	285	89.6	606	6	CD690290 EST6813 h
6	283.4	89.1	558	6	CD690030 EST6553 h
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9	282	88.7	605	6	CD688415 EST9437 h
10	281.8	88.6	472	6	CD702614 EST19139
11	280.2	87.1	497	6	CD696718 EST13241
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13	276.2	86.9	894	4	BG341803 602463535
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15	274.6	86.4	851	4	BG686018 602638582
16	274.2	86.2	818	3	CR597684 full-length
17	272	85.5	629	6	CD697149 EST13672
18	271.4	85.3	421	6	CD690477 EST17000 h
19	270.6	85.1	459	6	CD695600 EST12123
20	268.8	84.5	903	5	BQ706785 AGENCOURT
21	267.2	84.0	710	6	CD695065 EST11588
22	266.6	83.8	906	4	BG756264 602713576
23	265.8	83.6	484	6	CD696042 EST12565
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31	264.2	83.1	769	6	CB957759	CB957759 AGENCOURT
32	264.2	83.1	886	4	BG756818	BG756818 602710291
33	263.2	82.8	612	6	CB553710	CB553710 MMSFP0024
34	262.6	82.6	545	6	CD697196	CD697196 EST13719
35	262.6	82.6	677	6	CD692170	CD692170 EST8709 h
36	262.6	82.6	748	6	CB956867	CB956867 AGENCOURT
37	262.6	82.6	759	6	CB984469	CB984469 AGENCOURT
38	261	82.1	422	2	AM407904	AM407904 UI-HF-BL0
39	261	82.1	741	6	CB958688	CB958688 AGENCOURT
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41	259.4	81.6	447	2	AM405752	AM405752 UI-HF-BL0
42	259.4	81.6	689	6	CB055233	CB055233 NISC_gm08
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ALIGNMENTS

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DEFINITION BF976230
ACCESSION BF976230.1 GI:12343445
VERSION
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgaabp-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LILCM1208 row: j column: 02
High quality sequence stop: 721.

FEATURES

source

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for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 92.6%; Score 294.6; DB 4; Length 943;
Best Local Similarity 95.6%; Pred. No. 1,2e-82;
Matches 303; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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DB 91 AGATGACCCAGTCTCCATCTTCGGTCTGATCTGTAGAGACAGAGTCCATTAATT 150
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RESULT 2
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DEFINITION clone CSOD1026Y122 5-PRIME, mRNA sequence.
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VERSION BX336281.2 GI:46279255
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 774)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length CDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 2, 2003 this sequence version replaced gi:30341499.
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by life technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1696.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdnafs=CSOD1026DF11QPIK=1696.r.
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized."

ORIGIN
Query Match 91.1%; Score 289.8; DB 5; Length 774;

Best Local Similarity 94.6%; Pred. No. 4e-81;
Matches 300; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCCTCCGTCGTCTGATCTGTGAGACAGAGTCCATTAATT 61
DB 22 AGATGACCCAGTCTCCATCTTCGGTCTGATCTGTAGAGACAGAGTCCATTAATT 81
QY 62 GTCGGGCGAGTCAGGATTAAGCAGTTGGTTAGCCTGTATCAGCAAAACAGGAAAG 121
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QY 122 CCCCTAATCCGATCTATCTGATCCATTCAGTTGGCAAGGGGGTCCCGTCAAGTTCA 181
DB 142 CCCCTAATCCGATCTATCTGATCCATTCAGTTGGCAAGGGGGTCCCGTCAAGTTCA 201
QY 182 GCGGCACTGATCTGGGACAGATTTCACTCAGTCATCAGAGCCTGAGCTGAAGATT 241
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DB 322 TTGCACTTACTATTTGCAACAGGCTAACAGTTTCCGTCACCTTTGGCCAGGGAGCA 321
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ACCESSION BE939490.1 GI:10467987
VERSION BE939490.1
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 554)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20020263
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=kt2-QVO-UM0093-250
800-360-a09&kt3=2000-08-25&kt4=1)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 547.
FEATURES
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location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_stre="Adult"
/clone_lib="UM0093"

/note="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 90.6%; Score 288.2; DB 2; Length 554;
Best Local Similarity 94.3%; Pred. No. 1.2e-80;
Matches 299; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTTCGCTGTCGATCTGTAGAGACAGATCCATTAATT 61
DB 36 AGATGACCCAGTCTCCATCTTCGCTGTCGATCTGTAGAGACAGATCCATTAATT 95
QY 62 GTCGGGCGAGTCAGGCTATTAGCAGTTGGTTAGCTGTATCAGAGAACCAAGGAAAG 121
DB 96 GTCGGGCGAGTCAGGCTATTAGCAGTTGGTTAGCTGTATCAGAGAACCAAGGAAAG 155
QY 122 CCCCTAACTCCGATCTATCTGATCCAGTTGGCAAGTGGGTCCCGTCAAGTTCA 181
DB 156 CCCCTAACTCCGATCTATCTGATCCAGTTGGCAAGTGGGTCCCGTCAAGTTCA 215
QY 182 GCGGCACTGATCTGGGACAGATTTTCAGTCTCAGCATCAGAGCCTGAGCCTGAAGATT 241
DB 216 GCGGCACTGATCTGGGACAGATTTTCAGTCTCAGCATCAGAGCCTGAGCCTGAAGATT 275
QY 242 CTGCACTTACTATTGTCAACAGGCTAACAGTTTCCCTGACACTTTTGGCCAGGGAGCA 301
DB 276 TTGCACTTACTATTGTCAACAGGCTAACAGTTTCCCTGACACTTTTGGCCAGGGAGCA 335
QY 302 AGGTGAATCAACGA 318
DB 336 AGCTGAGATCAACGA 352

RESULT 4
BF663472 1100 bp mRNA linear EST 21-DEC-2000
LOCUS 602144635F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297736 5',
DEFINITION mRNA sequence.

ACCESSION BF663472
VERSION BF663472.1 GI:11937367
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1100)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@b-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: L10M152 row: f column: 09
High quality sequence stop: 704.
Location/Qualifiers
1..1100
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/db_xref="taxon:9606"
/clone_image="4297736"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"

FEATURES

source

1..1100
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="4297736"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACAGAG(G) size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 90.1%; Score 286.6; DB 2; Length 1100;
Best Local Similarity 94.0%; Pred. No. 4.6e-80;
Matches 298; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTTCGCTGTCGATCTGTAGAGACAGATCCATTAATT 61
DB 81 AGATGACCCAGTCTCCATCTTCGCTGTCGATCTGTAGAGACAGATCCATTAATT 140
QY 62 GTCGGGCGAGTCAGGCTATTAGCAGTTGGTTAGCTGTATCAGAGAACCAAGGAAAG 121
DB 141 GTCGGGCGAGTCAGGCTATTAGCAGTTGGTTAGCTGTATCAGAGAACCAAGGAAAG 200
QY 122 CCCCTAACTCCGATCTATCTGATCCAGTTGGCAAGTGGGTCCCGTCAAGTTCA 181
DB 201 CCCCTAACTCCGATCTATCTGATCCAGTTGGCAAGTGGGTCCCGTCAAGTTCA 260
QY 182 GCGGCACTGATCTGGGACAGATTTTCAGTCTCAGCATCAGAGCCTGAGCCTGAAGATT 241
DB 261 GCGGCACTGATCTGGGACAGATTTTCAGTCTCAGCATCAGAGCCTGAGCCTGAAGATT 320
QY 242 CTGCACTTACTATTGTCAACAGGCTAACAGTTTCCCTGACACTTTTGGCCAGGGAGCA 301
DB 321 TTGCACTTACTATTGTCAACAGGCTAACAGTTTCCCTGACACTTTTGGCCAGGGAGCA 380
QY 302 AGGTGAATCAACGA 318
DB 381 AGCTGAGATCAACGA 397

RESULT 5
CD690290 606 bp mRNA linear EST 25-JUN-2003
LOCUS CD690290
DEFINITION EST6813 human nasopharynx Homo sapiens cDNA, mRNA sequence.

ACCESSION CD690290
VERSION CD690290.1 GI:32210896
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 606)
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
1..606
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

FEATURES

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1..606
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

Db 625 GTCCGGGAGTCAGGATTTAGCAGCTGGTTAGCTGGTTTCACAGAAACAGGAAAG 566
Qy 122 CCCCTAAACTCTGATCTATCTGCATCTCAGTTTGCAAAAGGGGATCCCGTCAAGGTTCA 181
Db 565 CCCCTAAAGCTCTGATCTATCTGATCTGCATCTCAGTTTGCAAAAGGGGATCCCGTCAAGGTTCA 506
Qy 182 GCGGAGTGTGATCTGCGGACAGATTTCACTCTCACCATCAGCAGCTGAGCTTGAAGATT 241
Db 505 GCGGAGTGTGATCTGCGGACAGATTTCACTCTCACCATCAGCAGCTGAGCTTGAAGATT 446
Qy 242 CTGCACTTACTATTTGTCACAGGCTAACAGTTTCCGTCACCTTTGGCCAGGGGACCA 301
Db 445 TTGCACTTACTATTTGTCACAGGCTAACAGTTTCCGTCACCTTTGGCCAGGGGACCA 386
Qy 302 AGGTGAATCAACGA 318
Db 385 AGGTGAATCAACGA 369

RESULT 8
BG533970 755 bp mRNA linear EST 03-APR-2001
LOCUS 602553071.F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4663096 5',
DEFINITION mRNA sequence.
ACCESSION BG533970
VERSION BG533970.1 GI:13525510
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: csapba-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
Plate: LNCMI464 row: m column: 17
High quality sequence stop: 726.
Location/Qualifiers

FEATURES
source

1..755
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4663096"
/lab_host="DH10B (T1 phage-resistant)"
/clone_id="NIH_MGC_77"
/note="Torgan: lung; Vector: pMDR-LIB (Clontech); Site: 1:
SfiI (ggcgccctcgcc); Site: 2: SfiI (ggcgatagcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCGCGCATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 89.1%; Score 283.4; DB 4; Length 755;
Best Local Similarity 93.4%; Pred. No. 4,4e-79;
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
2 AGCTCAGCAGTCTCTCATCTTCCGTGTCAGCTGTGTGAGAGACAGATCACCATTAATT 61

Db 101 AGATGACCCAGTCTCCATCTTCCGTCTGCTGATCTGTAGAGACGAGTCAACATCACTT 160
Qy 62 GTCCGGGAGTCAAGGATTTAGCAGTTGTTAGCTTGATTCAGACAGAAACAGGAAAG 121
Db 161 GTCCGGGAGTCAAGGATTTAGCAGTTGTTAGCTTGATTCAGACAGAAACAGGAAAG 220
Qy 122 CCCCTAAACTCTGATCTATCTGCATCTCAGTTTGCAAAAGGGGATCCCGTCAAGGTTCA 181
Db 221 CCCCTAAAGCTCTGATCTATCTGATCTGCATCTCAGTTTGCAAAAGGGGATCCCGTCAAGGTTCA 280
Qy 182 GCGGAGTGTGATCTGCGGACAGATTTCACTCTCACCATCAGCAGCTGAGCTTGAAGATT 241
Db 281 GCGGAGTGTGATCTGCGGACAGATTTCACTCTCACCATCAGCAGCTGAGCTTGAAGATT 340
Qy 242 CTGCACTTACTATTTGTCACAGGCTAACAGTTTCCGTCACCTTTGGCCAGGGGACCA 301
Db 341 TTGCACTTACTATTTGTCACAGGCTAACAGTTTCCGTCACCTTTGGCCAGGGGACCA 400
Qy 302 AGGTGAATCAACGA 318
Db 401 AGGTGAATCAACGA 417

RESULT 9
CD688415 605 bp mRNA linear EST 25-JUN-2003
LOCUS CD688415
DEFINITION EST4937 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD688415
VERSION CD688415.1 GI:32207195
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 605)
JOURNAL Lnu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
COMMENT Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
Contact: Yixun Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsuns.edu.cn
Location/Qualifiers

FEATURES
source

1..605
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_id="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN

Query Match 88.7%; Score 282; DB 6; Length 605;
Best Local Similarity 93.6%; Pred. No. 1.1e-78;
Matches 294; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
5 TCAGCAGTCTCCATCTTCCGTCTGATCTGTAGAGACAGAGTCAACATTAATTCTTC 64
Db 123 TCAGCAGTCTCCATCTTCTGTCTGATCTGTGTGAGACAGAGTCAACATTAATTCTTC 182
Qy 65 GCGGAGTCAAGGATTTAGCAGTTGTTAGCTTGATTCAGACAGAAACAGGAAAGCC 124
Db 183 GCGGAGTCAAGGATTTAGCAGTTGTTAGCTTGATTCAGACAGAAACAGGAAAGCC 242
Qy 125 CTAAATCTCTATCTATTTGTCATCTCAGTTTGCAAAAGGGGATCCCGTCAAGGTTCAAGC 184
Db 243 CTAAATCTCTATCTATCTCAGTTTGTCATCTCAGTTTGCAAAAGGGGATCCCGTCAAGGTTCAAGC 302

QY	185	GCAGTGGATCTGGGACACAGATTTTCAGTCTTCACCATATGACAGCCTGACGCTTGAAGATTCTG	244
Db	303	GCAGTGGATCTGGGACACAGATTTTCAGTCTTCACCATATGACAGCCTGACGCTTGAAGATTCTG	362
QY	245	CAACTTACTATTGTCAACAGGAGTAAAGTTTCCGTACACTTTTGGCCAGGGGACCAAG	304
Db	363	CAACTTACTATTGTCAACAGGAGTAAAGTTTCCGTACACTTTTGGCCAGGGGACCAAG	422
QY	305	TGGAAATCAACGA	318
Db	423	TGGAGATCAACGA	436
RESULT 10			
CD702614			
LOCUS	CD702614	472 bp	mRNA linear EST 25-JUN-2003
DEFINITION	EST19139 human nasopharynx Homo sapiens cDNA, mRNA sequence.		
ACCESSION	CD702614		
VERSION	CD702614.1	GI:32233244	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 472) Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.		
JOURNAL	Transcriptional Gene Expression Profile of Human Nasopharynx		
COMMENT	Unpublished (2003) Contact: Yixin Zeng Cancer Center Sun Yat-sen University 651 Dongfeng Road East, Guangzhou 510060, China Tel: 86-1380-9770-743 Fax: 86-20-8775-4506 Email: yxzeng@gzsums.edu.cn. Location/Qualifiers		
FEATURES			
source	1..472 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /tissue_type="normal nasopharynx" /clone_lib="human nasopharynx" /note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"		
ORIGIN			
Query Match	88.6%;	Score 281.8;	DB 6; Length 472;
Best Local Similarity	93.1%;	Pred. No. 1.2e-78;	
Matches	295;	Conservative 0;	Mismatches 22; Indels 0; Gaps 0;
QY	2	AGCTCAGCAGCTCCTCATCTTCCGTCGTGATCTGTGAGAGACAGATCAACCATACTT	61
Db	125	AGATACCCAGTCTCATCTTCCGTCGTGATCTGTGAGAGACAGCTCAACCATACTT	184
QY	62	GTCGGGCGAGTCAGGGATTATAGCATTTGGTTGCTCGTATCAGACAGAAACAGGGAAG	121
Db	185	GTCGGGCGAGTCAGGGCTATTAGCACTGGTTAGCCTGTGATCAGAGAAACAGGGAAG	244
QY	122	CCCCTAAACTCTGATCTATTCTGCATCCAGTTTGCAAAAGTGGGTCCTCCGTCAAGTTCA	181
Db	245	CCCCTAACCTCTGATCTATTCTGCATCCAGTTTGCAAAAGTGGGTCCTCCATCAAGTTCA	304
QY	182	GCGGAGTGGATCTGGGACAGATTTCAAGTTCACATCAGACGCTGACGCTGAAGATT	241
Db	305	GCGGAGTGGATCTGGGACAGATTTCAAGTTCACATCAGACGCTGACGCTGAAGATT	364
QY	242	CTGCAACTTACTATTGTCAACAGGCTAAACAGTTTCCCGTACACTTTTGCCAGGGAGCA	301
Db	365	TTGCAACTTACTATTGTGTCAACAGGCTAAACAGTTTCCCTCTCACTTCCGCGAGGAGCA	424
QY	302	AGGTGAAATCAACGA	318

Db	425	AGGTGGAGATCAAAACGA	441	
RESULT 11				
LOCUS	CD696718	497 bp	mRNA	linear
DEFINITION	EST113241	human nasopharynx Homo sapiens cDNA, mRNA sequence.		EST 25-JUN-2003
ACCESSION	CD696718			
VERSION	CD696718.1	GI:32223477		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 497)			
	Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.			
TITLE	Transcriptional Gene Expression Profile of Human Nasopharynx			
JOURNAL	Unpublished (2003)			
COMMENT	Contact: Yixin Zeng Cancer Center Sun Yat-sen University 651 Dongfeng Road East, Guangzhou 510060, China Tel: 86-1580-9770-743 Fax: 86-20-8775-4506 Email: yxzeng@gzsums.edu.cn			
FEATURES	Location/Qualifiers			
source	1..497 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /tissue_type="normal nasopharynx" /clone_lib="human nasopharynx" /note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"			
ORIGIN				
Query Match	88.1%;	Score 280.2;	DB 6;	Length 497;
Best Local Similarity	92.7%;	Pred. No. 4.1e-78;		
Matches	294;	Conservative	0;	Mismatches 23; Indels 0; Gaps 0;
QY	2	AGCTCAGCCAGTCTTCACATCTTCGTGTGATCTGTAGAGACAGAGTCAACCTAACTT	61	
Db	120	AGATGATCCCAAGTCTTCACATCTTCGTGTGATCTGTAGAGAGACAGATCACTCACTT	179	
QY	62	GTCGGGGCAGTCAAGGATTTAGCAGTTGAGCTGGTATCAGCAGAAACAGAGGAAG	121	
Db	180	GTCGGGGCAGTCAAGGATTTAGCAGTTGAGCTGGTATCAGCAGAAACAGAGGAAG	239	
QY	122	CCCCCAAACTCTGATCTATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG	181	
Db	240	CCCCCAAACTCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG	299	
QY	182	GCGGAGTGTGATCTGGGACAGATTTCACTCTCACATCAGCAGCCTTGACGCTTGAAGATT	241	
Db	300	GCGGAGTGTGATCTGGGACAGATTTCACTCTCACATCAGCAGCCTTGACGCTTGAAGATT	359	
QY	242	CTGCAACTTACTATGTGCAACAGGCTAACATTTCCGTAACCTTTGGCCAGGGGACCA	301	
Db	360	TTGCAACTTACTATGTGCAACAGGCTAACATTTCCGTAACCTTTGGCCGCTGAGACCA	419	
QY	302	AGGTGAATCAAAACA	318	
Db	420	AAATGATATCAAAACA	436	
RESULT 12				
LOCUS	BF129120	912 bp	mRNA	linear
DEFINITION	60181158071 NIH_MGC_48	Homo sapiens cDNA clone IMAGE:4054530 5',		
ACCESSION	BF129120			
VERSION	BF129120.1	GI:10968160		

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 912)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
AUTHORS Contact: Robert Strausberg, Ph.D.
TITLE Email: cgapbs-remail.nih.gov
COMMENT Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LNLN)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: LNCM894 row: p column: 19
High quality sequence stop: 695.
Location/Qualifiers
1. .912
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4054530"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pORF7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 87.6%; Score 278.6; DB 2; Length 912;
Best Local Similarity 92.4%; Pred. No. 1.6e-77;
Matches 293; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 2 AGCTCAGCAGTCTCCATCTCCGCTGTCATCTGTAGAGACAGAGTCCACCAATCTT 61
DB 72 AGATGACCCAGCTCCATCTCCGCTGTCATCTGTAGAGACAGAGTCCACCAATCTT 131
QY 62 GTCCGGCGAGTCAGAGGATTTAGCAGTTGGTTAGCCTGTATCAGCAGAAACCAAGGAAAG 121
DB 132 GTCCGGCGAGTCAGAGGATTTAGCAGTTGGTTAGCCTGTATCAGCAGAAACCAAGGAAAG 191
QY 122 CCCCTAACTCTGATCTATCTGATCAGTTGGCAAGTGGGGTCCCTCAAGTTCA 181
DB 192 CCCCTAACTCTGATCTATCTGATCAGTTGGCAAGTGGGGTCCCTCAAGTTCA 251
QY 182 GCGGAGTGGATCTGGGACAGATTTCATCTCAGATCAGAGAGCTGAGAGCTGAAGTT 241
DB 252 GCGGAGTGGATCTGGGACAGATTTCATCTCAGATCAGAGAGCTGAGAGCTGAAGTT 311
QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCGCTACACTTTTGGCCAGGGAGCA 301
DB 312 TTGCAACTTACTATTGTCTACAGACTAACAGTTTCCCTCACTTTGGCCCTGGAGCA 371
QY 302 AGGTGAAATCAACGA 318
DB 372 AAGTGATATCAACGA 388

RESULT 13
BG341803 894 bp mRNA linear EST 27-FEB-2001
LOCUS BG341803
DEFINITION 602463535P1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576136 5',

ACCESSION mRNA sequence.
VERSION BG341803
KEYWORDS BG341803.1 GI:13148241
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 894)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
AUTHORS Contact: Robert Strausberg, Ph.D.
TITLE Email: cgapbs-remail.nih.gov
COMMENT Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: LNCM1288 row: f column: 09
High quality sequence stop: 636.
Location/Qualifiers
1. .894
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4576136"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pORF7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 86.9%; Score 276.2; DB 4; Length 894;
Best Local Similarity 94.0%; Pred. No. 9.1e-77;
Matches 298; Conservative 0; Mismatches 18; Indels 1; Gaps 1;
QY 2 AGCTCAGCAGTCTCCATCTCCGCTGTCATCTGTAGAGACAGAGTCCACCAATCTT 61
DB 86 AGATGACCCAGTCTCCATCTCCGCTGTCATCTGTAGAGACAGAGTCCACCAATCTT 145
QY 62 GTCCGGCGAGTCAGAGGATTTAGCAGTTGGTTAGCCTGTATCAGCAGAAACCAAGGAAAG 121
DB 146 GTCCGGCGAGTCAGAGGATTTAGCAGTTGGTTAGCCTGTATCAGCAGAAACCAAGGAAAG 204
QY 122 CCCCTAACTCTGATCTATCTGATCAGTTGGCAAGTGGGGTCCCTCAAGTTCA 181
DB 205 CCCCTAACTCTGATCTATCTGATCAGTTGGCAAGTGGGGTCCCTCAAGTTCA 264
QY 182 GCGGAGTGGATCTGGGACAGATTTCATCTCAGATCAGAGAGCTGAGAGCTGAAGTT 241
DB 265 GCGGAGTGGATCTGGGACAGATTTCATCTCAGATCAGAGAGCTGAGAGCTGAAGTT 324
QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCGCTACACTTTTGGCCAGGGAGCA 301
DB 325 TTGCAACTTACTATTGTCTACAGACTAACAGTTTCCCTCACTTTGGCCCTGGAGCA 384
QY 302 AGGTGAAATCAACGA 318
DB 385 AAGTGATATCAACGA 401

RESULT 14

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CD706288      CD706288      561 bp      mRNA      linear      EST 25-JUN-2003
LOCUS          EST22815 human nasopharynx Homo sapiens cDNA, mRNA sequence.
DEFINITION     CD706288
ACCESSION     CD706288
VERSION       CD706288.1 GI:32236918
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 561)
AUTHORS        Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
                Zeng, Y.-X.
TITLE          Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL        Unpublished (2003)
COMMENT        Contact: Yixin Zeng
                Cancer Center
                Sun Yat-sen University
                651 Dongfeng Road East, Guangzhou 510060, China
                Tel.: 86-1380-9770-743
                Fax: 86-20-8775-4506
                Email: yxzeng@gzsums.edu.cn.
                Location/Qualifiers
                1..561
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /tissue_type="normal nasopharynx"
                /clone_lib="human nasopharynx"
                /note="ESTs generated from a normal nasopharynx cDNA
                library from southern Chinese"

ORIGIN
Query Match      86.6%; Score 275.4; DB 6; Length 561;
Best Local Similarity 91.8%; Pred. No. 1.4e-76;
Matches 291; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY      2 AGCTCAGCAGCTTCATCTTCCTCGTGTGATCTGTGAGAGACAGAGTCACCATTAATT 61
        |||
        |||
        |||
DB      117 AGATGACCCAGTCTCCATCTTCCTCGTGTGATCTGTGAGAGACAGAGTCACCATTAATT 176
        |||
        |||
        |||
QY      62 GTGGGGGAGTCAAGGATTAAGAGTGGTGAAGCTGATCAGAGAAACAGGGAAG 121
        |||
        |||
        |||
DB      177 GTGGGGGAGTCAAGGATTAAGAGTGGTGAAGCTGATCAGAGAAACAGGGAAG 236
        |||
        |||
        |||
QY      122 CCCCTAAATCTCTATCTATCTGCATCCAGTTGGCAAGTGGGTCCTCCGTCAGATTCA 181
        |||
        |||
        |||
DB      237 CCCCTAAATCTCTATCTATCTGCATCCAGTTGGCAAGTGGGTCCTCCGTCAGATTCA 296
        |||
        |||
        |||
QY      182 GCGGCAAGTGAATCGGAGACAGATTTCAGTCTCACCATCAGACGCTGCAAGCTTGAATT 241
        |||
        |||
        |||
DB      297 GCGGCAAGTGAATCGGAGACAGATTTCAGTCTCACCATCAGACGCTGCAAGCTTGAATT 356
        |||
        |||
        |||
QY      242 CTGCACTTACTATTGTCAAGGCTACAGTTTCCGTCAGCTTTTGGCCAGGGAACA 301
        |||
        |||
        |||
DB      357 TTGCACTTACTATTGTGAGAGACTTAACAGTTTCCGTCAGCAATTGGCCAGGGAACA 416
        |||
        |||
        |||
QY      302 AGGTGAATCAACGA 318
        |||
        |||
        |||
DB      417 AGGTGAATCAACGA 433
        |||
        |||
        |||

RESULT 15
BG686018      851 bp      mRNA      linear      EST 01-MAY-2001
LOCUS          602638582F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4766157 5',
DEFINITION     mRNA sequence.
ACCESSION     BG686018
VERSION       BG686018.1 GI:13917415
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE      1 (bases 1 to 851)
AUTHORS        NIH-MGC http://mgi.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: cgabs-remail.nih.gov
                Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
                cDNA Library Preparation: Ling Hong/Rubin Laboratory
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LNL at:
                http://image.lnl.gov
                Plate: LNCM1626 row: c column: 22
                High quality sequence stop: 851.
                Location/Qualifiers
                1..851
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:4766157"
                /tissue_type="primary B-cells from tonsils (cell line)"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_48"
                /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                Site_2: EcoRI; cDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCAAGAG(G). Size-selected >500bp
                for average insert size 1.8kb. Library constructed by Ling
                Hong in the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH_MGC library."

ORIGIN
Query Match      86.4%; Score 274.6; DB 4; Length 851;
Best Local Similarity 93.7%; Pred. No. 2.9e-76;
Matches 297; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY      2 AGCTCAGCAGCTTCATCTTCCTCGTGTGATCTGTGAGAGACAGAGTCACCATTAATT 61
        |||
        |||
        |||
DB      81 AGATGACCCAGTCTCCATCTTCCTCGTGTGATCTGTGAGAGACAGAGTCACCATTAATT 140
        |||
        |||
        |||
QY      62 GTGGGGGAGTCAAGGATTAAGAGTGGTGAAGCTGATCAGAGAAACAGGGAAG 121
        |||
        |||
        |||
DB      141 GTGGGGGAGTCAAGGATTAAGAGTGGTGAAGCTGATCAGAGAAACAGGGAAG 199
        |||
        |||
        |||
QY      122 CCCCTAAATCTCTATCTATCTGCATCCAGTTGGCAAGTGGGTCCTCCGTCAGATTCA 181
        |||
        |||
        |||
DB      200 CCCCTAAATCTCTATCTATCTGCATCCAGTTGGCAAGTGGGTCCTCCGTCAGATTCA 259
        |||
        |||
        |||
QY      182 GCGGCAAGTGAATCGGAGACAGATTTCAGTCTCACCATCAGACGCTGCAAGCTTGAATT 241
        |||
        |||
        |||
DB      260 GCGGCAAGTGAATCGGAGACAGATTTCAGTCTCACCATCAGACGCTGCAAGCTTGAATT 319
        |||
        |||
        |||
QY      242 CTGCACTTACTATTGTCAAGGCTACAGTTTCCGTCAGCTTTTGGCCAGGGAACA 301
        |||
        |||
        |||
DB      320 TTGCACTTACTATTGTCAAGGCTACAGTTTCCGTCAGCTTTTGGCCAGGGAACA 379
        |||
        |||
        |||
QY      302 AGGTGAATCAACGA 318
        |||
        |||
        |||
DB      380 AGGTGAATCAACGA 396
        |||
        |||
        |||

Search completed: July 27, 2005, 12:32:16
Job time : 1962.75 secs

```


PF 27-DEC-2001; 2001WO-SE002908.
XX
XX 29-DEC-2000; 2000SE-00004892.
XX
XX (PFAA) PHARMACIA DIAGNOSTICS AB.
XX
XX Flicker S, Steinberger P, Kraft D, Valenta R;
XX WPI; 2002-583604/62.
XX P-PSDB; ABG30450.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
XX Disclosure; Page 35-36; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have anti-allergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to Phl p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific Fabs of the invention may be useful for environmental
CC allergen detection and for standardization of allergen extracts. The Fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific Fabs of the invention are useful for
CC inner alla, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to Phl p 2. The present sequence represents the DNA
CC encoding the human IgG Fab, clone 100 light chain protein of the
XX invention
XX
XX Sequence 318 BP; 80 A; 81 C; 81 G; 76 T; 0 U; 0 Other:
SQ
Query Match 100.0%; Score 318; DB 6; Length 318;
Best Local Similarity 100.0%; Pred. No. 9.6e-93;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCTCAGCGAGTCCATCTTCGTCGATCTGTAGAGACAGAGTCAACCTACT 60
DB 1 GAGCTCAGCGAGTCCATCTTCGTCGATCTGTAGAGACAGAGTCAACCTACT 60
QY 61 TGTGCGGAGTCAAGGATATTAGAGAGTTGAGCTGTATCAGAGAAACAGGAAA 120
DB 61 TGTGCGGAGTCAAGGATATTAGAGAGTTGAGCTGTATCAGAGAAACAGGAAA 120
QY 121 GCCCTTAACTCTGATCTATTTCGATCCAGTTTGCAAGTGGGCTCCGTCAGAGTTTC 180
DB 121 GCCCTTAACTCTGATCTATTTCGATCCAGTTTGCAAGTGGGCTCCGTCAGAGTTTC 180
QY 181 AGCGGCGATGATCTGGGAGAGATTTCAGTCCACACACAGCTTCGACCTGAAGAT 240
DB 181 AGCGGCGATGATCTGGGAGAGATTTCAGTCCACACACAGCTTCGACCTGAAGAT 240
QY 241 TCTGCAACTTACTATTGTCACACAGGCTTACAGTTTCCGTCACCTTTGGCAGGGAGCC 300
DB 241 TCTGCAACTTACTATTGTCACACAGGCTTACAGTTTCCGTCACCTTTGGCAGGGAGCC 300
QY 301 AAGGTGGAATCAACGA 318
DB 301 AAGGTGGAATCAACGA 318
RESULT 2
AAS99473
ID AAS99473 standard; cDNA; 974 BP.
XX AAS99473;
AC
XX
DT 12-MAR-2002 (first entry)

XX
XX Anti-human AILIM monoclonal antibody clone Jmab-136, light chain cDNA.
DE
XX
XX Human; antirheumatic; antiarthritis; antidiabetic; antipsoriatic;
KW antiallergic; antitumor; neuroprotective; antihypertoid; vasotrophic;
KW immunosuppressive; dermatological; antinflammatory; hepatotropic;
KW activation inducible lymphocyte immunomodulatory molecule; AILIM;
KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
KW allergic contact-type dermatitis; chronic inflammatory dermatosis;
KW systemic lupus erythematosus; autoimmune disorder; inflammation; SS;
KW graft versus host reaction; immune rejection; intestinal immunity;
KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
OS
XX Homo sapiens.
XX
XX WO200187981-A2.
XX
XX 22-NOV-2001.
XX
XX 15-MAY-2001; 2001WO-JP004035.
XX
XX 18-MAY-2000; 2000JP-00147116.
XX 30-MAR-2001; 2001JP-00099508.
XX
XX (NISE) JAPAN TOBACCO INC.
XX
XX Tsuji T, Tezuka K, Hori N;
XX WPI; 2002-075313/10.
XX P-PSDB; AAU74297.
XX
XX New human monoclonal antibody that binds to activation inducible
PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid
PT arthritis, multiple sclerosis and inflammation.
XX
XX Claim 45; Page 267-270; 300pp; English.
XX
XX The invention relates to a novel human antibody (I), preferably a human
CC monoclonal antibody which binds to an activation inducible lymphocyte
CC immunomodulatory molecule (AILIM). (I) is useful for modulating signal
CC transduction into a cell mediated by AILIM, for modulating proliferation
CC of AILIM-expressing cells, for modulating production of a cytokine from
CC AILIM-expressing cells, and for inducing antibody-dependent cytotoxicity
CC against AILIM-expressing cells and/or immune cytotoxicity or apoptosis of
CC AILIM-expressing cells. (I) is useful for treating, preventing or
CC prophylaxis of delayed type allergy. (I) is useful for treating and
CC preventing various diseases associated with AILIM-mediated costimulatory
CC transduction, and for inhibiting the onset and/or advancement of the
CC diseases. (I) is useful for suppression, prevention and/or treatment of
CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,
CC allergic contact-type dermatitis, chronic inflammatory dermatosis,
CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,
CC psoriasis, autoimmune or allergic disorders, inflammation, graft versus
CC host reaction, graft versus host disease, immune rejection, disorders
CC caused by abnormal intestinal immunity, specifically inflammatory
CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,
CC nephritis, vasculitis, and pancreatitis. (I) induces no serious
CC immunorejection due to antigenicity to human, i.e., human anti-mouse
CC antigenicity (HAMA) in a host. AAS99444-AAS99477 represent anti-human
CC AILIM monoclonal antibody coding sequences and PCR primers of the
CC invention
XX
SQ Sequence 974 BP; 246 A; 282 C; 232 G; 214 T; 0 U; 0 Other;
Query Match 91.6%; Score 291.4; DB 6; Length 974;
Best Local Similarity 95.0%; Pred. No. 6.4e-84;
Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 2 AGCTCAGCAGTCCATCTTCGTCGATCTGTAGAGACAGAGTCAACCTACT 61
DB 112 AGATGACCCAGTCTTCATCTTCGTCGATCTGTAGAGACAGAGTCAACCTACT 171

QY 62 GTCCGGCGAGTCAGGGTATTAGCACTTGTTAGCTGGTATCAGCAAGAAACAGGGAAG 121
Db GTCCGGCGAGTCAGGGTATTAGCACTTGTTAGCTGGTATCAGCAAGAAACAGGGAAG 231
QY 122 CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGTGGGGTCCCGTCAAGTTCA 181
Db CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGTGGGGTCCCGTCAAGTTCA 291
QY 182 GCGGAGTGTATCTGGGACAGATTTCACTTCACCATCAGCAGCTGCAGCCTGAAGATT 241
Db GCGGAGTGTATCTGGGACAGATTTCACTTCACCATCAGCAGCTGCAGCCTGAAGATT 351
QY 242 CTGCACTTACTATTGTCAACAGGCTAACAGTTTCCGTAACCTTTTGCCAGGGGACCA 301
Db TTGCACTTACTATTGTCAACAGGCTAACAGTTTCCGTAACCTTTTGCCAGGGGACCA 411
QY 302 AGGTGAAATCAACGA 318
Db AGGTGAAATCAACGA 428

RESULT 3

AAAT73441

AAAT73441 standard; DNA, 388 BP.
AAAT73441;
03-DEC-1997 (first entry)

Human immunoglobulin light chain variable region partial transcript.

Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
transplant rejection; ss.

Homo sapiens.

MO9713852-A1.

17-APR-1997.

10-OCT-1996; 96WO-US016433.

10-OCT-1995; 95US-00544404.

(GENP-) GENPHARM INT INC.

Lonberg N, Kay RM;

WPI, 1997-235888/21.

Novel anti-CD4 antibody produced by transgenic mice - used in the
treatment of auto-immune disease etc.

Claim 44; Page 255; 396pp; English.

A novel composition has been developed which comprises an immunoglobulin
(Ig) having an affinity constant (Ka) of at least 2 multiply 100000000 M
-1 for binding to a predetermined human antigen. The present sequence
represents a human light chain variable region partial nucleotide
sequence, 10C5 kappa, which encodes an amino acid sequence from a claimed
immunoglobulin that specifically binds human CD4. The anti-CD4 antibodies
may be used in therapeutic and diagnostic applications, especially for
the treatment of human diseases. These antibodies reduce activity of CD4
cells and reduce undesirable autoimmune reactions, inflammatory response
and transplant rejection. Transgenic animals are capable of producing
heterologous antibodies of multiple isotypes by undergoing isotype
switching. These animals produce a first Ig type that is necessary for
antigen-stimulated B-cell maturation and can switch to encode and produce
one or more subsequent heterologous isotypes

Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 U; 0 Other;

Query Match 91.5%; Score 291; DB 2; Length 388;
Best Local Similarity 95.2%; Pred. No. 6e-84;
Matches 300; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2 AGCTCAACCACTTCCATCTCCGTCGTGATCTGTGAGACAGACATCACTT 61
Db AGAATGACCACTTCCATCTCCGTCGTGATCTGTGAGACAGACATCACTT 133
QY 62 GTCCGGCGAGTCAGGGTATTAGCACTTGTTAGCTGGTATCAGCAAGAAACAGGGAAG 121
Db GTCCGGCGAGTCAGGGTATTAGCACTTGTTAGCTGGTATCAGCAAGAAACAGGGAAG 193
QY 122 CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGTGGGGTCCCGTCAAGTTCA 181
Db CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGTGGGGTCCCGTCAAGTTCA 253
QY 182 GCGGAGTGTATCTGGGACAGATTTCACTTCACCATCAGCAGCTGCAGCCTGAAGATT 241
Db GCGGAGTGTATCTGGGACAGATTTCACTTCACCATCAGCAGCTGCAGCCTGAAGATT 313
QY 242 CTGCACTTACTATTGTCAACAGGCTAACAGTTTCCGTAACCTTTTGCCAGGGGACCA 301
Db TTGCACTTACTATTGTCAACAGGCTAACAGTTTCCGTAACCTTTTGCCAGGGGACCA 373
QY 302 AGGTGAAATCAAC 316
Db AGGTGAAATCAAC 388

RESULT 4

AAV39239

AAV39239 standard; DNA, 388 BP.
AAV39239;
18-DEC-1998 (first entry)

Functional kappa transcript isolated from transgenic cell line 10C5.

Transgenic animal; human heterologous antibody; transgene;

isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;

autoimmune reaction; inflammatory response; transplant rejection;

acid induced lung injury; acute adult respiratory distress syndrome;

ARDS; vasculitis; septic shock; allergic reaction; asthma;

cytic fibrosis; ss.

Synthetic.

Homo sapiens.

Mus sp.

MO9824884-A1.

11-JUN-1998.

01-DEC-1997; 97WO-US021803.

02-DEC-1996; 96US-00758417.

(GENP-) GENPHARM INT.

Lonberg N, Kay RM;

WPI, 1998-333306/29.

Hybridoma producing antibody specific for interleukin-8 - used to prevent
efflux of neutrophils from vasculature, and treat reperfusion injury.

Example 41; Page 304; 452pp; English.
AAV39232-41 represent functional transcripts of a human IgGkappa anti-CD4
antibody. The sequences are isolated from 5 different transgenic mouse
hybridoma cell lines. The specification describes transgenic non-human
animals, especially a mouse, which are capable of producing a human

CC heterologous antibodies of multiple isotypes by undergoing isotype
CC switching. The transgenic animals have human heavy and light chain
CC transgenes. The transgenes are capable of functionally rearranging a
CC heterologous diversity (D) gene in a variable-diversity-junction (V-D-J)
CC recombination. The transgenes include a heavy chain transgene comprising
CC at least one V, D and J gene segment, and one constant region gene
CC segment. The immunoglobulin (Ig) light chain transgene comprises at least
CC one V and J gene segment and one constant region gene segment. The gene
CC segments are heterologous to the transgenic animal. The antibody can be
CC used to prevent efflux of neutrophils from vasculature. It can also be
CC used to treat reperfusion injury. CD4 binding antibodies are used to
CC reduce undesirable autoimmune reactions, inflammatory responses and
CC rejection of transplanted organs. The anti-IL-8 antibodies can reduce
CC tissue damage and prolong survival in animal models of acute adult
CC respiratory distress syndrome (ARDS) and acid induced lung injury. The
CC anti-IL-8 antibodies can also be used for the treatment of vasculitis,
CC septic shock, allergic reactions (e.g. asthma) and cystic fibrosis
XX
SQ Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 U; 0 Other;
Query Match 91.5%; Score 291; DB 2; Length 388;
Best Local Similarity 95.2%; Pred. No. 6e-84;
Matches 300; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 2 AGCTCAGGCAAGTCCCATCTCCGTCGTGATCTGTAGAGACAGAGTCAACCTAATT 61
DB 74 AGATGACCCAGTCTCCATCTTCGTCGTGATCTGTAGAGACAGAGTCAACCTAATT 133
QY 62 GTCGGGCGAGTCAGGAGTATTAGCAGTTGGTTCGCTGATCAGCAGAAACAGGGAAG 121
DB 134 GTCGGGCGAGTCAGGAGTATTAGCAGTTGGTTCGCTGATCAGCAGAAACAGGGAAG 193
QY 122 CCCCTAAATCTCTGATCTATTTCGCATCCAGTTTGCAAAAGTGGGGTCCCGTCAAGTTCA 181
DB 194 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCGTCAAGTTCA 253
QY 182 GCGGCAAGTGCATCTGGGACAGATTTCAGTCACATCAGAGCCTGAGAGCTTAAAGTT 241
DB 254 GCGGCAAGTGCATCTGGGACAGATTTCAGTCACATCAGAGCCTGAGAGCTTAAAGTT 313
QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCGTAACATTTTGGCCAGGGGACCA 301
DB 314 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCGTAACATTTTGGCCAGGGGACCA 373
QY 302 AGGTGAATCAAC 316
DB 374 AGCTGAGATCAAC 388
RESULT 5
AAZ21993 standard; DNA; 388 BP.
ID AAZ21993
AC AAZ21993;
XX
DT 24-NOV-1999 (first entry)
XX
DE Partial nucleotide sequence for a functional transcript 10C5-kappa.
XX
KW Transgenic animal; heterologous antibody; hybridoma; B cell;
KW transgenic mouse; human heavy chain transgene; digoxin; PCR primer;
KW human light chain transgene; immortalized cell; immunoglobulin;
KW Shinga-like toxin; autoimmune disease; cancer; infectious disease;
KW transplant rejection; blood disorder; coagulation disorder; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX MO9945962-A1.
XX
XX 16-SEP-1999.
PD
XX
PF 12-MAR-1999; 99WO-US005535.

XX
PR 13-MAR-1998; 98US-00042353.
XX
PA (GENP-) GENPHARM INT INC.
XX
PI Lonberg N, Fishwild DM, Ball WJ;
XX WPI; 1999-551219/46.
DR
XX
PT Novel transgenic non-human animals used to produce heterologous
PT antibodies.
PS Example 41; Page 305; 484pp; English.
XX
XX The specification describes transgenic animals that are capable of
XX producing a heterologous antibody. The antibodies are isolated from a
XX hybridoma, comprising B cells, that is obtained from a transgenic mouse
XX having a genome comprising a human heavy chain transgene and a human
XX light chain transgene. The B cells are fused to immortalized cells
XX suitable for generating a hybridoma, which produces a detectable amount
XX of an immunoglobulin that specifically binds digoxin or Shinga-like
XX toxin. B cells from transgenic animals can be used to generate hybridomas
XX expressing monoclonal high affinity human sequence antibodies. Antibodies
XX produced from the transgenic animals of the invention can be used to
XX treat human diseases, e.g. autoimmune diseases, cancer, infectious
XX disease, transplant rejection, blood disorders such as coagulation
XX disorders and other diseases. The present sequence represents a partial
XX nucleotide sequence for a functional transcript used in the course of the
XX invention
SQ Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 U; 0 Other;
Query Match 91.5%; Score 291; DB 2; Length 388;
Best Local Similarity 95.2%; Pred. No. 6e-84;
Matches 300; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 2 AGCTCAGGCAAGTCCCATCTCCGTCGTGATCTGTAGAGACAGAGTCAACCTAATT 61
DB 74 AGATGACCCAGTCTCCATCTTCGTCGTGATCTGTAGAGACAGAGTCAACCTAATT 133
QY 62 GTCGGGCGAGTCAGGAGTATTAGCAGTTGGTTCGCTGATCAGCAGAAACAGGGAAG 121
DB 134 GTCGGGCGAGTCAGGAGTATTAGCAGTTGGTTCGCTGATCAGCAGAAACAGGGAAG 193
QY 122 CCCCTAAATCTCTGATCTATTTCGCATCCAGTTTGCAAAAGTGGGGTCCCGTCAAGTTCA 181
DB 194 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCGTCAAGTTCA 253
QY 182 GCGGCAAGTGCATCTGGGACAGATTTCAGTCACATCAGAGCCTGAGAGCTTAAAGTT 241
DB 254 GCGGCAAGTGCATCTGGGACAGATTTCAGTCACATCAGAGCCTGAGAGCTTAAAGTT 313
QY 242 CTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCGTAACATTTTGGCCAGGGGACCA 301
DB 314 TTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCGTAACATTTTGGCCAGGGGACCA 373
QY 302 AGGTGAATCAAC 316
DB 374 AGCTGAGATCAAC 388
RESULT 6
ADM47072 standard; DNA; 711 BP.
ID ADM47072
AC ADM47072;
XX
XX 03-JUN-2004 (first entry)
DT
XX
DE Mouse anti-human G-CSF antibody light chain gene.
XX
XX methylotroph yeast; mammalian sugar chain; OCH1; alpha-1;
KW 6-mannosyl transferase; alpha-1; 2-mannosidase;
KW

KW orotidin-5'-phosphate decarboxylase; URA3;
 KW phosphoribosyl-5'-phosphate decarboxylase; ADE1;
 KW imidazole-glycerol-phosphate dehydratase; HIS3;
 KW 3-isopropyl malate dehydrogenase; LEU2; proteinase A; proteinase B; PRB1;
 KW PEP4; YPS1; KTR1; MN9; AOX; GAPDH; mannose 6-phosphate transferase;
 KW glyceraldehyde 3-phosphate dehydrogenase; mannose 6-phosphate transferase; ds; gene.
 XX Mus sp.
 OS WO2003091431-A1.
 PN 06-NOV-2003.
 PD 28-APR-2003; 2003WO-JP005464.
 PF 26-APR-2002; 2002JP-00127677.
 PR (KIRI) KIRIN BEER KK.
 PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX Kobayashi K, Kitagawa Y, Komeda T, Kawashima N, Jigami Y;
 PI Chiba Y;
 XX WPI; 2003-854401/79.
 DR Producing methylotrophic yeast that expresses mammalian sugar chains by
 PT disrupting the OCH1 gene and inserting an alpha-1,2-mannosidase gene.
 XX Example 28; SEQ ID NO 91; 247pp; Japanese.
 PS The invention relates to the production of a methylotrophic yeast that
 CC produces mammalian sugar chains, comprising disrupting the OCH1 gene in
 CC the yeast that encodes for alpha-1,6-mannosyl transferase and inserting
 CC and expressing the alpha-1,2-mannosidase gene. The specification also
 CC includes DNA sequences encoding: (a) orotidin-5'-phosphate decarboxylase
 CC (URA3); (b) phosphoribosyl-5'-phosphate decarboxylase (HIS3); (d) 3-
 CC isopropyl malate dehydrogenase (LEU2); (e) alpha-1,6-mannosyl transferase
 CC (OCH1); (f) proteinase A (PEP4); (g) proteinase B (PRB1); and (h)
 CC aspartic protease (YPS1), mannose 6-phosphate transferase (KTR1 or MN9), alcohol
 CC oxidase (AOX) and glyceraldehyde 3-phosphate dehydrogenase (GAPDH) gene
 CC sequences. The yeast is used for the production of human and mammalian
 CC high mannose glycoproteins with high yield and purity. The method is also
 CC useful for producing hybrid or complex sugar chains containing mammalian
 CC type chains. This sequence represents the gene encoding a mouse anti-
 CC human G-CSF antibody light chain used in the invention.
 XX Sequence 711 BP; 176 A; 203 C; 182 G; 150 T; 0 U; 0 Other;
 SQ Query Match 90.3%; Score 287.2; DB 11; Length 711;
 Best Local Similarity 94.3%; Pred. No. 1.3e-82;
 Matches 298; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 302 AGGTGAAATCAACG 317
 Db 374 AGGTGAAATCAACG 389
 RESULT 7
 ADP22215
 ID ADP22215 standard; cDNA; 321 BP.
 AC ADP22215;
 XX 09-SEP-2004 (first entry)
 DE Human anti-TNFA antibody heavy chain variable region cDNA SEQ ID NO:121.
 XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;
 KW anti-TNFA antibody; anabolic; antiarteriosclerotic; antiarthritic;
 KW antibacterial; antiinflammatory; antiproliferative; antitumour;
 KW eating disorder; immunomodulator; immunosuppressive; nephrotoxic;
 KW neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;
 KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KW prostate cancer; immuno-mediated inflammatory disease;
 KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KW septic shock; autoimmune disease; Crohn's disease; graft-host reaction;
 KW sexex shock; cachexia; anorexia; multiple sclerosis; gene; ss.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 XX FH 1.321
 FT CDS /tag= a
 FT /product= "human anti-TNFA antibody heavy chain variable
 FT region"
 FT
 XX MO204050683-A2.
 XX 17-JUN-2004.
 XX 02-DEC-2003; 2003WO-US038281.
 XX 02-DEC-2002; 2002US-0430729P.
 PA (ABGE-) ABGENIX INC.
 XX Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
 PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang MT, Lee R;
 PI Manchulenko K, Fegioni R, Senaldi G, Qiaojuan JS;
 XX WPI; 2004-480601/45.
 DR P-PSDB; ADP22216.
 XX New recombinant human monoclonal antibody that specifically binds to
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.
 XX Example 10; SEQ ID NO 121; 213pp; English.
 PS The present invention describes a human monoclonal antibody (I) that
 CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:
 CC (a) a heavy chain complementarily determining region 1 (CDR1) having the
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
 CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
 CC (M1) the level of TNFA in a patient sample, comprising contacting with
 CC (I), and detecting the level of binding between the antibody and TNFA in
 CC the sample; (2) a composition comprising the antibody or its functional
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFA induced

CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNF α induced apoptosis by administering the human monoclonal antibody of
 CC (1). (1) has anabolic, antiarteriosclerotic, antiarthritic,
 CC antibacterial, antiinflammatory, antiproliferative, antineoplastic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotoxic,
 CC neuroprotective, vasotropic and antiproliferative activities, and can be used
 CC as a TNF α antagonist. The antibody (1) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease, such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence encodes a human anti-TNF α
 CC antibody heavy chain variable region, which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 321 BP; 81 A; 82 C; 83 G; 75 T; 0 U; 0 Other;
 Query Match 90.2%; Score 286.8; DB 12; Length 321;
 Best Local Similarity 94.6%; Pred. No. 1.3e-82;
 Matches 297; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
 QY 2 AGCTCAGCGAGTCCATCTCCGTCGATCTGTAGAGACAGAGTCACTTAATT 61
 Db 8 AGATGACCCAGTCTCCATCTCCGTCGATCTGTAGAGACAGAGTCACTTAATT 67
 QY 62 GTCCGGGAGTCAAGGATTAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 121
 Db 68 GTCCGGGAGTCAAGGATTAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 127
 QY 122 CCCCTAACTCTGATCTATTTCTGATCAGTTGGCAAGTGGGGTCCCGTAAAGTTCA 181
 Db 128 CCCCTAACTCTGATCTATCTGATCAGTTGGCAAGTGGGGTCCCGTAAAGTTCA 187
 QY 182 GCGGAGTCAAGTCAAGGATTAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 241
 Db 188 GCGGAGTCAAGTCAAGGATTAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 247
 QY 242 CTGCAACTTATTTGTAACAGGCTTAACAGTTTCCCTGACACTTTGGCCAGGGAGCA 301
 Db 248 TTGCAAGTATATTTGTAACAGGCTTAACAGTTTCCCTGACACTTTGGCCAGGGAGCA 307
 QY 302 AGGTGAAATCAAA 315
 Db 308 AGGTGAAATCAAA 321
 RESULT 8
 AB22309 standard; DNA; 632 BP.
 XX ID AB22309 standard; DNA; 632 BP.
 AC AB22309;
 XX
 DT 20-MAR-2003 (first entry)
 XX
 DE S. pneumoniae PPS-3 antibody 3H1 light chain DNA sequence SEQ ID NO:4.
 XX
 KW Antipneumococcal; antibody; monoclonal antibody; infection; PPS-3;
 KW Streptococcus pneumoniae; capsular polysaccharide; gene; ds.
 XX
 OS Streptococcus pneumoniae.
 OS Synthetic.
 XX
 PN WO200292017-A2.
 XX
 PD 21-NOV-2002.
 XX
 PF 16-MAY-2002; 2002WO-US018363.
 XX
 PR 16-MAY-2001; 2001US-0291492P.
 XX

PA (PIRO/) PIROSKY L.
 PA (ZHON/) ZHONG Z.
 PA (CHAN/) CHANG Q.
 PI Pirofsky L, Zhong Z, Chang Q;
 DR WPI; 2003-120598/11.
 XX
 XX New antibody or its antigen-binding fragment that specifically binds the
 PT capsular polysaccharide of Streptococcus pneumoniae serotype 3, useful
 PT for treating, inhibiting or preventing S. pneumoniae infections.
 XX
 PS Claim 13; Fig 6B; 56pp; English.
 XX
 XX The present invention describes an antibody or its antigen-binding
 CC fragment (1) that specifically binds the capsular polysaccharide of
 CC Streptococcus pneumoniae serotype 3 (S. pneumoniae PPS-3), comprising a
 CC heavy and/or light chain amino acid sequence. (1) has antibacterial
 CC activity and can be used in vaccines. The anti-S. pneumoniae PPS-3
 CC antibody or its antigen-binding fragment is useful for treating,
 CC inhibiting or preventing S. pneumoniae infections or conditions or
 CC disorders caused by the infection. Methods from the present invention can
 CC be used for preventing or reducing the severity of conditions or
 CC disorders caused by S. pneumoniae serotype 3 infection, or for increasing
 CC the resistance of a subject to infection by S. pneumoniae serotype 3. The
 CC present sequence represents a S. pneumoniae PPS-3 antibody light chain
 CC DNA sequence from the present invention
 XX
 SQ Sequence 632 BP; 165 A; 175 C; 159 G; 133 T; 0 U; 0 Other;
 Query Match 90.1%; Score 286.4; DB 8; Length 632;
 Best Local Similarity 94.9%; Pred. No. 2.3e-82;
 Matches 296; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
 QY 7 ACGAGTCTCATCTTCCGTCGATCTGTAGAGACAGAGTCACTTAATTGTCGG 66
 Db 12 ACGAGTCTCATCTTCCGTCGATCTGTAGAGACAGAGTCACTTAATTGTCGG 71
 QY 67 GCGAGTCAAGGATTAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 126
 Db 72 GCGAGTCAAGGATTAAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 131
 QY 127 AAATCTCTGATCTATTTGTAACAGGCTTAACAGTTTCCCTGACACTTTGGCCAGGGAGCA 186
 Db 132 AAATCTCTGATCTATTTGTAACAGGCTTAACAGTTTCCCTGACACTTTGGCCAGGGAGCA 191
 QY 187 AGTGAATCTGGGACAGATTTCAAGTCAAGGCTTCCGTCGATCTGTAGAGACAGAGTCACTTAATTGTCGG 246
 Db 192 AGTGAATCTGGGACAGATTTCAAGTCAAGGCTTCCGTCGATCTGTAGAGACAGAGTCACTTAATTGTCGG 251
 QY 247 ACTTACTATTTGTAACAGGCTTAACAGTTTCCCTGACACTTTGGCCAGGGAGCAAGGTG 306
 Db 252 ACTTACTATTTGTAACAGGCTTAACAGTTTCCCTGACACTTTGGCCAGGGAGCAAGGTG 311
 QY 307 GAAATCAAAACA 318
 Db 312 GAAATCAAAACA 323
 RESULT 9
 AAH47735 standard; DNA; 321 BP.
 XX ID AAH47735 standard; DNA; 321 BP.
 AC AAH47735;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Nucleotide sequence of seq Id No. 78.
 XX
 KW Gene library; immunoglobulin; antibody library; human; ds.
 XX
 OS Homo sapiens.
 XX

PN WO200162907-A1.
XX
XX 30-AUG-2001.
XX
XX 22-FEB-2001; 2001WO-JP001298.
XX
XX 22-FEB-2000; 2000JP-00050543.
XX
XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
XX Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M,
PI Okuno Y, Shiraki K;
XX
XX WPI; 2001-565420/63.
XX
XX P-PSDB; AAG65571.
XX
XX Producing gene libraries and antibody libraries, involves selecting a
PT light chain that binds to a heavy chain product to produce a functional
PT formation, and producing a gene library of the light chain variable
PT regions.
XX
XX Examples; p 151; 181pp; Japanese.
XX
XX The invention relates to producing gene libraries, comprising
CC immunoglobulin light and heavy variable region. The method involves
CC selecting light chain that binds with the heavy chain product to produce
CC a functional conformation, producing a gene library comprising a
CC collection of these light chain variable genes, and combining with gene
CC library of heavy chain variable genes. The method is used for production
CC of gene and antibody libraries
XX
XX Sequence 321 BP; 80 A; 85 C; 80 G; 76 T; 0 U; 0 Other;
SQ
Query Match 89.7%; Score 285.2; DB 4; Length 321;
Best Local Similarity 94.3%; Pred. No. 4.3e-82;
Matches 296; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 2 AGCTACGCGAGTCTCCATCTTCCGTCGTCGATCTGTAGAGACAGAGTCAACATTAATT 61
DB 8 AGATGACCCAGTCTTCATCTTCCGTCGTCGATCTGTAGAGACAGAGTCAACATTAATT 67
QY 62 GTGCGGCGAGTCAAGGATTAAGACAGTTGTTAGCTGTATACAGAAACAGGGAAG 121
DB 68 GTGCGGCGAGTCAAGGATTAAGACAGTTGTTAGCTGTATACAGAAACAGGGAAG 127
QY 122 CCCCTAACTCTGATCTATTTCTGATCCAGTTTGCAAAAGTGGGTCCCGTCAAGTTCA 181
DB 128 CCCCTAACTCTGATCTATGCTGATCCAGTTTGCAAAAGTGGGTCCCGTCAAGTTCA 187
QY 182 GCGGAGTGAATCTGGGACAGATTTCACTCAGTCACATCAGAGCCTGAGCCTGAAGATT 241
DB 188 GCGGAGTGAATCTGGGACAGATTTCACTCAGTCACATCAGAGCCTGAGCCTGAAGATT 247
QY 242 CTGCAACTTACTATTTGTCACAGGCTAACAGTTTCCGTACACTTTTGGCCAGGGAGCA 301
DB 248 TTGCAACTTACTATTTGTCACAGGCTAACAGTTTCCGTACACTTTTGGCCAGGGAGCA 307
QY 302 AGGTGGAATCAAA 315
DB 308 AGGTGGAATCAAA 321
RESULT 10
ADHS6388
ID ADHS6388 standard; DNA; 401 BP.
XX
XX ADHS6388;
XX
XX 25-MAR-2004 (first entry)
XX
XX Variable region of the human 9F11 antibody k-chain DNA SEQ ID NO:2.
XX
XX human; immunoglobulin M; IgM; monoclonal antibody; HIV infection;

KW anti-HIV; HIV; human 9F11 antibody; gene; ds.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO2004003196-A1.
XX
XX 08-JAN-2004.
XX
XX 30-JUN-2003; 2003WO-JP008306.
XX
XX 01-JUL-2002; 2002JP-00227952.
XX
XX 18-MAR-2003; 2003JP-00074312.
XX
XX (OKAD/) OKADA H.
XX
XX (OKAD/) OKADA N.
XX
XX Okada H, Okada N;
XX
XX WPI; 2004-083055/08.
XX
XX Human IgM monoclonal antibody against activated human lymphocytes or HIV
PT infected cells for treatment of HIV.
XX
XX Claim 4; SEQ ID NO 2; 27pp; Japanese.
XX
XX The present invention describes a human immunoglobulin M (IgM) monoclonal
CC antibody (I) against activated human lymphocytes or HIV infected cells,
CC mediated by homologous complement. Also described: (1) an
CC immunocontrolling agent and HIV treatment containing the antibody; and
CC (2) cells PERM PB-8379 that produce the antibody. (I) has anti-HIV
CC activity, and can be used in the treatment of HIV. The present sequence
CC represents the variable region of the human 9F11 antibody k-chain
CC nucleotide sequence, which is used in the exemplification of the present
CC invention.
XX
XX Sequence 401 BP; 92 A; 110 C; 105 G; 94 T; 0 U; 0 Other;
SQ
Query Match 89.2%; Score 283.6; DB 12; Length 401;
Best Local Similarity 93.9%; Pred. No. 1.5e-81;
Matches 295; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 2 AGCTACGCGAGTCTCCATCTTCCGTCGTCGATCTGTAGAGACAGAGTCAACATTAATT 61
DB 8 AGATGACCCAGTCTTCATCTTCCGTCGTCGATCTGTAGAGACAGAGTCAACATTAATT 147
QY 62 GTGCGGCGAGTCAAGGATTAAGACAGTTGTTAGCTGTATACAGAAACAGGGAAG 121
DB 148 GTGCGGCGAGTCAAGGATTAAGACAGTTGTTAGCTGTATACAGAAACAGGGAAG 207
QY 122 CCCCTAACTCTGATCTATTTCTGATCCAGTTTGCAAAAGTGGGTCCCGTCAAGTTCA 181
DB 128 CCCCTAACTCTGATCTATGCTGATCCAGTTTGCAAAAGTGGGTCCCGTCAAGTTCA 267
QY 182 GCGGAGTGAATCTGGGACAGATTTCACTCAGTCACATCAGAGCCTGAGCCTGAAGATT 241
DB 208 GCGGAGTGAATCTGGGACAGATTTCACTCAGTCACATCAGAGCCTGAGCCTGAAGATT 327
QY 242 CTGCAACTTACTATTTGTCACAGGCTAACAGTTTCCGTACACTTTTGGCCAGGGAGCA 301
DB 248 TTGCAACTTACTATTTGTCACAGGCTAACAGTTTCCGTACACTTTTGGCCAGGGAGCA 387
QY 302 AGGTGGAATCAAA 315
DB 388 AGGTGGAATCAAA 401
RESULT 11
AAT73445
ID AAT73445 standard; DNA; 420 BP.
XX
XX AAT73445;
XX

DT 03-DEC-1997 (first entry)
XX
DE Human immunoglobulin light chain variable region partial transcript.
XX
KM Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
KM transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
KM transplant rejection; ss.
XX
OS Homo sapiens.
XX
PN MO9713852-A1.
XX
PD 17-APR-1997.
XX
PF 10-OCT-1996; 96WO-US016433.
XX
PR 10-OCT-1995; 95US-00544404.
XX
PA (GENP-) GENPHARM INT INC.
XX
PI Lonberg N, Kay RM;
XX
DR WPI; 1997-235888/21.
XX
PT Novel anti-CD4 antibody produced by transgenic mice - used in the
PT treatment of auto-immune disease etc.
XX
PS Claim 45; Page 272-273; 396pp; English.
XX
CC A novel composition has been developed which comprises an immunoglobulin
CC (Ig) having an affinity constant (Ka) of at least 2 multiply 1000000000 M
CC -1 for binding to a predetermined human antigen. The present sequence
CC represents a human light chain variable region partial nucleotide
CC sequence, LC6G5, which encodes an amino acid sequence from a claimed
CC immunoglobulin that specifically binds human CD4. The anti-CD4 antibodies
CC may be used in therapeutic and diagnostic applications, especially for
CC the treatment of human diseases. These antibodies reduce activity of CD4
CC cells and reduce undesirable autoimmune reactions, inflammatory response
CC and transplant rejection. Transgenic animals are capable of producing
CC heterologous antibodies of multiple isotypes by undergoing isotype
CC switching. These animals produce a first Ig type that is necessary for
CC antigen-stimulated B-cell maturation and can switch to encode and produce
CC one or more subsequent heterologous isotypes
XX
SQ Sequence 420 BP; 98 A; 116 C; 98 G; 108 T; 0 U; 0 Other;
Query Match 89.1%; Score 283.4; DB 2; Length 420;
Best Local Similarity 93.4%; Pred. No. 1.8e-81;
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 2 AGCTCAGCAGCTTCATCTTCCGTCTGCATCTGTGAGAGACAGAGTCAACCATTA 61
DB 80 AGATGACCCAGTCTCCATCTTCCGTCTGCATCTGTGAGAGACAGAGTCAACCATTA 139
QY 62 GTGGGGGAGTCAGGAGTATGAGAGTGGTATGAGTATCAGAGAAACAGGAAAG 121
DB 140 GTCCGGGCGAGTCAGATATGAGAGCTGTGAGCTGTATCAGATAAACAGGAAAG 199
QY 122 CCCCTAAACTCTGATCTATCTGCATCCAGTTTGCAAGTGGGTCCTCCGTCAGAGTTCA 181
DB 200 CACCTAAGCTCTATCTATCTGATCAGTTCAGTTTGCAAGTGGTCTCCATCAAGTTCA 259
QY 182 GCGGCACTGATCTGGGACAGATTTCACTTCACCATCAGAGCCTGACGCTGAAAGTT 241
DB 260 GCGGAACTGATCTGGGACAGATTTCACTTCACCATCAGAGCCTGACGCTGAAAGTT 319
QY 242 CTGCACTTACTATTTGTCAACAGGTAACAGTTTCCGTCAGACTTTGGCCAGGGGACCA 301
DB 320 TTGGAACCTACTATTTGTCAACAGGTAACAGTTTCCGTCAGACTTTGGTCAGGGAAACA 379
QY 302 AGGTGAAATCAACGA 318
DB 380 AGCTGAGATCAACGA 396

RESULT 12
AAV39293
ID AAV39293 standard; DNA; 420 BP.
XX
AC AAV39293;
XX
DT 18-DEC-1998 (first entry)
XX
DE Synthetic kappa light chain sequence LC6G5.
XX
KM Transgenic animal; human heterologous antibody; transgene;
KM isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;
KM autoimmune reaction; inflammatory response; transplant rejection;
KM acid induced lung injury; acute adult respiratory distress syndrome;
KM ARDS; vasculitis; septic shock; allergic reaction; asthma;
KM cystic fibrosis; ss.
XX
OS Synthetic.
XX
PN Homo sapiens.
XX
PD MO9824884-A1.
XX
PD 11-JUN-1998.
XX
PF 01-DEC-1997; 97WO-US021803.
XX
PR 02-DEC-1996; 96US-00758417.
XX
PA (GENP-) GENPHARM INT.
XX
PI Lonberg N, Kay RM;
XX
DR WPI; 1998-333306/29.
XX
PT Hybridoma producing antibody specific for interleukin-8 - used to prevent
PT efflux of neutrophils from vasculature, and treat reperfusion injury.
XX
PS Example 42; Page 324-325; 452pp; English.
XX
CC The present sequence represents a synthetic kappa light sequence (created
CC using oligonucleotides AAV39267-78). This synthetic sequence differs from
CC natural sequences in that strings of repeated oligonucleotides are
CC interrupted (to facilitate oligonucleotide synthesis and PCR
CC amplification), optimal translation initiation sites are incorporated and
CC HindIII sites were engineered upstream of the translation initiation
CC sites. The sequence is used to make plasmid pHC6G5, which is used in the
CC construction of minigenes for expression of Igkappa anti-CD4 antibodies,
CC in the transgenic mouse of the invention. The specification describes
CC transgenic non-human animals, especially a mouse, which are capable of
CC producing a human heterologous antibodies of multiple isotypes by
CC undergoing isotype switching. The transgenic animals have human heavy and
CC light chain heterologous. The transgenes are capable of functionally
CC rearranging a heterologous diversity (D) gene in a variable-diversity-
CC junction (V-D-J) recombination. The transgenes include a heavy chain
CC transgene comprising at least one V, D and J gene segment, and one
CC constant region gene segment. The immunoglobulin (Ig) light chain
CC transgene comprises at least one V and J gene segment and one constant
CC region gene segment. The gene segments are heterologous to the transgenic
CC animal. The antibody can be used to prevent efflux of neutrophils from
CC vasculature. It can also be used to treat reperfusion injury. CD4 binding
CC antibodies are used to reduce undesirable autoimmune reactions,
CC inflammatory responses and rejection of transplanted organs. The anti-IL-
CC 8 antibodies can reduce tissue damage and prolong survival in animal
CC models of acute adult respiratory distress syndrome (ARDS) and acid
CC induced lung injury. The anti-IL-8 antibodies can also be used for the
CC treatment of vasculitis, septic shock, allergic reactions (e.g. asthma)
CC and cystic fibrosis
XX
SQ Sequence 420 BP; 98 A; 116 C; 98 G; 108 T; 0 U; 0 Other;
Query Match 89.1%; Score 283.4; DB 2; Length 420;

Best Local Similarity 93.4%; Pred. No. 1.8e-81;
Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```
QY 2 AGCTCAGCAGTCTCCATCTTCCGTCGATCTGTGAGAGACAGAGTCAACATTAATT 61
    |||
Db 80 AGATGACCCAGTCTCCATCTTCCGTCGATCTGTGAGAGACAGAGTCAACATTAATT 139
    |||

QY 62 GTGCGGAGTCAAGGATTTAGCAGTTGGTTAGCTGGTATCAGCAAAACAGGAAAG 121
    |||
Db 140 GTGCGGAGTCAAGGATTTAGCAGTTGGTTAGCTGGTATCAGCAAAACAGGAAAG 199
    |||

QY 122 CCCCTAACTCTGATCTATTTGTCATCAGTTGGCAAAAGGGGTCCCGTCAAGTTCA 181
    |||
Db 200 CACCTAAGCTCTGATCTATTTGTCATCAGTTGGCAAAAGGGGTCCCGTCAAGTTCA 259
    |||

QY 182 GCGGAGTGAATCTGGGACAGATTTCACTCACCATAGCAGCTGAGGCTGAAATT 241
    |||
Db 260 GCGGAGTGAATCTGGGACAGATTTCACTCACCATAGCAGCTGAGGCTGAAATT 319
    |||

QY 242 CTGCAACTTACTATTTGTCACAGGCTTAACAGTTTCCGTACACTTTGGCCAGGGAACA 301
    |||
Db 320 TTGCAACTTACTATTTGTCACAGGCTTAACAGTTTCCGTACACTTTGGCCAGGGAACA 379
    |||

QY 302 AGGTGAAATCAACGA 318
    |||
Db 380 AGGTGAAATCAACGA 396
    |||
```

RESULT 13

AA22047
ID AA22047 standard; DNA; 420 BP.

AC AA22047;

DT 24-NOV-1999 (first entry)

DE Nucleotide sequence of LC6G5.

XX Transgenic animal; heterologous antibody; hybridoma; B cell;

KW transgenic mouse; human heavy chain transgene; digoxin;

KW human light chain transgene; immortalized cell; immunoglobulin;

KW Shiga-like toxin; autoimmune disease; cancer; infectious disease;

KW transplant rejection; blood disorder; coagulation disorder; ss.

XX Synthetic.

OS

XX

PN W09945962-A1.

XX

PD 16-SEP-1999.

XX

PF 12-MAR-1999; 99WO-US005535.

XX

PR 13-MAR-1998; 98US-00042353.

XX

PA (GENP-) GENPHARM INT INC.

XX

PI Lonberg N, Fishwild DM, Ball WJ;

DR WPI; 1999-551219/46.

XX Novel transgenic non-human animals used to produce heterologous

PT antibodies.

XX

PS Example 42; Page 325-326; 484pp; English.

XX

CC The specification describes transgenic animals that are capable of

CC producing a heterologous antibody. The antibodies are isolated from a

CC hybridoma, comprising B cells, that is obtained from a transgenic mouse

CC having a genome comprising a human heavy chain transgene and a human

CC light chain transgene. The B cells are fused to immortalized cells

CC suitable for generating a hybridoma, which produces a detectable amount

CC of an immunoglobulin that specifically binds digoxin or Shiga-like

CC toxin. B cells from transgenic animals can be used to generate hybridomas

CC expressing monoclonal high affinity human sequence antibodies. Antibodies

CC produced from the transgenic animals of the invention can be used to

CC treat human diseases, e.g. autoimmune diseases, cancer, infectious

CC disease, transplant rejection, blood disorders such as coagulation

CC disorders and other diseases. The present sequence is used in the course

CC of the invention

XX

SQ Sequence 420 BP; 98 A; 116 C; 98 G; 108 T; 0 U; 0 Other;

XX

Query Match 89.1%; Score 283.4; DB 2; Length 420;

Best Local Similarity 93.4%; Pred. No. 1.8e-81;

Matches 296; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTTCCGTCGATCTGTGAGAGACAGAGTCAACATTAATT 61

Db 80 AGATGACCCAGTCTCCATCTTCCGTCGATCTGTGAGAGACAGAGTCAACATTAATT 139

QY 62 GTGCGGAGTCAAGGATTTAGCAGTTGGTTAGCTGGTATCAGCAAAACAGGAAAG 121

Db 140 GTGCGGAGTCAAGGATTTAGCAGTTGGTTAGCTGGTATCAGCAAAACAGGAAAG 199

QY 122 CCCCTAACTCTGATCTATTTGTCATCAGTTGGCAAAAGGGGTCCCGTCAAGTTCA 181

Db 200 CACCTAAGCTCTGATCTATTTGTCATCAGTTGGCAAAAGGGGTCCCGTCAAGTTCA 259

QY 182 GCGGAGTGAATCTGGGACAGATTTCACTCACCATAGCAGCTGAGGCTGAAATT 241

Db 260 GCGGAGTGAATCTGGGACAGATTTCACTCACCATAGCAGCTGAGGCTGAAATT 319

QY 242 CTGCAACTTACTATTTGTCACAGGCTTAACAGTTTCCGTACACTTTGGCCAGGGAACA 301

Db 320 TTGCAACTTACTATTTGTCACAGGCTTAACAGTTTCCGTACACTTTGGCCAGGGAACA 379

QY 302 AGGTGAAATCAACGA 318

Db 380 AGGTGAAATCAACGA 396

XX

RESULT 14

AA778825

ID AA778825 standard; DNA; 3819 BP.

AC AA778825;

DT 23-JAN-1998 (first entry)

XX

DE Kappa light chain plasmid pLC65.

XX Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;

KW transgenic; mouse; CD4; antibody; autoimmune; inflammatory;

KW transplant rejection; immunoglobulin; ss.

XX Synthetic.

OS Homo sapiens.

XX

PN W09713852-A1.

XX

PD 17-APR-1997.

XX

PF 10-OCT-1996; 96WO-US016433.

XX

PR 10-OCT-1995; 95US-00544404.

XX

PA (GENP-) GENPHARM INT INC.

XX

PI Lonberg N, Kay RM;

DR WPI; 1997-235888/21.

XX Novel anti-CD4 antibody produced by transgenic mice - used in the

PT treatment of auto-immune disease etc.

XX

PS Example 42; Page 266-268; 396pp; English.

XX	A novel composition has been developed which comprises an immunoglobulin
CC	(Ig) having an affinity constant (Ka) of at least 2 multiply 10000000 M
CC	-1 for binding to a predetermined human antigen. The present sequence
CC	represents the kappa light chain plasmid pLC6G5 which includes the kappa
CC	constant region and polyadenylation site. Anti- CD4 antibodies may be
CC	used in therapeutic and diagnostic applications, especially for the
CC	treatment of human diseases. These antibodies reduce activity of CD4
CC	cells and reduce undesirable autoimmune reactions, inflammatory response
CC	and transplant rejection. Transgenic animals are capable of producing
CC	heterologous antibodies of multiple isotypes by undergoing isotype
CC	switching. These animals produce a first Ig type that is necessary for
CC	antigen-stimulated B-cell maturation, and can switch to encode and produce
CC	one or more subsequent heterologous isotypes.
XX	
SQ	Sequence 3819 BP; 947 A; 1015 C; 912 G; 945 T; 0 U; 0 Other;
SO	
Query Match	89.1%; Score 283.4; DB 2; Length 3819;
Best Local Similarity	93.4%; Pred. No. 4,3e-81;
Matches 296; Conservative	0; Mismatches 21; Indels 0; Gaps 0;
OY	2 AGCTCAGCAGTCTCCATCTTCGCCGTCTGCATCTGTGGAGACAGATCAACATAACTT 61
Db	2513 AGATGACCACGCTCATCTTCGCCGTCTGCATCTGTGGAGACAGATCAACATCACTT 257Z
OY	62 GTCGGGCAGTCAAGGGATTAGACAGTTGGTTAGCCTGGTATCAGCAAAACAGGGAAG 121
Db	2573 GTCGGGCAGTCAAGGATTAATVAGCAGCTGGTTAGCCTGGTATCAGCATAAACAGGTAAAG 263Z
OY	122 CCCCAAACCTCGTATCTAATTCCTGCATCAAGTTTGCAAAAGTGGGTCGCCGTCAAGTTCA 181
Db	2633 CACTTAACCTCTGTATCTAATGTCTGATCAAGTTTGCAAAAGTGTTCATCAATCAAGTTCA 2692Z
OY	182 GCGCAGTGAATCTGGGACAGATTTTCAGTCTCACCATCAGACAGCCTGACGCTGAAGATT 241
Db	2693 GCGGAAGTGAATCTGGGACAAGTTTCACTCTCACCATCAGACAGCCTGAGCCTGAAGATT 275S
OY	242 CTGCACTTACTATTGTCAACAGGCTAACAGTTTCCCGTACACTTTTGCCAGGGAGCCA 301
Db	2753 TTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGTCAGGGAGCCA 2812Z
OY	302 AGGTGGAATCAACGA 318
Db	2813 AGCTGGAGATCAACGA 2829
RESULT 15	
AAV39266	
ID	AAV39266 standard; DNA; 3819 BP.
XX	
AC	AAV39266;
XX	
DT	18-DEC-1998 (first entry)
XX	
DE	Plasmid pLC6G5 nucleotide sequence.
XX	
KW	Transgenic animal; human heterologous antibody; transgene;
KM	isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;
KW	autoimmune reaction; inflammatory response; transplant rejection;
KM	acid induced lung injury; acute adult respiratory distress syndrome;
KW	ARDS; vasculitis; septic shock; allergic reaction; asthma;
KM	cystic fibrosis; ss.
XX	
OS	Synthetic.
XX	
PN	Homo sapiens.
XX	
PD	WO9824884-A1.
XX	
PE	11-JUN-1998.
XX	
PR	01-DEC-1997; 97WO-US021803.
XX	
PR	02-DEC-1996; 96US-00758417.

Thu Jul 28 05:42:27 2005

us-10-027-725a-6.rng

Page 11

Job time : 303.048 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 09:08:49 ; Search time 476.839 Seconds

(without alignments)
4312.305 Million cell updates/sec

Title: US-10-027-725A-6

Perfect score: 318

Sequence: 1 gagctcagcagctccatc.....ccaagtcgaatcaacga 318

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7277826 seqs, 3233139505 residues 14555652

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Listing first 45 summaries

Published Applications NA:
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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5: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
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8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
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16: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	318	100.0	318	14	US-10-027-725A-6
2	291.4	91.6	974	19	US-09-859-053-29
3	291.4	91.6	974	19	US-10-635-105-29
4	291.4	91.6	974	22	US-10-800-250-29
5	288.2	90.6	711	21	US-10-901-901-11
6	286.8	90.2	321	21	US-10-727-155-121
7	286.4	90.1	632	21	US-10-714-079C-4

8	286.2	90.0	322	17	US-10-309-762-224	Sequence 224, App
9	284.6	89.5	322	21	US-10-638-265-75	Sequence 75, Appl
10	284.6	89.5	711	21	US-10-910-901-3	Sequence 3, Appl
11	283.6	89.2	387	21	US-10-693-576-1	Sequence 1, Appl
12	281.8	88.6	705	17	US-10-292-088-23	Sequence 23, Appl
13	280.8	88.3	728	9	US-09-844-684-15	Sequence 15, Appl
14	280.8	88.3	728	14	US-10-040-244-15	Sequence 15, Appl
15	280.8	88.3	728	19	US-10-693-629-63	Sequence 63, Appl
16	280.4	88.2	321	15	US-10-324-493-21	Sequence 21, Appl
17	280.2	88.1	705	17	US-10-292-088-47	Sequence 47, Appl
18	279.8	88.0	322	16	US-10-041-860-85	Sequence 85, Appl
19	279.8	88.0	322	18	US-10-269-711-28	Sequence 28, Appl
20	279.8	88.0	322	19	US-10-665-183-63	Sequence 63, Appl
21	279.8	88.0	322	19	US-10-684-109-24	Sequence 24, Appl
22	278.8	87.7	321	17	US-10-292-088-19	Sequence 19, Appl
23	278.2	87.5	322	18	US-10-269-711-16	Sequence 16, Appl
24	278.2	87.5	322	19	US-10-684-109-16	Sequence 16, Appl
25	277.6	87.3	716	9	US-09-844-684-13	Sequence 13, Appl
26	277.6	87.3	716	14	US-10-040-244-13	Sequence 13, Appl
27	277.2	87.2	321	17	US-10-292-088-43	Sequence 43, Appl
28	277	87.1	405	21	US-10-783-111-23	Sequence 23, Appl
29	277	87.1	405	21	US-10-783-111-24	Sequence 24, Appl
30	277	87.1	752	19	US-10-684-109-83	Sequence 83, Appl
31	277	87.1	752	19	US-10-684-109-84	Sequence 84, Appl
32	276.6	87.0	322	18	US-10-269-711-24	Sequence 24, Appl
33	276.6	87.0	322	19	US-10-684-109-32	Sequence 32, Appl
34	276.6	87.0	321	15	US-10-091-100-22	Sequence 22, Appl
35	275.6	86.7	321	20	US-10-482-630-84	Sequence 84, Appl
36	275.4	86.6	384	20	US-10-723-860-2996	Sequence 2996, Ap
37	275	86.5	322	17	US-10-309-762-213	Sequence 213, App
38	275	86.5	322	17	US-10-309-762-215	Sequence 215, App
39	275	86.5	322	17	US-10-309-762-228	Sequence 228, App
40	275	86.5	322	17	US-10-309-762-238	Sequence 238, App
41	275	86.5	322	18	US-10-269-711-8	Sequence 8, Appl
42	275	86.5	322	19	US-10-684-109-8	Sequence 8, Appl
43	274	86.2	321	19	US-10-703-714-7	Sequence 7, Appl
44	274	86.2	321	19	US-10-703-714-7	Sequence 7, Appl
45	274	86.2	321	19	US-10-703-714-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-10-027-725A-6
; Sequence 6, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific Igb-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259, 436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-6

QY	1	GAGCTCAGCAGCTCCATCTTCGTCCTCAGCTGATGAGACAGAGTACACT	60
DB	1	GAGCTCAGCAGCTCCATCTTCGTCCTCAGCTGATGAGACAGAGTACACT	60
QY	61	TGTCGGGAGTCAAGGATATTAGAGTTGTTAGCTGTATCAGACAGAAACAGGAA	120

Db 61 TGTGGGCGAGTCAGGGGATTAGCAGTTGGTTAGCTGTATCAGCAGAAACAGGAAA 120
Qy 121 GCCCTTAACTCTGATCTATTTCTGCATCCAGTTTGCAAGTGGGGTCCGCTCAAGTTTC 180
Db 121 GCCCTTAACTCTGATCTATTTCTGCATCCAGTTTGCAAGTGGGGTCCGCTCAAGTTTC 180
Qy 181 AGCGGAGTGGATCTGGGACAGATTTCAGTCTCAGCCATCAGCAGCTGGACCTGAAAT 240
Db 181 AGCGGAGTGGATCTGGGACAGATTTCAGTCTCAGCCATCAGCAGCTGGACCTGAAAT 240
Qy 241 TCTGCACTTACTATTTGTCACAGGCTTACAGTTTCCGCTACACTTTTGGCCAGGGACC 300
Db 241 TCTGCACTTACTATTTGTCACAGGCTTACAGTTTCCGCTACACTTTTGGCCAGGGACC 300
Qy 301 AAGGTGGAATCAACGA 318
Db 301 AAGGTGGAATCAACGA 318

RESULT 2

US-09-859-053-29
; Sequence 29, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(38)
; NAME/KEY: CDS
; LOCATION: (39)...(746)
; NAME/KEY: 3'UTR
; LOCATION: (750)...(974)
; NAME/KEY: sig_peptide
; LOCATION: (39)...(104)
US-09-859-053-29

Query Match 91.6%; Score 291.4; DB 9; Length 974;
Best Local Similarity 95.0%; Pred. No. 2.7e-85;
Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 2 AGCTCAGCAGATCTTCATCTTCCGTGCTGATCTGTGGAGACAGAGTCAACATTAATT 61
Db 112 AGATGACCCAGTCTTCATCTTCCGTGCTGATCTGTGGAGACAGAGTCAACATTAATT 171
Qy 62 GTGGGCGAGTCAGGGATTATAGCAAGTTGATTAGCTGTGTATCAGCAGAAACAGGGAAG 121
Db 172 GTGGGCGAGTCAGGGATTATAGCAAGTTGATTAGCTGTGTATCAGCAGAAACAGGGAAG 231
Qy 122 CCCCTTAACTCTGATCTATTTCTGCATCCAGTTTGCAAGTGGGGTCCGCTCAAGTTTC 181
Db 232 CCCCTTAACTCTGATCTATTTCTGCATCCAGTTTGCAAGTGGGGTCCGCTCAAGTTTC 291
Qy 182 GCGGAGTGGATCTGGGACAGATTTCAGTCTCAGCCATCAGCAGCTGGACCTGAAAT 241
Db 292 GCGGAGTGGATCTGGGACAGATTTCAGTCTCAGCCATCAGCAGCTGGACCTGAAAT 351

Qy 242 CTGCACTTACTATTTGTCACAGGCTTACAGTTTCCGCTACACTTTTGGCCAGGGACC 301
Db 352 TTGCACTTACTATTTGTCACAGGCTTACAGTTTCCGCTACACTTTTGGCCAGGGACC 411
Qy 302 AGGTGGAATCAACGA 318
Db 412 AGGTGGAATCAACGA 428

RESULT 3

US-10-625-105-29
; Sequence 29, Application US/10625105
; Publication No. US20040180052A1
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, Nobuaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/10/625,105
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US/09/859,053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(38)
; NAME/KEY: CDS
; LOCATION: (39)...(746)
; NAME/KEY: 3'UTR
; LOCATION: (750)...(974)
; NAME/KEY: sig_peptide
; LOCATION: (39)...(104)
US-10-625-105-29

Query Match 91.6%; Score 291.4; DB 19; Length 974;
Best Local Similarity 95.0%; Pred. No. 2.7e-85;
Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 2 AGCTCAGCAGATCTTCATCTTCCGTGCTGATCTGTGGAGACAGAGTCAACATTAATT 61
Db 112 AGATGACCCAGTCTTCATCTTCCGTGCTGATCTGTGGAGACAGAGTCAACATTAATT 171
Qy 62 GTGGGCGAGTCAGGGATTATAGCAAGTTGATTAGCTGTGTATCAGCAGAAACAGGGAAG 121
Db 172 GTGGGCGAGTCAGGGATTATAGCAAGTTGATTAGCTGTGTATCAGCAGAAACAGGGAAG 231
Qy 122 CCCCTTAACTCTGATCTATTTCTGCATCCAGTTTGCAAGTGGGGTCCGCTCAAGTTTC 181
Db 232 CCCCTTAACTCTGATCTATTTCTGCATCCAGTTTGCAAGTGGGGTCCGCTCAAGTTTC 291
Qy 182 GCGGAGTGGATCTGGGACAGATTTCAGTCTCAGCCATCAGCAGCTGGACCTGAAAT 241
Db 292 GCGGAGTGGATCTGGGACAGATTTCAGTCTCAGCCATCAGCAGCTGGACCTGAAAT 351
Qy 242 CTGCACTTACTATTTGTCACAGGCTTACAGTTTCCGCTACACTTTTGGCCAGGGACC 301
Db 352 TTGCACTTACTATTTGTCACAGGCTTACAGTTTCCGCTACACTTTTGGCCAGGGACC 411

QY 302 AGGTGAAATCAACGA 318
Db 412 AGGTGAAATCAACGA 428

RESULT 4

US-10-800-250-29
; Sequence 29, Application US/10800250
; Publication No. US2004014691A1
; GENERAL INFORMATION:
; APPLICANT: Teuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, Nobuaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/10/800,250
; PRIOR FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: US/09/859,053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(38)
; NAME/KEY: CDS
; LOCATION: (39)...(746)
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (750)...(974)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (39)...(104)
US-10-800-250-29

Query Match 91.6%; Score 291.4; DB 22; Length 974;
Best Local Similarity 95.0%; Pred. No. 2.7e-85;
Matches 301; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTTCATCTTCCGTCGATCTGTGAGAGACAGAGTCAACATTAATT 61
Db 112 AGATGACCCAGTCTTCATCTTCCGTCGATCTGTGAGAGACAGAGTCAACATTAATT 171
QY 62 GTCCGGGAGTCAAGGATTTAGCAGTGTAGAGCTGATGAGAGAAACAGGGAAG 121
Db 172 GTCCGGGAGTCAAGGATTTAGCAGTGTAGAGCTGATGAGAGAAACAGGGAAG 231
QY 122 CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGTGGGCTCCGTCAGGTTCA 181
Db 232 CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGTGGGCTCCGTCAGGTTCA 291
QY 182 GCGGAGTGTGATCTGGGACAGATTTGATCAGTCAAGCAGGCTGCAAGTTCA 241
Db 292 GCGGAGTGTGATCTGGGACAGATTTGATCAGTCAAGCAGGCTGCAAGTTCA 351
QY 242 CTGCAACTTACTATTTGCAAGGCTTAACAGTTTCCGTCAGGTTTGCCAGGGAACA 301
Db 352 TTGCAACTTACTATTTGCAAGGCTTAACAGTTTCCGTCAGGTTTGCCAGGGAACA 411
QY 302 AGGTGAAATCAACGA 318
Db 412 AGGTGAAATCAACGA 428

RESULT 5

US-10-910-901-11
; Sequence 11, Application US/10910901
; Publication No. US20050054019A1
; GENERAL INFORMATION:
; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO C-MET
; FILE REFERENCE: ABX-PP5
; CURRENT APPLICATION NUMBER: US/10/910,901
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 11
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-910-901-11

Query Match 90.6%; Score 288.2; DB 21; Length 711;
Best Local Similarity 94.3%; Pred. No. 2.8e-84;
Matches 299; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTTCATCTTCCGTCGATCTGTGAGAGACAGAGTCAACATTAATT 61
Db 74 AGATGACCCAGTCTTCATCTTCCGTCGATCTGTGAGAGACAGAGTCAACATTAATT 133
QY 62 GTCCGGGAGTCAAGGATTTAGCAGTGTAGAGCTGATGAGAGAAACAGGGAAG 121
Db 134 GTCCGGGAGTCAAGGATTTAGCAGTGTAGAGCTGATGAGAGAAACAGGGAAG 193
QY 122 CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGTGGGCTCCGTCAGGTTCA 181
Db 194 CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGTGGGCTCCGTCAGGTTCA 253
QY 182 GCGGAGTGTGATCTGGGACAGATTTGATCAGTCAAGCAGGCTGCAAGTTCA 241
Db 254 GCGGAGTGTGATCTGGGACAGATTTGATCAGTCAAGCAGGCTGCAAGTTCA 313
QY 242 CTGCAACTTACTATTTGCAAGGCTTAACAGTTTCCGTCAGGTTTGCCAGGGAACA 301
Db 314 TTGCAACTTACTATTTGCAAGGCTTAACAGTTTCCGTCAGGTTTGCCAGGGAACA 373
QY 302 AGGTGAAATCAACGA 318
Db 374 AGGTGAAATCAACGA 390

RESULT 6

US-10-727-155-121
; Sequence 121, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaepal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendescho
; APPLICANT: Palaniswami Rathnaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenko
; APPLICANT: Raffaella Paggioli
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FACTOR AND USES THEREOF

FILE REFERENCE: AGENIX 073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 121
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
US-10-727-155-121

Query Match 90.2%; Score 286.8; DB 21; Length 321;
Best Local Similarity 94.6%; Pred. No. 6.7e-84;
Matches 297; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTTCCGCTGCTGATCTGTGAGACAGAGTCAACATTAATT 61
DB 8 AGATGACCCAGTCTCCATCTTCCGCTGCTGATCTGTGAGACAGAGTCAACATTAATT 67
QY 62 GTCGGGCGAGTCAAGGATTAAGAGTTGTTAGCTGATCAGAGAAACAGGGAAG 121
DB 68 GTCGGGCGAGTCAAGGATTAAGAGTTGTTAGCTGATCAGAGAAACAGGGAAG 127
QY 122 CCCCTAACTCTGATCTATTTCTGATCAGTTTGCAAGTGGGCTCCGTCAGAGTTCA 181
DB 128 CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGTGGGCTCCGTCAGAGTTCA 187
QY 182 GCGGAGTGAATCTGGGACAGATTTCACTTCACCATCAGAGCTGAGGCTGAAGTT 241
DB 188 GCGGAGTGAATCTGGGACAGATTTTACTTCACCATCAGAGCTGAGGCTGAAGTT 247
QY 242 CTGCAACTTACTATTTGTCACAGGCTAACAGTTTCCCTGACATTTTGGCCAGGGACCA 301
DB 248 TTGCAAGTACTATTTGTCACAGGCTAACAGTTTCCCTGACATTTTGGCCAGGGACCA 307
QY 302 AGGTGGAATCAAA 315
DB 308 AGGTGGAATCAAA 321

RESULT 7
US-10-714-079C-4
Sequence 4, Application US/10714079C
Publication No. US20050014931A1
GENERAL INFORMATION:
APPLICANT: PIROFSKI, LISE-ANNE
APPLICANT: ZHONG, ZHAOJING
TITLE OF INVENTION: HUMAN ANTIPEUNOCOCAL ANTIBODIES FROM NON-HUMAN
FILE REFERENCE: ABX-AE1 CON
CURRENT APPLICATION NUMBER: US/10/714,079C
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: PCT/US02/18363
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/291,492
PRIOR FILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 632
TYPE: DNA
ORGANISM: Homo sapiens
US-10-714-079C-4

Query Match 90.1%; Score 286.4; DB 21; Length 632;
Best Local Similarity 94.9%; Pred. No. 1.1e-83;
Matches 296; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 7 ACGAGTCTCATCTTCCGCTGCTGATCTGTGAGACAGAGTCAACATTAATTGTGG 66
DB 7 ACGAGTCTCATCTTCCGCTGCTGATCTGTGAGACAGAGTCAACATTAATTGTGG 66

DB 12 ACGAGTCTCATCTTCCGCTGCTGATCTGTGAGACAGAGTCAACATTAATTGTGG 71
QY 67 GCGAGTCAAGGATTAAGAGTTGTTAGCTGATCAGAGAAACAGGGAAGCCCTT 126
DB 72 GCGAGTCAAGGATTAAGAGTTGTTAGCTGATCAGAGAAACAGGGAAGCCCTT 131
QY 127 AAATCTGATCTATTTGTCACAGGCTAACAGTTTCCCTGACATTTTGGCCAGGGACCA 186
DB 132 AAATCTGATCTATTTGTCACAGGCTAACAGTTTCCCTGACATTTTGGCCAGGGACCA 191
QY 187 AGTGAATCTGGGACAGATTTCACTTCACCATCAGAGCTGAGCTGAAGATTTTGA 246
DB 192 AGTGAATCTGGGACAGATTTTCACTTCACCATCAGAGCTGAGCTGAAGATTTTGA 251
QY 247 ACTTACTATTTGTCACAGGCTAACAGTTTCCCTGACATTTTGGCCAGGGACCAAGG 306
DB 252 ACTTACTATTTGTCACAGGCTAACAGTTTCCCTGACATTTTGGCCAGGGACCAAGG 311
QY 307 GAATCAACGA 318
DB 312 GAATCAACGA 323

RESULT 8
US-10-309-762-224
Sequence 224, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
FILE REFERENCE: AGENIX .027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 224
LENGTH: 322
TYPE: DNA
ORGANISM: Homo sapiens
US-10-309-762-224

Query Match 90.0%; Score 286.2; DB 17; Length 322;
Best Local Similarity 94.3%; Pred. No. 1.1e-83;
Matches 297; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTCCATCTTCCGCTGCTGATCTGTGAGACAGAGTCAACATTAATT 61
DB 8 AGATGACCCAGTCTCCATCTTCCGCTGCTGATCTGTGAGACAGAGTCAACATTAATT 67
QY 62 GTCGGGCGAGTCAAGGATTAAGAGTTGTTAGCTGATCAGAGAAACAGGGAAG 121
DB 68 GTCGGGCGAGTCAAGGATTAAGAGTTGTTAGCTGATCAGAGAAACAGGGAAG 127
QY 122 CCCCTAACTCTGATCTATTTCTGATCAGTTTGCAAGTGGGCTCCGTCAGAGTTCA 181
DB 128 CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGTGGGCTCCGTCAGAGTTCA 187
QY 182 GCGGAGTGAATCTGGGACAGATTTCACTTCACCATCAGAGCTGAGGCTGAAGTT 241
DB 188 GCGGAGTGAATCTGGGACAGATTTTCACTTCACCATCAGAGCTGAGGCTGAAGTT 247
QY 242 CTGCAACTTACTATTTGTCACAGGCTAACAGTTTCCCTGACATTTTGGCCAGGGACCA 301
DB 248 TTGCAAGTACTATTTGTCACAGGCTAACAGTTTCCCTGACATTTTGGCCAGGGACCA 307
QY 302 AGGTGGAATCAAA 316
DB 302 AGGTGGAATCAAA 316

Db 308 AAGTGATATCAAC 322

RESULT 9

US-10-638-265-75

Sequence 75, Application US/10638265

Publication No. US20050031614A1

GENERAL INFORMATION:

APPLICANT: Roskos, Lorin

APPLICANT: Politz, Ian

APPLICANT: King, Chadwick

TITLE OF INVENTION: ANTIBODIES DIRECTED TO PARATHYROID

TITLE OF INVENTION: HORMONE (PTH) AND USES THEREOF

FILE REFERENCE: AGENIX.092A

CURRENT APPLICATION NUMBER: US/10/638,265

CURRENT FILING DATE: 2003-08-08

NUMBER OF SEQ ID NOS: 97

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 75

LENGTH: 322

TYPE: DNA

ORGANISM: Homosapien

US-10-638-265-75

Query Match 89.5%; Score 284.6; DB 21; Length 322;

Best Local Similarity 94.0%; Pred. No. 3.5e-83;

Matches 296; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTTCATCTTCCGTCTGCATCTGTGAGAGACAGATCACTTAATT 61

DB 8 AGATGACCCAGTCTTCATCTTCCGTCTGCATCTGTGAGAGACAGATCACTTAATT 67

QY 62 GTCCGGGAGTCAAGGATTTAGCAGTTGGTACCTGATACAGAGAAACAGGGAAG 121

DB 68 GTCCGGGAGTCAAGGATTTAGCAGTTGGTACCTGATACAGAGAAACAGGGAAG 127

QY 122 CCCCTAACTCTGATCTTATCTGATCCAGTTGGCAAGTGGGGTCCCGTCAAGTTCA 181

DB 128 CCCCTAACTCTGATCTTATCTGATCCAGTTGGCAAGTGGGGTCCCGTCAAGTTCA 187

QY 182 GCGGAGTGAATCTGGGACAGATTTCACTTCACATCAGAGCCTGCAAGCTTGAATT 241

DB 188 GCGGAGTGAATCTGGGACAGATTTCACTTCACATCAGAGCCTGCAAGCTTGAATT 247

QY 242 CTGCACTTACTATTTGTAAGAGCTACAGTTCCGCTACACTTTGGCCAGGGAGCA 301

DB 248 TTGCACTTACTATTTGTAAGAGCTACAGTTCCGCTACACTTTGGCCAGGGAGCA 307

QY 302 AGTGGAATCAAC 316

DB 308 AAGTGATATCAAC 322

RESULT 10

US-10-910-901-3

Sequence 3, Application US/10910901

Publication No. US20050054019A1

GENERAL INFORMATION:

APPLICANT: MICHAUD, NEIL R., et al.

TITLE OF INVENTION: ANTIBODIES TO C-MET

FILE REFERENCE: ABX-PFS

CURRENT APPLICATION NUMBER: US/10/910,901

CURRENT FILING DATE: 2004-08-03

PRIOR APPLICATION NUMBER: US 60/492,432

PRIOR FILING DATE: 2003-08-04

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 3

LENGTH: 711

TYPE: DNA

ORGANISM: Homo sapiens

US-10-910-901-3

Query Match 89.5%; Score 284.6; DB 21; Length 711;

Best Local Similarity 93.4%; Pred. No. 4.3e-83;

Matches 296; Conservative 1; Mismatches 20; Indels 0; Gaps 0;

RESULT 11

US-10-893-576-1

Sequence 1, Application US/10893576

Publication No. US20050118643A1

GENERAL INFORMATION:

APPLICANT: BURGESS, TERESA L.

APPLICANT: COXON, ANGELA

APPLICANT: GREEN, LARRY L.

APPLICANT: ZHANG, KE

TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR

FILE REFERENCE: 06843.0051-00000

CURRENT APPLICATION NUMBER: US/10/893,576

CURRENT FILING DATE: 2004-07-16

PRIOR APPLICATION NUMBER: US 60/488,681

PRIOR FILING DATE: 2003-07-18

NUMBER OF SEQ ID NOS: 194

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 1

LENGTH: 387

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic HGF 1.24.1 light

OTHER INFORMATION: chain V region (VK, 1-L15)

US-10-893-576-1

Query Match 89.2%; Score 283.6; DB 21; Length 387;

Best Local Similarity 93.9%; Pred. No. 7.9e-83;

Matches 295; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2 AGCTCAGCAGTCTTCATCTTCCGTCTGCATCTGTGAGAGACAGATCACTTAATT 61

DB 74 AGATGACCCAGTCTTCATCTTCCGTCTGCATCTGTGAGAGACAGATCACTTAATT 133

QY 62 GTCCGGGAGTCAAGGATTTAGCAGTTGGTACCTGATACAGAGAAACAGGGAAG 121

DB 134 GTCCGGGAGTCAAGGATTTAGCAGTTGGTACCTGATACAGAGAAACAGGGAAG 193

QY 122 CCCCTAACTCTGATCTTATCTGATCCAGTTGGCAAGTGGGGTCCCGTCAAGTTCA 181

DB 194 CCCCTAACTCTGATCTTATCTGATCCAGTTGGCAAGTGGGGTCCCGTCAAGTTCA 253

QY 182 GCGGAGTGAATCTGGGACAGATTTCACTTCACATCAGAGCCTGCAAGCTTGAATT 241

Db 254 GCGGCACTGATCTGGAGACAGATTTCACCTCTCACATCAGACGCTGACGCTGAAGATT 313
Qy 242 CTGCAACTTACTATTGTCAACAGGCTTAACAGTTCCGCTACACTTTTGGCCAGGGAAACA 301
Db 314 TTGCAACTTACTATTGTCAACAGGCTTAACAGGCTTCCGCTGAGCGTTGCGCCAGGAAACA 373
Qy 302 AGGTGAATCAAA 315
Db 374 AGGTGAATCAAA 387

RESULT 12

US-10-292-088-23
; Sequence 23, Application US/10292088
; Publication No. US2003211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 23
; LENGTH: 705
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-292-088-23

Query Match 88.6%; Score 281.8; DB 17; Length 705;
Best Local Similarity 93.1%; Pred. No. 3,6e-82;
Matches 295; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 2 AGCTCAGCAGTCTCCATCTTCGCTGCTGCATCTGTAAGAGACAGAGTCAACATACTT 61
Db 68 AGATGACCCAGTCTCCATCTTCGCTGCTGCATCTGTAAGAGAGAGATCAACATACTT 127
Qy 62 GTCGGGAGAGTCAAGGATTTAGCAGTTGCTTACCTGATACAGCAAAACAGGAAAG 121
Db 128 GTCGGGAGAGTCAAGGATTTAGCAGTTGCTTACCTGATACAGCAAAACAGGAAAG 187
Qy 122 CCCCTAACTCTGATCTATCTGCATCTCAGTTTGCAGAAAGTGGGGTCCGCTCAAGTTCA 181
Db 188 CCCCTAACTCTGATCTATCTGCATCTCAGTTTGCAGAAAGTGGGGTCCGCTCAAGTTCA 247
Qy 182 GCGGCACTGATCTGGGACAGATTTCAGTCTCACCATCAGACGCTGACGCTGAAGATT 241
Db 248 GCGGCACTGATCTGGGACAGATTTCAGTCTCACCATCAGACGCTGACGCTGAAGATT 307
Qy 242 CTGCAACTTACTATTGTCAACAGGCTTAACAGTTCCGCTACACTTTTGGCCAGGGAAACA 301
Db 308 TTGCAACTTACTATTGTCAACAGGCTTAACAGTTCCGCTACACTTTTGGCCAGGGAAACA 367
Qy 302 AGGTGAATCAAA 318
Db 368 AGGTGAATCAAA 384

RESULT 13

US-09-844-684-15
; Sequence 15, Application US/09844684
; Patent No. US20020142358A1
; GENERAL INFORMATION:
; APPLICANT: GEMINI SCIENCE, INC.
; APPLICANT: LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY
; TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME
; FILE REFERENCE: 21286/0276339

; CURRENT APPLICATION NUMBER: US/09/844,684
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/200,601
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 15
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-844-684-15

Query Match 88.3%; Score 280.8; DB 9; Length 728;
Best Local Similarity 93.0%; Pred. No. 7,8e-82;
Matches 294; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 2 AGCTCAGCAGTCTCCATCTTCGCTGCTGCATCTGTAAGAGACAGATCAACATACTT 61
Db 132 AGATGACCCAGTCTCCATCTTCGCTGCTGCATCTGTAAGAGAGAGATCAACATACTT 191
Qy 62 GTCGGGAGAGTCAAGGATTTAGCAGTTGCTTACCTGATACAGCAAAACAGGAAAG 121
Db 192 GTCGGGAGAGTCAAGGATTTAGCAGTTGCTTACCTGATACAGCAAAACAGGAAAG 251
Qy 122 CCCCTAACTCTGATCTATCTGCATCTCAGTTTGCAGAAAGTGGGGTCCGCTCAAGTTCA 181
Db 252 CCCCTAACTCTGATCTATCTGCATCTCAGTTTGCAGAAAGTGGGGTCCGCTCAAGTTCA 311
Qy 182 GCGGCACTGATCTGGGACAGATTTCAGTCTCACCATCAGACGCTGACGCTGAAGATT 241
Db 312 GCGGCACTGATCTGGGACAGATTTCAGTCTCACCATCAGACGCTGACGCTGAAGATT 371
Qy 242 CTGCAACTTACTATTGTCAACAGGCTTAACAGTTCCGCTACACTTTTGGCCAGGGAAACA 301
Db 372 TTGCAACTTACTATTGTCAACAGGCTTAACAGTTCCGCTACACTTTTGGCCAGGGAAACA 431
Qy 302 AGGTGAATCAAA 317
Db 432 AGGTGAATCAAA 447

RESULT 14

US-10-040-244-15
; Sequence 15, Application US/10040244
; Publication No. US20030059427A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: FORCE, WALKER F.
; APPLICANT: TAKAHASHI, NOBUAKI
; APPLICANT: MIYAYAMA, TOSHITOMI
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBOD
; FILE REFERENCE: 021286/0272501
; CURRENT APPLICATION NUMBER: US/10/040,244
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/200,601
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 09/844,684
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 3.0
; SEQ ID NO 15
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-244-15

Query Match 88.3%; Score 280.8; DB 14; Length 728;
Best Local Similarity 93.0%; Pred. No. 7,8e-82;
Matches 294; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 2 AGCTCAGCAGTCTCCATCTTCGCTGCTGCATCTGTAAGAGAGAGATCAACATACTT 61

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Db      132 AGATGACCCAGTCCCATCTTCCGTCGTGATCTGTGAGAGACAGATCAACATCACTT 191
Qy      62  GTCCGGCAGTCAAGGATATTAGAGTTAGCTGTGATCAGAGAAACAGAGGAAG 121
Db      192 GTCCGGCAGTCAAGGATATTAGAGTTAGCTGTGATCAGAGAAACAGAGGAAG 251
Qy      122 CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGTGGGGTCCCGTCAAGTTCA 181
Db      252 CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGTGGGGTCCCGTCAAGTTCA 311
Qy      182 GCGGCACTGATCTGAGCAGATTTCACTTCACATCAGAGCCTGCAAGCTGAAGTT 241
Db      312 GCGGCACTGATCTGAGCAGATTTCACTTCACATCAGAGCCTGCAAGCTGAAGTT 371
Qy      242 CTGCACTTACTATTTGCAAGGCTAACAGTTTCCCTACATTTTGGCCAGGGAGCA 301
Db      372 TTGCACTTACTATTTGCAAGGCTAACAGTTTCCCTACATTTTGGCCAGGGAGCA 431
Qy      302 AGTGAATCAACG 317
Db      432 AGTGAATCAACG 447

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RESULT 15

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US-10-693-629-65
; Sequence 65, Application US/10693629
; Publication No. US20040120948A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: MIRAYAMA, Toshifumi
; APPLICANT: YOSHIDA, Hiroshi
; APPLICANT: FORCE, Walker, R.
; APPLICANT: CHEN, Xingjie
; APPLICANT: TAKAHASHI, Nobuaki
; TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY
; FILE REFERENCE: 021286-0306473
; CURRENT APPLICATION NUMBER: US/10/693,629
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US09/844,684
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP2001/142482
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: JP2001/310535
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US10/040,244
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-693-629-65

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Query Match 88.3%; Score 280.8; DB 19; Length 728;
 Best Local Similarity 93.0%; Pred. No. 7.8e-82;
 Matches 294; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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Qy      2  AGCTCAGCAGTCTTCATCTTCCGTCGTGATCTGTAGAGAGACAGATCAACATCACTT 61
Db      132 AGATGACCCAGTCCCATCTTCCGTCGTGATCTGTGAGAGACAGATCAACATCACTT 191
Qy      62  GTCCGGCAGTCAAGGATATTAGAGTTAGCTGTGATCAGAGAAACAGAGGAAG 121
Db      192 GTCCGGCAGTCAAGGATATTAGAGTTAGCTGTGATCAGAGAAACAGAGGAAG 251
Qy      122 CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGTGGGGTCCCGTCAAGTTCA 181
Db      252 CCCCTAACTCTGATCTATCTGATCAGTTTGCAAGTGGGGTCCCGTCAAGTTCA 311

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Qy      182 GCGGCACTGATCTGAGCAGATTTCACTTCACATCAGAGCCTGCAAGCTGAAGTT 241
Db      312 GCGGCACTGATCTGAGCAGATTTCACTTCACATCAGAGCCTGCAAGCTGAAGTT 371
Qy      242 CTGCACTTACTATTTGCAAGGCTAACAGTTTCCCTACATTTTGGCCAGGGAGCA 301
Db      372 TTGCACTTACTATTTGCAAGGCTAACAGTTTCCCTACATTTTGGCCAGGGAGCA 431
Qy      302 AGTGAATCAACG 317
Db      432 AGTGAATCAACG 447

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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:42:26 ; Search time 88.6545 Seconds
(without alignment)
5869.253 Million cell updates/sec

Title: US-10-027-725A-5
Perfect score: 318
Sequence: 1 gagctcaccagctccatc.....ccaactgagatcaacga 318

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 240568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	276.4	86.9	321	US-09-240-274-102	Sequence 102, App
2	276.4	86.9	321	US-09-240-274-199	Sequence 199, App
3	273.2	85.9	321	US-09-240-274-107	Sequence 107, App
4	273.2	85.9	321	US-09-240-274-113	Sequence 113, App
5	273.2	85.9	321	US-09-240-274-201	Sequence 201, App
6	273.2	85.9	321	US-09-240-274-211	Sequence 211, App
7	273.2	85.9	321	US-09-240-274-218	Sequence 218, App
8	271.6	85.4	321	US-09-240-274-106	Sequence 106, App
9	271.6	85.4	321	US-09-240-274-205	Sequence 205, App
10	271.6	85.4	321	US-09-240-274-221	Sequence 221, App
11	271.6	85.4	321	US-09-240-274-222	Sequence 222, App
12	271.2	85.3	720	US-09-192-854-1	Sequence 1, App11
13	270	84.9	321	US-09-240-274-215	Sequence 215, App
14	270	84.9	321	US-09-240-274-217	Sequence 217, App
15	268.4	84.4	321	US-09-240-274-105	Sequence 105, App
16	267.4	84.1	714	US-09-472-087-62	Sequence 62, App1
17	265.2	83.4	321	US-09-240-274-109	Sequence 109, App
18	265.2	83.4	321	US-09-240-274-216	Sequence 216, App
19	263.6	82.8	321	US-09-240-274-207	Sequence 207, App
20	263.4	82.8	324	US-09-240-274-101	Sequence 101, App
21	263.4	82.8	324	US-09-240-274-112	Sequence 112, App
22	263.4	82.8	324	US-09-240-274-210	Sequence 210, App
23	262.4	82.5	451	US-09-472-087-50	Sequence 50, App1
24	262	82.4	321	US-09-240-274-104	Sequence 104, App
25	261.8	82.3	324	US-09-240-274-110	Sequence 110, App
26	261.8	82.3	324	US-09-240-274-206	Sequence 206, App
27	261.4	82.2	402	US-09-472-087-49	Sequence 49, App1

28	261.2	82.1	321	US-08-378-939-13	Sequence 13, App1
29	260.4	81.9	321	US-09-240-274-103	Sequence 103, App
30	260	81.8	672	US-09-456-090A-47	Sequence 47, App1
31	260	81.8	672	US-09-453-234-47	Sequence 47, App1
32	256.6	80.7	417	US-09-472-087-48	Sequence 48, App1
33	256.2	80.6	458	US-09-472-087-44	Sequence 44, App1
34	255.4	80.3	324	US-09-240-274-224	Sequence 224, App
35	254.8	80.1	318	US-08-844-215-20	Sequence 20, App
36	254	79.9	321	US-09-240-274-200	Sequence 200, App
37	254	79.9	321	US-09-240-274-213	Sequence 213, App
38	252.4	79.4	318	US-09-240-274-202	Sequence 202, App
39	250.8	78.9	318	US-09-240-274-208	Sequence 208, App
40	250.8	78.9	321	US-09-240-274-108	Sequence 108, App
41	250.8	78.9	321	US-09-240-274-114	Sequence 114, App
42	250.8	78.9	321	US-09-240-274-203	Sequence 203, App
43	247.2	77.7	705	US-08-488-376-16	Sequence 16, App1
44	247.2	77.7	705	US-08-634-223-16	Sequence 16, App1
45	247.2	77.7	705	US-08-634-224-16	Sequence 16, App1

ALIGNMENTS

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RESULT 1
US-09-240-274-102
; Sequence 102, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT FILING DATE: 1998-04-10
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 102
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-240-274-102
Query Match 86.9%, Score 276.4; DB 3; Length 321;
Best Local Similarity 91.8%; Pred. No. 1.5e-85;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
1 GAGCTACCCAGTCTCCATCTCTGCTGCTGTAGAGACAGATCACTACT 60
4 GAGCTACCCAGTCTCCATCTCTGCTGCTGTAGAGACAGATCACTACT 63
61 TGGCGGCACTGAGATTAAGCACTTAATGATGTCGCGAAGCGGGAG 120
64 TGGCGGCACTGAGATTAAGCACTTAATGATGTCGCGAAGCGGGAA 123
121 GCCCTAAGCTCCGATCTGATGATCACTTGGCAAGTGGGGTCCATCAGTT 180
124 GCCCTAAGCTCCGATCTGATGATCACTTGGCAAGTGGGGTCCATCAGTT 183
181 AGTGGAGTGTGATGAGACAGATTAAGCACTTGGCAAGTGGAGAC 240
184 AGTGGAGTGTGATGAGACAGATTAAGCACTTGGCAAGTGGAGAT 243
241 TTTCAGTGTCTGATGAGACAGATTAAGCACTTGGCAAGTGGAGAC 300
244 TTTCAGTGTCTGATGAGACAGATTAAGCACTTGGCAAGTGGAGAC 303
301 AAACGTGAGATCAACGA 318
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Db 304 AAGCTGGAATCAACGA 321

RESULT 2

US-09-240-274-199
Sequence 199, Application US/09240274
Patent No. 6255455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 199

LENGTH: 321

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH13

US-09-240-274-199

Query Match 86.9%; Score 276.4; DB 3; Length 321;

Best Local Similarity 91.8%; Pred. No. 1.5e-85;

Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GAGCTCACCAGTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCCATCACT 60

Db 4 GAGCTCACCAGTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCCATCACT 63

QY 61 TCCCGGACGTCAGAGTATTAGCACTATTAAATTGATCAGCAGAAACCGGGAG 120

Db 64 TCCCGGACGTCAGAGTATTAGCACTATTAAATTGATCAGCAGAAACCGGGAG 123

QY 121 GCCCTAAGCTCCGATCTGATGATGATGATGATGATGATGATGATGATGATG 180

Db 124 GCCCTAAGCTCCGATCTGATGATGATGATGATGATGATGATGATGATGATG 183

QY 181 AGTGGCAGTGGATCGGACAGAGTTCATCTCAACATTCGCAACTGGAAGAC 240

Db 184 AGTGGCAGTGGATCGGACAGAGTTCATCTCAACATTCGCAACTGGAAGAT 243

QY 241 TTTCGAAGTACTACTGTCAACAGAGTTACATCTTATACCTTGGCCCTGGAGC 300

Db 244 TTTCGAAGTACTACTGTCAACAGAGTTACATCTTATACCTTGGCCCTGGAGC 303

QY 301 AAAGTGAAGATCAACGA 318

Db 304 AAGCTGGAATCAACGA 321

RESULT 3

US-09-240-274-107

Sequence 107, Application US/09240274
Patent No. 6255455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 107
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 107

US-09-240-274-107

Query Match 85.9%; Score 273.2; DB 3; Length 321;

Best Local Similarity 91.2%; Pred. No. 2e-84;

Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 GAGCTCACCAGTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCCATCACT 60

Db 4 GAGCTCACCAGTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCCATCACT 63

QY 61 TCCCGGACGTCAGAGTATTAGCACTATTAAATTGATCAGCAGAAACCGGGAG 120

Db 64 TCCCGGACGTCAGAGTATTAGCACTATTAAATTGATCAGCAGAAACCGGGAG 123

QY 121 GCCCTAAGCTCCGATCTGATGATGATGATGATGATGATGATGATGATGATG 180

Db 124 GCCCTAAGCTCCGATCTGATGATGATGATGATGATGATGATGATGATGATG 183

QY 181 AGTGGCAGTGGATCGGACAGAGTTCATCTCAACATTCGCAACTGGAAGAC 240

Db 184 AGTGGCAGTGGATCGGACAGAGTTCATCTCAACATTCGCAACTGGAAGAT 243

QY 241 TTTCGAAGTACTACTGTCAACAGAGTTACATCTTATACCTTGGCCCTGGAGC 300

Db 244 TTTCGAAGTACTACTGTCAACAGAGTTACATCTTATACCTTGGCCCTGGAGC 303

QY 301 AAAGTGAAGATCAACGA 318

Db 304 AAGCTGGAATCAACGA 321

RESULT 4

US-09-240-274-113

Sequence 113, Application US/09240274
Patent No. 6255455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202

CURRENT APPLICATION NUMBER: US/09/240,274

CURRENT FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/028,550

EARLIER FILING DATE: 1996-10-11

NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 113

LENGTH: 321

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: anti-Rh(D) chain 113

US-09-240-274-113

Query Match 85.9%; Score 273.2; DB 3; Length 321;

Best Local Similarity 91.2%; Pred. No. 2e-84;

Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 GAGCTCACCAGTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCCATCACT 60

Db 4 GAGCTCACCAGTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCCATCACT 63

QY 61 TCCCGGACGTCAGAGTATTAGCACTATTAAATTGATCAGCAGAAACCGGGAG 120

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Db      64 TCCGGGCAAGTCAGAGATTAGCAGGATATTAAATTGATTCAGCAGAAACCGAGGGAAA 123
Qy      121 GCGCCCTAAGCTCCGATCTGATAGTATGCAATTCGAATGGGGTCCCATCCAGGTTTC 180
Db      124 GCGCCCTAAGCTCCGATCTGATAGTATGCAATTCGAATGGGGTCCCATCCAGGTTTC 183
Qy      181 AGTGGCAGTGGATCTGGGACAGATTTCATCTCAACATCAGCAATCTGCAACTGAAGAC 240
Db      184 AGTGGCAGTGGATCTGGGACAGATTTCATCTCAACATCAGCAAGTCTGCAACTGAAGAT 243
Qy      241 TTTCGAAGTACTACTGTCAACAGAGTTACACTTAATATACCTTGCGCCCTGGGAGCC 300
Db      244 TTTCGAAGTACTACTGTCAACAGAGTTACCGTACCCCTCAGATTGCGCGGGGAGCC 303
Qy      301 AAAGTGAGATCAACGA 318
Db      304 AAGCTGAGATCAACGA 321
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RESULT 5

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US-09-240-274-201
; Sequence 201, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 201
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-09-240-274-201
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Query Match 85.9%; Score 273.2; DB 3; Length 321;

Best Local Similarity 91.2%; Pred. No. 2e-84;

Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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Qy      1 GAGCTCACCCAGTCCATCTCCCTGCTGCTGCTGAGAGACAGAGTCAACATCACT 60
Db      4 GAGCTCACCCAGTCCATCTCCCTGCTGCTGCTGAGAGACAGAGTCAACATCACT 63
Qy      61 TCCCGGACAGCTCAGAGTATTAGCACTATTAAATTGGTATCAGCAGAAAACCGGGGAAG 120
Db      64 TCCCGGACAGCTCAGAGATTTAGCAGCTATTAAATTGGTATCAGCAGAAAACCGGGAAA 123
Qy      121 GCGCCCTAAGCTCCGATCTGATAGTATGCAATTCGAATGGGGTCCCATCCAGGTTTC 180
Db      124 GCGCCCTAAGCTCCGATCTGATAGTATGCAATTCGAATGGGGTCCCATCCAGGTTTC 183
Qy      181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACATCAGCAATCTGCAACTGAAGAC 240
Db      184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACATCAGCAAGTCTGCAACTGAAGAT 243
Qy      241 TTTCGAAGTACTACTGTCAACAGAGTTACACTTAATATACCTTGCGCCCTGGGAGCC 300
Db      244 TTTCGAAGTACTACTGTCAACAGAGTTACACTTAATATACCTTGCGCCCTGGGAGCC 303
Qy      301 AAAGTGAGATCAACGA 318
Db      304 AAGCTGAGATCAACGA 321
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RESULT 6

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US-09-240-274-211
; Sequence 211, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH36
US-09-240-274-211
```

Query Match 85.9%; Score 273.2; DB 3; Length 321;

Best Local Similarity 91.2%; Pred. No. 2e-84;

Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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Qy      1 GAGCTCACCCAGTCCATCTCCCTGCTGCTGCTGAGAGACAGAGTCAACATCACT 60
Db      4 GAGCTCACCCAGTCCATCTCCCTGCTGCTGCTGAGAGACAGAGTCAACATCACT 63
Qy      61 TCCCGGACAGCTCAGAGTATTAGCACTATTAAATTGGTATCAGCAGAAAACCGGGGAAG 120
Db      64 TCCCGGACAGCTCAGAGATTTAGCAGCTATTAAATTGGTATCAGCAGAAAACCGGGAAA 123
Qy      121 GCGCCCTAAGCTCCGATCTGATAGTATGCAATTCGAATGGGGTCCCATCCAGGTTTC 180
Db      124 TCCCTAAGCTCCGATCTGATAGTATGCAATTCGAATGGGGTCCCATCCAGGTTTC 183
Qy      181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACATCAGCAATCTGCAACTGAAGAC 240
Db      184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACATCAGCAAGTCTGCAACTGAAGAT 243
Qy      241 TTTCGAAGTACTACTGTCAACAGAGTTACACTTAATATACCTTGCGCCCTGGGAGCC 300
Db      244 TTTCGAAGTACTACTGTCAACAGAGTTACAGTTACCCCTCGGCTTTCGGCCCTGGGAGCC 303
Qy      301 AAAGTGAGATCAACGA 318
Db      304 AAGCTGAGATCAACGA 321
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RESULT 7

```
US-09-240-274-218
; Sequence 218, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
```


Sequence 221, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1998-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 221
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-240-274-221

Query Match 85.4%; Score 271.6; DB 3; Length 321;
Best Local Similarity 90.9%; Pred. No. 7e-84;
Matches 289; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 GAGCTACCCAGTCTCCATCTCCCTGCTGCTCTGAGAGACAGAGTCCATCACT 60
DB 4 GAGCTACCCAGTCTCCATCTCCCTGCTGCTCTGAGAGACAGAGTCCATCACT 63
QY 61 TGCCGGGACGTCAGAGTATTAGACCTATTAAATTGGATACAGAGAAACCGGGGAG 120
DB 64 TGCCGGGACGTCAGAGTATTAGACCTATTAAATTGGATACAGAGAAACCGGGGAA 123
QY 121 GCCCTTAAGCTCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 124 GCCCTTAAGCTCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 183
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACCTCAGCAGCAGTCACTGAGAAC 240
DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACCTCAGCAGCAGTCACTGAGAAC 243
QY 241 TTTCGAAGTCTACTGTCACAGAGTTCACCTTATATACCTTGGGCTGGGACC 300
DB 244 TTTCGAAGTCTACTGTCACAGAGTTCACCTTATATACCTTGGGCTGGGACC 303
QY 301 AAAGTGGAGATCAACGA 318
DB 304 AAAGTGGAGATCAACGA 321

RESULT 11
US-09-240-274-222
Sequence 222, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 222
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-222

Query Match 85.4%; Score 271.6; DB 3; Length 321;
Best Local Similarity 90.9%; Pred. No. 7e-84;
Matches 289; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 GAGCTACCCAGTCTCCATCTCCCTGCTGCTCTGAGAGACAGAGTCCATCACT 60
DB 4 GAGCTACCCAGTCTCCATCTCCCTGCTGCTCTGAGAGACAGAGTCCATCACT 63
QY 61 TGCCGGGACGTCAGAGTATTAGACCTATTAAATTGGATACAGAGAAACCGGGGAG 120
DB 64 TGCCGGGACGTCAGAGTATTAGACCTATTAAATTGGATACAGAGAAACCGGGGAA 123
QY 121 GCCCTTAAGCTCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 124 GCCCTTAAGCTCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 183
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACCTCAGCAGCAGTCACTGAGAAC 240
DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACCTCAGCAGCAGTCACTGAGAAC 243
QY 241 TTTCGAAGTCTACTGTCACAGAGTTCACCTTATATACCTTGGGCTGGGACC 300
DB 244 TTTCGAAGTCTACTGTCACAGAGTTCACCTTATATACCTTGGGCTGGGACC 303
QY 301 AAAGTGGAGATCAACGA 318
DB 304 AAAGTGGAGATCAACGA 321

RESULT 12
US-09-192-854-1
Sequence 1, Application US/09192854
Patent No. 6696245
GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian
TITLE OF INVENTION: Methods for Selecting Functional Peptides
FILE REFERENCE: 3789/72916
CURRENT APPLICATION NUMBER: US/09/192,854
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: 60/066,729
EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 720
TYPE: DNA
ORGANISM: Homo sapiens
US-09-192-854-1

Query Match 85.3%; Score 271.2; DB 4; Length 720;
Best Local Similarity 91.1%; Pred. No. 1.4e-83;
Matches 289; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 2 AGCTACCCAGTCTCCATCTCCCTGCTGCTCTGAGAGACAGAGTCCATCACT 61
DB 404 AGATGACCCAGTCTCCATCTCCCTGCTGCTCTGAGAGACAGAGTCCATCACT 463
QY 62 GCCGGGACGTCAGAGTATTAGACCTATTAAATTGGATACAGAGAAACCGGGGAG 121
DB 64 GCCGGGACGTCAGAGTATTAGACCTATTAAATTGGATACAGAGAAACCGGGGAG 523
QY 122 CCCCTTAAGCTCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 181
DB 524 CCCCTTAAGCTCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 583
QY 182 GTGGCAGTGGATCTGGGACAGAGTTCACCTCAGCAGCAGTCACTGAGAAC 241
DB 584 GTGGCAGTGGATCTGGGACAGAGTTCACCTCAGCAGCAGTCACTGAGAAC 643

QY	Db	QY	Db
242	TTTGCAAGTACTACTCTGCAACAGAGTTACACTACCTTATATPCTTGGCCCTGGAGCA	302	AACTGGAGATCAAAAGC 317
644	TTTGCACTTACTACTCTGCAACAGAGTTACAGTACCCTTAATATCGTTGGCAAGAGACCA	704	AGGTGAAATCAACGC 719

RESULT 13
US-09-240-274-215
; Sequence 215, Application US/09240274
; Patent No. 636666

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/ TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
/ TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
/ FILE REFERENCE: 09596-4202
/ CURRENT APPLICATION NUMBER: US/09/240,274
/ CURRENT FILING DATE: 1999-01-29
/ EARLIER APPLICATION NUMBER: 60/081,380
/ EARLIER FILING DATE: 1998-04-10
/ EARLIER APPLICATION NUMBER: 60/028,550
/ EARLIER FILING DATE: 1996-10-11
/ NUMBER OF SEQ ID NOS: 224
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 215
/ LENGTH: 321
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: anti-Rh(D) antibody clone SH46
/ OS-09-240-274-215

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Query Match	84.9%;	Score 270;	DB 3;	Length 321;
Best Local Similarity	90.6%;	Pred. No. 2.5e-83;		
Matches 288; Conservative	0;	Mismatches 30;	Indels 0;	Gaps 0;

Qy	1	GACGTACCCAGAGTCTCAATCTCCGATCTGGCTCTGAGAGAGACAGATCAACATCACT	60
Db	4	GACGTACCCAGTCTCATCTCTCCGTGTGATCTGTAGAGAGACAGATCAACATCACT	63
Qy	61	TGCGGGGACAGTCTAGAGATATTAGACCTTATTTAAATTGGTATCAGACGAAACCGGGGAG	120
Db	64	TGCGGGGCAAGTCAAGTACATTAGACACTTATTTAAATTGGTATCAGACGAAACCGGGGAA	123
Qy	121	GCCCTTAAGCTCTGATCTGTAGTGCATCCAAATTTGCAAAAGTGGGTCCCATCCAGGTTT	180
Db	124	GCCCTTAATCTCTGATCTGTATGTGTGATCCAGTTTGCAAAAGTGGGTCCCATCAAGTTTC	183
Qy	181	AGTGGCAGTGGATCTCTGGACAGAGTTCACTTCCACATGACGATCTTGCAACTTGAAAC	240
Db	184	AGTGGCAGTGGATCTCTGGACAGATTTTCACTTCCACATGACGATCTTCAACTTGAAAT	243
Qy	241	TTTGGCAAGTTACTACTGTCAACAGATGTACACTTATATATCTTGGGCGCTGGAGCC	300
Db	244	TTTGGCAACTTACTACTGTCAACAGATTTACAGTTTCCCTTAGCATTTTGGGCGCTGGAGCC	303
Qy	301	AAACTGGAGATCAAACGA 318	
Db	304	AAAGTGATATCAAACGA 321	

RESULT 14
US-09-240-274-217

Sequence 217, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4202

```

CURRENT APPLICATION NUMBER: US/09/240, 274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 217
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH48
US-09-240-274-217

Query Match      84.9%;   Score 270;   DB 3;   Length 321;
Best Local Similarity 90.6%;   Pred. No. 2.5e-83;
Matches 288;   Conservative 0;   Mismatches 30;   Indels 0;   Gaps 0

```

OTHER INFORMATION: anti-Rh(D) antibody clone SH48
US-09-240-274-217

Query Match	84.9%;	Score 270;	Length 321;
Best Local Similarity	90.6%;	Pred. No. 2.5e-83;	
Matches 288;	Conservative	0;	Mismatches 30; Indels 0; Gaps 0
QY	1	GAGCTCACCCAGTCTCCATCTCCCTGTCTGSCCTCTGTAGAGACAGAGTCCATCACT	60
Db	4	GAGCTCACCCAGTCTCCATCTCCCTGTCTGSCATCTGTAGAGACAGAGTCCATCACT	63
QY	61	TGCCCCGACACTCAGAGATTAGACACCTATTTAATTGGTATCAGCAGAAAACCGGGGAG	120
Db	64	TGCCGGGACATCAGTACATTAGACAGCTATTTTAAATTGGTATCAGCAGAAAACCGAGGAAA	123
QY	121	GCCCCTAAGCTCTCGATCTGTAGTGCATCCAAATTGSCAAAGTGGGGTCCCATCCAGGTTT	180
Db	124	GCCCCATTCTCTGATCTATGCTGTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTT	183
QY	181	AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTTGAAGTC	240
Db	184	AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCAGCTGCAACTGAAGAT	243
QY	241	TTTTCGAAGTATCTACTGTCAACAGAGTTACACTACTTATATACCTTTGGCCCTTGGAGC	300
Db	244	TTTTCGAATTATCTACTGTCAACAGACTTACAGTTTCCCTAGACATTTTGGCCCTTGGAGC	303
QY	301	AAACTGGAGATCAAAACGA 318	
Db	304	AAAGTGATATCAAAACGA 321	

RESULT 15
US-09-240-274-105
; Sequence 105, Application US/09240274

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? TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
? TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
? FILE REFERENCE: 09596-4202
? CURRENT APPLICATION NUMBER: US/09/240, 274
? CURRENT FILING DATE: 1999-01-29
? EARLIER APPLICATION NUMBER: 60/081,380
? EARLIER FILING DATE: 1998-04-10
? EARLIER APPLICATION NUMBER: 60/028,550
? EARLIER FILING DATE: 1996-10-11
? NUMBER OF SEQ ID NOS: 224
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 105
? LENGTH: 321
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: anti-Rh(D) chain I05
US-09-240-274-105

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ORGANISM: *Homo sapiens*
FEATURE:

Query Match	84.4%	Score 268.4	DB 3	Length 321
Best Local Similarity	90.3%	Pred. No. 9e-83		
Match 287; Conservative	0	Mismatches 31	Indels 0	Gaps 0

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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:15:56 ; Search time 1958.75 Seconds
(without alignments)
6179.670 Million cell updates/sec

Title: US-10-027-725A-5
Perfect score: 318
Sequence: 1 gagctcaccagctctcatc.....ccaactcgagatcaacga 318

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: gb_est1:
2: gb_est2:
3: gb_hc3:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est1:
9: gb_ges82:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	270.6	85.1	422	2	AM407904 UI-HF-BLO
2	270.6	85.1	1084	6	CB986592 AGENCOURT
3	269	84.6	493	2	AM405753 UI-HF-BLO
4	269	84.6	624	6	CD690145 EST6668 h
5	269	84.6	770	4	BG685444 602637305
6	269	84.6	797	6	CB987347 AGENCOURT
7	267.4	84.1	525	6	CD705928 EST72455
8	267.4	84.1	750	6	CB985395 AGENCOURT
9	265.8	83.6	431	2	AM406886 UI-HF-BLO
10	265.8	83.6	693	6	CD684441 EST1961 hu
11	265.8	83.6	799	6	CB984750 AGENCOURT
12	265.8	83.6	819	6	CB985931 AGENCOURT
13	265.8	83.6	864	4	BG548281 602575248
14	265.8	83.6	933	4	BQ899146 AGENCOURT
15	265.8	83.6	992	5	BQ708832 AGENCOURT
16	264.2	83.1	391	2	AM404992 UI-HF-BLO
17	264.2	83.1	447	2	AM405752 UI-HF-BLO
18	264.2	83.1	487	2	AM405301 UI-HF-BLO
19	264.2	83.1	498	6	CD684450 EST970 hu
20	264.2	83.1	499	6	CD685478 EST1998 h
21	264.2	83.1	608	2	AM404714 UI-HF-BLO
22	264.2	83.1	619	6	CD693603 EST10126
23	264.2	83.1	724	6	CB959008 AGENCOURT
24	264.2	83.1	745	6	CB958128 AGENCOURT

25	264.2	83.1	748	6	CB956867	CB956867 AGENCOURT
26	262.8	82.6	471	2	AM406294	AM406294 UI-HF-BLO
27	262.6	82.6	550	6	CD709957	CD709957 EST26484
28	262.6	82.6	708	6	CB956923	CB956923 AGENCOURT
29	262.6	82.6	725	6	CB987519	CB987519 AGENCOURT
30	262.6	82.6	742	6	CB984723	CB984723 AGENCOURT
31	262.6	82.6	923	5	BQ882857	BQ882857 AGENCOURT
32	261.8	82.3	921	4	BG341239	BG341239 602463904
33	261.2	82.1	854	5	BX397739	BX397739 EST7739
34	261	82.1	598	6	CD692150	CD692150 EST8689 h
35	261	82.1	671	4	BM830977	BM830977 K-EST0104
36	261	82.1	684	4	BM769909	BM769909 K-EST0053
37	261	82.1	753	6	CB955708	CB955708 AGENCOURT
38	261	82.1	855	6	CB995312	CB995312 AGENCOURT
39	259.4	81.6	460	2	AM405906	AM405906 UI-HF-BLO
40	259.4	81.6	532	4	BM823145	BM823145 K-EST0094
41	259.4	81.6	566	2	AM406081	AM406081 UI-HF-BLO
42	259.4	81.6	743	6	CB957909	CB957909 AGENCOURT
43	259.4	81.6	754	6	CB986767	CB986767 AGENCOURT
44	259.4	81.6	762	6	CB958057	CB958057 AGENCOURT
45	259.4	81.6	793	6	CB987506	CB987506 AGENCOURT

ALIGNMENTS

RESULT 1
AM407904
LOCUS
DEFINITION
UI-HF-BLO-add-a-01-0-UI.r2 NIH MGC_37 Homo sapiens cDNA clone
IMAGE:3061128 5', mRNA sequence.
AM407904
ACCESSION
AM407904.1 GI:6926961
VERSION
AM407904.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 422)
NIH-MGC <http://mgs.nci.nih.gov/>.
NATIONAL INSTITUTE OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
JOURNAL
UNPUBLISHED (1999)
CONTACT: ROBERT STRAUSBERG, Ph.D.
COMMENT
Email: cgabs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Louis M. Staudt, M.D., Ph.D.
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLND at:
www-bio.illn.gov/bdnp/image/image.html
Seq primer: M13 Forward.

FEATURES

source
1..422
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3061128"
/cistype="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_id="NIH_MGC_37"
/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonafide, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
Query Match 85.1%; Score 270.6; DB 2; Length 422;
Best Local Similarity 90.9%; Pred. No. 9.2e-75;

	Matches	288;	Conservative	0;	Mismatches	29;	Indels	0;	Gaps	0;
Qy	2	AGCTCACCCAGTCTTCATCTCCCTGTCTGTCTGTGTGAGACAGAGTCAACATCACTT	61							
Db	30	AGATGACCCCAATCTCCATCTCCCTCTGTGTGATCTGTGTGAGACAGAGTCAACATCACTT	89							
Qy	62	GCCGGGACGTCAGAGTATTAGACCTATTATTAATTTGATATCAGACGAAACCGGGGAAAG	121							
Db	90	GCCGGGACGTCAGAGTATTAGACCTATTATTAATTTGATATCAGACGAAACCGGGGAAAG	149							
Qy	122	CCCCTAAGCTCCTGATCTGTAGTGATCCAAATTTTSCAAAGTGGGGTCCCATTCAGAGTTCA	181							
Db	150	CCCCTAAGCTCCTGATCTGTAGTGATCCAAATTTTSCAAAGTGGGGTCCCATTCAGAGTTCA	209							
Qy	182	GTGCGAGTGATCTTGGGACAGAGTTCACTCTTCACCATCAGCAATCTGCAACTGGAAGCT	241							
Db	210	GTGCGAGTGATCTTGGGACAGAGTTCACTCTTCACCATCAGCAAGTCTGCAACTGGAAGTT	269							
Qy	242	TTTGCAGTTACTACTGTCTCAACAGAGTTACACTTATATCTTTGGCCCTGGGACCA	301							
Db	270	TTTGCAGTTACTACTGTCTCAACAGAGTTACAGTATCCCGGTGACGTTTGGCCMAAGGACCA	329							
Qy	302	AACTGAGATCAAAACGA 318								
Db	330	AGGTGGAATCAAAACGA 346								

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RESULT 2
CB986592
LOCUS
DEFINITION
CB986592
ACCESSION
CB986592
VERSION
CB986592.1
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
REFERENCE
Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS
Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
TITLE
1 (bases 1 to 1084)
JOURNAL
NIH-MGC http://mgc.ncbi.nlm.gov/.
COMMENT
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing: Arrayed by: The I.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: NDCM134 row: n column: 06
High quality sequence stop: 330.
FEATURES
source
1..1084
location/Qualifiers

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30326813"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1ib="NH MGC 184"
/notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggcgcatatggcgc); Site_2: SfiI (ggcgccgcctggcgc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTAGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGGAGCGGCGACATC-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones

```

and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

RESULT 3					
LOCUS	AM405753				
DEFINITION	AM405753	493 bp	mRNA	linear	EST 16-FEB-2000
ACCESSION	U1-HF-BL0-abp-a-02-0-UI.r1 NIH_MGC_37			Homo sapiens	CDNA clone
VERSION	IMAGE:3057230 5'				mRNA sequence.
KEYWORDS	AM405753				
SOURCE	AM405753.1	GI:6924810			
ORGANISM	EST.				
	Homo sapiens (human)				
	Homo sapiens				
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 493)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D., Email: cgabbs@email.nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.linnl.gov/bdip/image/image.html Seq primer: M13 Forward.				

FEATURES	SOURCE
location/Qualifiers	
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/organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone="IMAGE:3057290"	
/tissue_type="lymph"	
/cell_type="germinal center B cells"	
/cell_line="MGC85"	
/lab_host="DH10B (LTI)"	
/clone_1b="NH_MGC_37"	
/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA"	

ORIGIN

(1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

Query Match 84.6%; Score 269; DB 2; Length 493;

Best Local Similarity 90.5%; Pred. No. 3.1e-74;

Matches 287; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 2 AGCTACCCAGTCCATCCCTCCGTCCTGTCGTGAGAGACAGAGTCAACATCTT 61
 DB 79 AGATGACCCAGTCTCCATCCCTCCGTCCTGTCGTGAGAGACAGAGTCAACATCTT 138
 QY 62 GCCGGGCAAGTCAGAGATTTAGACCTATTTAAATTTGGTATCAGAGAAACAGGGAAG 121
 DB 139 GCCGGGCAAGTCAGAGATTTAGACCTATTTAAATTTGGTATCAGAGAAACAGGGAAG 198
 QY 122 CCCCTAAGCTCTGATCTGATGATGATCAATTTGCAAAAGTGGGTCCTCATCAAGTTCA 181
 DB 199 CCCCTAAGCTCTGATCTGATGATGATCAATTTGCAAAAGTGGGTCCTCATCAAGTTCA 258
 QY 182 GTGGCAGTGTCTGGGACAGATTTCACTTCACATCAGATCTGCAACCTGAAGACT 241
 DB 259 GTGGCAGTGTCTGGGACAGATTTCACTTCACATCAGATCTGCAACCTGAAGACT 318
 QY 242 TTGCAAGTCTACTGTCAACAGAGTTACATCTTATATACCTTGCCCTGGGACCA 301
 DB 319 TTGCAAGTCTACTGTCAACAGAGTTACATCTTATATACCTTGCCCTGGGACCA 378
 QY 302 AACTGAGATCAACGA 318
 DB 379 AGTGAATCAACGA 395

RESULT 4 624 bp mRNA linear EST 25-JUN-2003
 LOCUS CD690145
 DEFINITION EST6668 human nasopharynx Homo sapiens cDNA, mRNA sequence.
 ACCESSION CD690145
 VERSION CD690145.1 GI:32210615

KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 624)
 AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-Y., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
 TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
 JOURNAL Unpublished (2003)

COMMENT Contact: Yixin Zeng
 Cancer Center
 Sun Yat-sen University
 651 Dongfeng Road East, Guangzhou 510060, China
 Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506
 Email: yxzeng@gszums.edu.cn

FEATURES
 source
 Location/Qualifiers
 1..624
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cfeature_type="normal nasopharynx"
 /clone_lib="human nasopharynx"
 /note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 84.6%; Score 269; DB 6; Length 624;

Best Local Similarity 90.5%; Pred. No. 3.4e-74;

Matches 287; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 2 AGCTACCCAGTCTCCATCCCTCCGTCCTGTCGTGAGAGACAGAGTCAACATCTT 61

DB 121 AGATGACCCAGTCTCCATCCCTCCGTCCTGTCGTGAGAGACAGAGTCAACATCTT 180
 QY 62 GCCGGGCAAGTCAGAGATTTAGACCTATTTAAATTTGGTATCAGAGAAACAGGGAAG 121
 DB 181 GCCGGGCAAGTCAGAGATTTAGACCTATTTAAATTTGGTATCAGAGAAACAGGGAAG 240
 QY 122 CCCCTAAGCTCTGATCTGATGATGATCAATTTGCAAAAGTGGGTCCTCATCAAGTTCA 181
 DB 241 CCCCTAAGCTCTGATCTGATGATGATCAATTTGCAAAAGTGGGTCCTCATCAAGTTCA 300
 QY 182 GTGGCAGTGTCTGGGACAGATTTCACTTCACATCAGATCTGCAACCTGAAGACT 241
 DB 301 GTGGCAGTGTCTGGGACAGATTTCACTTCACATCAGATCTGCAACCTGAAGACT 360
 QY 242 TTGCAAGTCTACTGTCAACAGAGTTACATCTTATATACCTTGCCCTGGGACCA 301
 DB 361 TTGCAAGTCTACTGTCAACAGAGTTACATCTTATATACCTTGCCCTGGGACCA 420
 QY 302 AACTGAGATCAACGA 318
 DB 421 AGTGAATCAACGA 437

RESULT 5 770 bp mRNA linear EST 01-MAY-2001
 LOCUS BG685444
 DEFINITION 602637305F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4765129 5', mRNA sequence.

ACCESSION BG685444
 VERSION BG685444.1 GI:13916841
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 770)
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITLE NIH-MGC http://mgi.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at:
 http://image.llnl.gov

Plate: L10M1623 row: 1 column: 02
 High quality sequence stop: 713.
 Location/Qualifiers
 1..770
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_image="4765129"
 /cfeature_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 48"
 /note="Organ: B-cells; Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

FEATURES
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 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_image="4765129"
 /cfeature_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 48"
 /note="Organ: B-cells; Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 84.6%; Score 269; DB 4; Length 770;

Best Local Similarity 90.5%; Pred. No. 3.6e-74;

QY 2 AGCTACCCAGTCTCCATCCCTCCGTCCTGTCGTGAGAGACAGAGTCAACATCTT 61

Matches 287; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 2 AGCTACCCAGTCTTCATCTCTCTGCTGCTGAGAGACAGAGTCACTT 61
|||
Db 80 AGATGACCCAGTCTTCATCTCTCTGCTGCTGAGAGACAGAGTCACTT 139
|||
Qy 62 GCCGGGACGTCAGAGTATAGACCTTAAATGCTATCAGAGAAACCGGGAAG 121
|||
Db 140 GCCGGGACGTCAGAGTATAGACCTTAAATGCTATCAGAGAAACCGGGAAG 199
|||
Qy 122 CCCCTAAGCTCTGATCTGATGATCCTATTCGAAAGTGGGCTCCATCAGATTCA 181
|||
Db 200 CCCCTAAGCTCTGATCTGATGATCCTATTCGAAAGTGGGCTCCATCAGATTCA 259
|||
Qy 182 GTGCGAGTGATCTGGGACAGAGTTCACTCTCACCATCAGAACTCGCACTGAAGCT 241
|||
Db 260 GTGCGAGTGATCTGGGACAGAGTTCACTCTCACCATCAGAACTCGCACTGAAGTT 319
|||
Qy 242 TTGCAAGTACTACTCTGCAACAGAGTTCACTCTTATACCTTGGGCTCCGAGCA 301
|||
Db 320 TTGCAAGTACTACTCTGCAACAGAGTTCACTCTTATACCTTGGGCTCCGAGCA 379
|||
Qy 302 AACTGAGATCAAAACA 318
|||
Db 380 AAGTGATATCAAAACA 396
|||

RESULT 6
CB987347 797 bp mRNA linear EST 01-MAY-2003
LOCUS AGENCOURT_13591809 NIH_MGC_184 Homo sapiens cDNA clone
DEFINITION IMAGE:30326300 5', mRNA sequence.
ACCESSION CB987347
VERSION CB987347.1 GI:30281867
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgsb@rcmail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILMN at:
http://image.llnl.gov
Plate: NDCM133 row: h column: 21
High quality sequence stop: 437.
Location/Qualifiers

FEATURES
SOURCE

1..797
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30326300"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccatcgcc); Site_2: SfiI (ggccgccgccc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCATATGAGC-3' and 3' adaptor sequence:
5'-ATTTCAGAGCGCCGCGCAGCATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 84.6%; Score 269; DB 6; Length 797;
Best Local Similarity 90.5%; Pred. No. 3.6e-74;
Matches 287; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 2 AGCTACCCAGTCTTCATCTCTCTGCTGCTGAGAGACAGAGTCACTT 61
|||
Db 106 AGATGACCCAGTCTTCATCTCTCTGCTGCTGAGAGACAGAGTCACTT 165
|||
Qy 62 GCCGGGACGTCAGAGTATAGACCTTAAATGCTATCAGAGAAACCGGGAAG 121
|||
Db 166 GCCGGGACGTCAGAGTATAGACCTTAAATGCTATCAGAGAAACCGGGAAG 225
|||
Qy 122 CCCCTAAGCTCTGATCTGATGATCCTATTCGAAAGTGGGCTCCATCAGATTCA 181
|||
Db 226 CCCCTAAGCTCTGATCTGATGATCCTATTCGAAAGTGGGCTCCATCAGATTCA 285
|||
Qy 182 GTGCGAGTGATCTGGGACAGAGTTCACTCTCACCATCAGAACTCGCACTGAAGCT 241
|||
Db 286 GTGCGAGTGATCTGGGACAGAGTTCACTCTCACCATCAGAACTCGCACTGAAGTT 345
|||
Qy 242 TTGCAAGTACTACTCTGCAACAGAGTTCACTCTTATACCTTGGGCTCCGAGCA 301
|||
Db 346 TTGCAAGTACTACTCTGCAACAGAGTTCACTCTTATACCTTGGGCTCCGAGCA 405
|||
Qy 302 AACTGAGATCAAAACA 318
|||
Db 406 AAGTGATATCAAAACA 422
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RESULT 7
CD705928 525 bp mRNA linear EST 25-JUN-2003
LOCUS EST22455 human nasopharynx Homo sapiens cDNA, mRNA sequence.
DEFINITION CD705928
ACCESSION CD705928
VERSION CD705928.1 GI:32236558
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-X., Pan, Z.-G. and
Zeng, Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers

FEATURES
SOURCE

1..525
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match 84.1%; Score 267.4; DB 6; Length 525;
Best Local Similarity 90.2%; Pred. No. 1e-73;
Matches 286; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 2 AGCTACCCAGTCTTCATCTCTCTGCTGCTGAGAGACAGAGTCACTT 61
|||

Db 124 AGATGACCCAGTCTTCATCTCCCTGTGTCATCTGTAGAGACAGACATCCATCACTT 183
Qy 62 GCCGGGACGTCAGAGATTAGACACCTATTAAATTTGGTATCAGACAAAACCGGGGAAG 121
Db 184 GCCGGGACGTCAGAGATTAGACACCTATTAAATTTGGTATCAGACAAAACCGGGGAAG 243
Qy 122 CCCCTAAGCTTCGATCTGTAGTCATCCAAATTTGCAAGTGGGGTCCCATCCAGTTCA 181
Db 244 CCCCTAAGCTTCGATCTGTAGTCATCCAAATTTGCAAGTGGGGTCCCATCCAGTTCA 303
Qy 182 GTGCGATGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCACCTGAAGACT 241
Db 304 GTGCGATGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCACCTGAAGACT 363
Qy 242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTGCGCCCTGGACCA 301
Db 364 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTGCGCCCTGGACCA 423
Qy 302 AACTGAGATCAAAACA 318
Db 424 AACTGAGATCAAAACA 440

RESULT 8
LOCUS CB985395
DEFINITION AGENCOURT 13643437 NIH_MGC_184 Homo sapiens cDNA clone
IMAGE:3028513 5', mRNA sequence.

ACCESSION CB985395
VERSION CB985395.1 GI:30279919
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 750)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: NDCM139 row: e column: 02
High quality sequence stop: 555.

FEATURES
Source
1..750
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3028513"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccatctggcc); Site_2: SfiI (ggccggccggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies containing inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 84.1%; Score 267.4; DB 6; Length 750;
Best Local Similarity 90.2%; Pred. No. 1.1e-73;
Matches 286; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 2 AGCTACCCAGTCTCCATCTCCCTGTGTCATCTGTAGAGACAGATCCATCACTT 61
Db 104 AGATGACCCAGTCTTCATCTCCCTGTGTCATCTGTAGAGACAGATCCATCACTT 163
Qy 62 GCCGGGACGTCAGAGATTAGACACCTATTAAATTTGGTATCAGACAAAACCGGGGAAG 121
Db 164 GCCGGGACGTCAGAGATTAGACACCTATTAAATTTGGTATCAGACAAAACCGGGGAAG 223
Qy 122 CCCCTAAGCTTCGATCTGTAGTCATCCAAATTTGCAAGTGGGGTCCCATCCAGTTCA 181
Db 244 CCCCTAAGCTTCGATCTGTAGTCATCCAAATTTGCAAGTGGGGTCCCATCCAGTTCA 283
Qy 182 GTGCGATGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCACCTGAAGACT 241
Db 284 GTGCGATGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCACCTGAAGACT 343
Qy 242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTGCGCCCTGGACCA 301
Db 344 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTGCGCCCTGGACCA 403
Qy 302 AACTGAGATCAAAACA 318
Db 404 AACTGAGATCAAAACA 420

RESULT 9
LOCUS AM406886
DEFINITION UT-HF-BLD-a49-b-06-0-UT_r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3061499 5', mRNA sequence.

ACCESSION AM406886
VERSION AM406886.1 GI:6925943
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 431)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staedt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bdrrp/image/image.html
Seq primer: M13 Forward.

FEATURES
Source
1..431
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3061499"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_37"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staedt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 83.6%; Score 265.8; DB 2; Length 431;
Best Local Similarity 89.9%; Pred. No. 3.1e-73;
Matches 285; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2 AGCTCACCAGCTCCATCCCTCCCTGCTGCTGCTGATGAGACAGATCCATCACTT 61
DB 67 AGATGACCCAGCTCCATCCCTCCCTGCTGCTGATGAGACAGATCCATCACTT 126
QY 62 GCCCGGACGTCAGAGTATTAGACCTTAATTTAAATGATACAGAGAAACCGGGAAG 121
DB 127 GCCCGGACGTCAGAGTATTAGACCTTAAATGATACAGAGAAACCGGGAAG 186
QY 122 CCCCTAAGCTCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 181
DB 187 CCCCTAAGCTCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 246
QY 182 GTGGCAGTGTATCTGGGACAGAGTCTCTCAGCATAGCATCTGCAACCTGAAGACT 241
DB 247 GTGGCAGTGTATCTGGGACAGAGTCTCTCAGCATAGCATCTGCAACCTGAAGACT 306
QY 242 TTGCAAGTATTACTGTGTCAGAGATTACTACTATATACCTTCCGCGCTGGAGCA 301
DB 307 TTGCAAGTATTACTGTGTCAGAGATTACTACTATATACCTTCCGCGCGGAGGACCA 366
QY 302 AACTGAGATCAAAACA 318
DB 367 AGGTGAGATCAAAACA 383

RESULT 10
CD684441 693 bp mRNA linear EST 25-JUN-2003
LOCUS CD684441
DEFINITION EST961 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD684441
VERSION CD684441.1 GI:32199435
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 693)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsun.edu.cn.

FEATURES
source
1..693
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN
Query Match 83.6%; Score 265.8; DB 6; Length 693;
Best Local Similarity 89.9%; Pred. No. 3.6e-73;
Matches 285; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2 AGCTCACCAGCTCTCCATCCCTCCCTGCTGCTGATGAGACAGATCCATCACTT 61
DB 127 AGATGACCCAGCTCTCCATCCCTCCCTGCTGCTGATGAGACAGATCCATCACTT 186
QY 62 GCCCGGACGTCAGAGTATTAGACCTTAATTTAAATGATACAGAGAAACCGGGAAG 121

DB 187 GCCCGGACCCAGAGATTAAGCCGCTATTAAATGATACAGAGAAACCGGGAAG 246
QY 122 CCCCTAAGCTCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 181
DB 247 CCCCTAAGCTCTGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 306
QY 182 GTGGCAGTGTATCTGGGACAGAGTCTCTCAGCATAGCATCTGCAACCTGAAGACT 241
DB 307 GTGGCAGTGTATCTGGGACAGAGTCTCTCAGCATAGCATCTGCAACCTGAAGACT 366
QY 242 TTGCAAGTATTACTGTGTCAGAGATTACTACTATATACCTTCCGCGCTGGAGCA 301
DB 367 TTGCAAGTATTACTGTGTCAGAGATTACTACTATATACCTTCCGCGGAGGACCA 426
QY 302 AACTGAGATCAAAACA 318
DB 427 AGGTGAGATCAAAACA 443

RESULT 11
CB984750 799 bp mRNA linear EST 01-MAY-2003
LOCUS CB984750
DEFINITION IMAGE:30326373 5', mRNA sequence.
ACCESSION CB984750
VERSION CB984750.1 GI:30279274
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 799)
AUTHORS NIH-MGC http://imgc.ncbi.nih.gov/
TITLE NIH-MGC
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palokovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: NDCM133 row: k column: 22
High quality sequence stop: 412.

FEATURES
source
1..799
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30326373"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccatcatgccc); Site_2: SfiI (ggccctccgccc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' adaptor
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTAATGCCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCCGGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 83.6%; Score 265.8; DB 6; Length 799;
Best Local Similarity 89.9%; Pred. No. 3.6e-73;
Matches 285; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

[illegible]

ORIGIN	CA . Note: this is a NIH_MGC Library."
Query Match	83.6%; Score 265.8; DB 6; Length 819;
Best Local Similarity	89.9%; Pred. No. 3.8e-73;
Matches 285; Conservative	0; Mismatches 32; Indels 0; Gaps 0;
QY	2 AGCTCACCAGTCTCCATCCCTCCCTGCTCTGTAGAGAGACAGATCCATTCCTT 61
DB	104 AGATGACCCAGTCTCCATCCCTCCCTGCTGTAGAGAGACAGATCCATTCCTT 163
QY	62 GCCGGGACGTCAGAGATTAGCAGCATTTAAATTGGTATCAGCAGAAACCGGGGAAG 121
DB	164 GCCGGGACGTCAGAGATTAGCAGCATTTAAATTGGTATCAGCAGAAACCGGGGAAG 223
QY	122 CCCCTAAGCTCTGATCTGTAGTCATCCAAATTTGCCAAAGTGGGATCCCATCCAGTTCA 181
DB	224 CCCCTAAGCTCTGATCTGTAGTCATCCAAATTTGCCAAAGTGGGATCCCATCCAGTTCA 283
QY	182 GTGCAAGTGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTTGAAGCT 241
DB	284 GTGCAAGTGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTTGAAGCT 343
QY	242 TTGCAAGTTACTACTGTCAACAGTTNCACTACTTATATACCTTGGGCCCTGGGACCA 301
DB	344 TTGCAAGTTACTACTGTCAACAGTTNCACTACTTATATACCTTGGGCCCTGGGACCA 403
QY	302 AACTGGAGATCAAAACA 318
DB	404 AGGTGAAATCAAAACA 420

RESULT	13
LOCUS	BG548281
DEFINITION	BG548281 864 bp mRNA linear EST 04-APR-2001
ACCESSION	60257524861 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4703483 5 ,
VERSION	RNA sequence.
KEYWORDS	BG548281
SOURCE	BG548281.1 GI:13546946
ORGANISM	EST.
	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL	1 (bases 1 to 864)
COMMENT	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: LNCMI541 row: p column: 12 High quality sequence stop: 726.
FEATURES	
SOURCE	Location/Qualifiers 1..864 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4703483" /lab_host="DH10B (TI phage-resistant)" /clone_id="NIH_MGC_77" /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site: 1: 5'fl (ggcgccctcgccc) ; Site 2: 5'fl (ggccattatgccc) ; 5' and 3' adaptor were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGCGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGCGGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9

kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 83.6%; Score 265.8; DB 4; Length 864;
Best Local Similarity 89.9%; Pred. No. 3.9e-73;
Matches 285; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2 AGCTCACCACAGTCTCCATCCCTGCTGCTGTGGAGACAGAGTCAACATCACTT 61
DB 100 AGATGACCCAGTCTCCATCCCTGCTGCTGTGGAGACAGAGTCAACATCACTT 159
QY 62 GCCGGGACGTCAGAGTATTGACACTATTAAATGGTATCAGAGAAACGAGGAAAG 121
DB 160 GCCGGGACGTCAGAGTATTGACACTATTAAATGGTATCAGAGAAACGAGGAAAG 219
QY 122 CCCCTAAGCTCTGATCTGTAGTGCATTCATTTGGCAAGTGGGGTCCCATCCAGTTCA 181
DB 220 CCCCTAAGCTCTGATCTGTAGTGCATTCATTTGGCAAGTGGGGTCCCATCCAGTTCA 279
QY 182 GTGGCAGTGCATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCACCTGAAAGT 241
DB 280 GTGGCAGTGCATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCACCTGAAAGT 339
QY 242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTGCGCCCTGGAGCA 301
DB 340 TTGCAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTGCGCCCTGGAGCA 399
QY 302 AACTGAGATCAAAACA 318
DB 400 CGGTGAGATCAAAACA 416

RESULT 14

BO899146

933 bp mRNA linear EST 16-AUG-2002

LOCUS

AGENCOURT 8585624 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6302530

DEFINITION

5', mRNA sequence.

ACCESSION

BO899146

VERSION

BO899146.1 GI:22291160

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov

FEATURES

CDNA Library Preparation: Rubin Laboratory

SOURCE

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DEFINITION

DNA Sequencing by: Agencourt Bioscience Corporation

AUTHORS

Clone distribution: MGC clone distribution information can be

TITLE

found through the I.M.A.G.E. Consortium/LNLN at:

JOURNAL

http://image.llnl.gov

COMMENT

Plate: LNCM2520 row: c column: 11

FEATURES

High quality sequence start: 9

SOURCE

Location/Qualifiers

DEFINITION

1..933

AUTHORS

/organism="Homo sapiens"

TITLE

/mol_type="mRNA"

JOURNAL

/db_xref="taxon:9606"

COMMENT

/clone="IMAGE:6302530"

FEATURES

/lab_host="DH10B (phage-resistant)"

SOURCE

/clone_lib="NIH_MGC_113"

DEFINITION

/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:

AUTHORS

EcoRI; CDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 83.6%; Score 265.8; DB 5; Length 933;
Best Local Similarity 89.9%; Pred. No. 4e-73;
Matches 285; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2 AGCTCACCACAGTCTCCATCCCTGCTGCTGTGGAGACAGAGTCAACATCACTT 61
DB 101 AGATGACCCAGTCTCCATCCCTGCTGCTGTGGAGACAGAGTCAACATCACTT 160
QY 62 GCCGGGACGTCAGAGTATTGACACTATTAAATGGTATCAGAGAAACGAGGAAAG 121
DB 161 GCCGGGACGTCAGAGTATTGACACTATTAAATGGTATCAGAGAAACGAGGAAAG 220
QY 122 CCCCTAAGCTCTGATCTGTAGTGCATTCATTTGGCAAGTGGGGTCCCATCCAGTTCA 181
DB 221 CCCCTAAGCTCTGATCTGTAGTGCATTCATTTGGCAAGTGGGGTCCCATCCAGTTCA 280
QY 182 GTGGCAGTGCATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCACCTGAAAGT 241
DB 281 GTGGCAGTGCATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCACCTGAAAGT 340
QY 242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTGCGCCCTGGAGCA 301
DB 341 TTGCAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTGCGCCCTGGAGCA 400
QY 302 AACTGAGATCAAAACA 318
DB 401 AGGTGAATCAAAACA 417

RESULT 15

BQ708832

992 bp mRNA linear EST 16-JUL-2002

LOCUS

AGENCOURT 8353479 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6279561

DEFINITION

5', mRNA sequence.

ACCESSION

BQ708832

VERSION

BQ708832.1 GI:21847731

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov

FEATURES

Tissue Procurement: Dr. Mark Watson

SOURCE

CDNA Library Preparation: Rubin Laboratory

DEFINITION

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

AUTHORS

DNA Sequencing by: Agencourt Bioscience Corporation

TITLE

Clone distribution: MGC clone distribution information can be

JOURNAL

found through the I.M.A.G.E. Consortium/LNLN at:

COMMENT

http://image.llnl.gov

FEATURES

Plate: LNCM2469 row: f column: 10

SOURCE

High quality sequence start: 5

DEFINITION

1..992

AUTHORS

Location/Qualifiers

TITLE

/organism="Homo sapiens"

JOURNAL

/mol_type="mRNA"

COMMENT

/db_xref="taxon:9606"

FEATURES

/clone="IMAGE:6279561"

SOURCE

/lab_host="DH10B (phage-resistant)"

DEFINITION

/clone_lib="NIH_MGC_113"

/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 83.6%; Score 265.8; DB 5; Length 992;
Best Local Similarity 89.9%; Pred. No. 4e-73;
Matches 285; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY	2	AGCTACCCAGCTTCATCTCCCTGTCGCTGTAGAGACAGAGTCACCATCACTT	61
Db	105	AGATGACCCAGCTTCATCTCCCTGTCGCTGTAGAGACAGAGTCACCATCACTT	164
QY	62	GCCGGGACGTCAGATTTAGCACCTATTAAATTGGTATCAGCAGAAACCGGGGAAG	121
Db	165	GCCGGGCAAGTCAGATTTAGCACCTTTAAATTGGTATCAGCAGAAACCGGGAAG	224
QY	122	CCCCAAGCTCTGATCTGTAGTCATTTGGCAAGTGGGGTCCCATCCAGGTCA	181
Db	225	CCCCCTCTCTGTGATCTTGTGTCATCAATTGCAAGTGGGGTCCCATCAAGGTCA	284
QY	182	GTGGCAGTGATCTGGACAGAGTTCACTTCACCATCAGCAATCTGCAACTGAAACT	241
Db	285	GTGGCAGTGATCTGGACAGATTTCACTTCACCATCAGCCGCTGCAACTGAAAGTT	344
QY	242	TTGCAAGTTACTTCTGTCACAGAGTTACACTTATATACCTTGGGCTTGGACCA	301
Db	345	TTGCAACTTACTTACTGTCACAGAGTTACATTAACCCCTGGACGTTTGGCCAAGGACCA	404
QY	302	AACTGGAGATCAAAAGA	318
Db	405	AGTGGAAATCAAAAGA	421

Search completed: July 27, 2005, 12:32:12
Job time : 1959.75 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 03:58:31 ; Search time 299.048 Seconds
(without alignments)
6294.891 Million cell updates/sec

Title: US-10-027-725A-5
Perfect score: 318
Sequence: 1 gagctcaccacgcgtccatc.....ccaactcgagatcaacga 318

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	316.4	99.5	318	6	ABK89641
2	276.4	86.9	321	5	AAH68647
3	276.4	86.9	321	5	AAH68701
4	276.4	86.9	321	9	ACD45311
5	276.4	86.9	321	9	ACD45365
6	273.2	85.9	321	5	AAV19761
7	273.2	85.9	321	5	AAH68720
8	273.2	85.9	321	5	AAH68658
9	273.2	85.9	321	5	AAH68652
10	273.2	85.9	321	5	AAH68713
11	273.2	85.9	321	5	AAH68703
12	273.2	85.9	321	9	ACD45377
13	273.2	85.9	321	9	ACD45367
14	273.2	85.9	321	9	ACD45384
15	273.2	85.9	321	9	ACD45316
16	273.2	85.9	321	9	ACD45322
17	272.2	85.6	735	13	ADR23329
18	272.2	85.6	735	13	ADR23331
19	272.2	85.6	735	13	ADR23317
20	272.2	85.6	736	12	ADH34564

21	272.2	85.6	738	13	ADR23319
22	272.2	85.6	750	13	ADR23321
23	272.2	85.6	750	13	ADR23325
24	271.6	85.4	321	5	AAH68723
25	271.6	85.4	321	5	AAH68651
26	271.6	85.4	321	5	AAH68724
27	271.6	85.4	321	5	AAH68707
28	271.6	85.4	321	9	ACD45371
29	271.6	85.4	321	9	ACD45388
30	271.6	85.4	321	9	ACD45387
31	271.6	85.4	321	9	ACD45315
32	271.2	85.3	720	2	AAH68700
33	271.2	85.3	720	10	ABZ76706
34	271.2	85.3	720	12	ADL92368
35	271.2	85.3	720	12	ADQ77166
36	270.6	85.1	396	2	AAT75423
37	270	84.9	321	5	AAH68717
38	270	84.9	321	5	AAH68719
39	270	84.9	321	9	ACD45383
40	270	84.9	321	9	ACD45381
41	269.2	84.7	321	12	ADL93583
42	269	84.6	729	3	AAH1630
43	269	84.6	729	6	ABL46009
44	268.4	84.4	321	5	AAH68650
45	268.4	84.4	321	9	ACD45314

ALIGNMENTS

RESULT 1	
ABK89641	
ID	ABK89641 standard; DNA; 318 BP.
XX	ABK89641;
AC	
XX	21-OCT-2002 (first entry)
DT	
XX	DNA encoding human IGE Fab clone 60 light chain.
XX	
KW	Human; fab; ds; gene; anti-allergic; vaccine; grass pollen; Phi p 2;
KW	timothy grass pollen allergen; passive immunotherapy.
XX	
OS	Homo sapiens.
XX	
XX	Location/Qualifiers
FT	1..318
FT	/product= "Fab clone 60 heavy chain"
FT	/transl_except= (pos:292..294, aa:Ser)
FT	7..63
FT	/*tag= b
FT	/note= "FRI region"
FT	64..96
FT	/*tag= c
FT	/note= "CDR1 region"
FT	97..141
FT	/*tag= d
FT	/note= "FRI region"
FT	142..162
FT	/*tag= e
FT	/note= "CDR2 region"
FT	163..258
FT	/*tag= f
FT	/note= "FRI region"
FT	259..285
FT	/*tag= g
FT	/note= "CDR3 region"
XX	
PN	WO200253595-A1.
XX	
XX	Adt23319 Human CD7
XX	Adt23321 Human CD7
XX	Adt23325 Human CD7
XX	Adt23317 Human CD7
XX	Adh34564 scfv SC02
XX	11-JUL-2002.

PF 27-DEC-2001; 2001MO-SE002908.
XX
XX 29-DEC-2000; 2000SE-00004892.
XX
XX (PHAA) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
XX WPI; 2002-583604/62.
DR P-PSDB; ABG30449.
XX
XX
PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs; useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
XX
PS Disclosure; Page 35; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have anti-allergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to Phl p 2 (a major Timothy grass pollen allergen). The group
CC 2 allergen-specific Fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The Fabs
CC - or a vaccine against a type I allergy is useful for diagnosing a type
CC I allergy. The allergen-specific Fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IgE antibodies to Phl p 2. The present sequence represents the DNA
CC encoding the human IgE Fab, clone 60 light chain protein of the invention
XX
SQ Sequence 318 BP; 83 A; 89 C; 72 G; 74 T; 0 U; 0 Other;

Query Match 99.5%; Score 316.4; DB 6; Length 318;
Best Local Similarity 99.7%; Pred. No. 1.4e-91;
Matches 317; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGTCAACCCAGTCTCCATCTCCCTGTCGTCGTAGAGAGACAGATCCATCACT 60
Db 1 GAGGTCAACCCAGTCTCCATCTCCCTGTCGTCGTAGAGAGACAGATCCATCACT 60

QY 61 TGGCGGGACGCTCAAGATTAGACACTATTAAATTGGATTCAGCAGAAAACCGGGAG 120
Db 61 TGGCGGGACGCTCAAGATTAGACACTATTAAATTGGATTCAGCAGAAAACCGGGAG 120

QY 121 GCCCCTTAAGCTCTGATCTGTAGTCATCAATTGGCAAATGGGGTCCCATCCAGGTTT 180
Db 121 GCCCCTTAAGCTCTGATCTGTAGTCATCAATTGGCAAATGGGGTCCCATCCAGGTTT 180

QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCAACCTGAAGAC 240
Db 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCAACCTGAAGAC 240

QY 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACTATATACCTTGGGCTGGAGCC 300
Db 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACTATATACCTTGGGCTGGAGCC 300

QY 301 AAATCGAGATCAACGCA 318
Db 301 AAATCGAGATCAACGCA 318

RESULT 2
ID AAH68647 standard; DNA; 321 BP.
XX
XX AAH68647;
XX
DT 14-SEP-2001 (first entry)
XX

DE Human anti-Rh(D) chain I02 nucleotide sequence.
XX
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic; db.
XX
XX Homo sapiens.
OS
PN US6255455-B1.
XX
XX 03-JUL-2001.
PD
XX
XX 29-JAN-1999; 99US-00240274.
PF
XX 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
XX
XX (UTPE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
PI
XX WPI; 2001-388931/41.
DR P-PSDB; AAG93590.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
PS Example 2; Col 54; 162pp; English.
XX
XX The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH6876 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;

Query Match 86.9%; Score 276.4; DB 5; Length 321;
Best Local Similarity 91.8%; Pred. No. 1.1e-78;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GAGGTCAACCCAGTCTCCATCTCCCTGTCGTCGTAGAGAGACAGATCCATCACT 60
Db 4 GAGGTCAACCCAGTCTCCATCTCCCTGTCGTCGTAGAGAGACAGATCCATCACT 63

QY 61 TGGCGGGACGCTCAAGATTAGACACTATTAAATTGGATTCAGCAGAAAACCGGGAG 120
Db 61 TGGCGGGACGCTCAAGATTAGACACTATTAAATTGGATTCAGCAGAAAACCGGGAG 123

QY 121 GCCCCTTAAGCTCTGATCTGTAGTCATCAATTGGCAAATGGGGTCCCATCCAGGTTT 180
Db 121 GCCCCTTAAGCTCTGATCTGTAGTCATCAATTGGCAAATGGGGTCCCATCCAGGTTT 183

QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCAACCTGAAGAC 240
Db 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCAACCTGAAGAC 243

QY 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACTATATACCTTGGGCTGGAGCC 300
Db 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACTATATACCTTGGGCTGGAGCC 303

QY 301 AAATCGAGATCAACGCA 318
Db 301 AAATCGAGATCAACGCA 321


```
RESULT 3
AAH68701
ID AAH68701 standard; DNA; 321 BP.
XX
XX AAH68701;
AC
XX
XX 14-SEP-2001 (first entry)
DT
XX
XX Human anti-Rh(D) antibody clone SH13 nucleotide sequence.
DE
XX
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic; de.
XX
XX Homo sapiens.
OS
XX US6255455-B1.
PN
XX 03-JUL-2001.
PD
XX
XX 29-JAN-1999; 99US-00240274.
PF
XX
XX 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
XX
XX (TYPE-) UNIV PENNSYLVANIA.
PA
XX
XX Siegel DL;
PI
XX
XX WPI; 2001-388931/41.
DR P-PSDB; AAG93644.
XX
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX Example 3; Col 74; 162pp; English.
XX
XX The present invention describes an isolated Rh(D) binding protein,
XX preferably a human antibody, (I) having an amino acid sequence comprising
XX one of the sequences (S) given in AAG93558 to AAG93669. (I) has
XX immunostimulant activity, and can be used as an immune system stimulant.
XX (I) can be used in diagnostic and therapeutic medicine. The antibodies
XX are used in diagnostics that require human antibodies instead of animal
XX antibodies, such as determine the Rh phenotype of human red blood cells.
XX AAH68615 to AAH68726 represent the nucleotide sequence which encode
XX AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
XX chain CDR3 amino acid sequences which are given in the exemplification of
XX the present invention
XX
XX Sequence 321 BP; 84 A; 89 C; 74 G; 74 T; 0 U; 0 Other;
SQ
Query Match 86.9%; Score 276.4; DB 5; Length 321;
Best Local Similarity 91.8%; Pred. No. 1.1e-78;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Oy 1 GAGCTCACCAGTCTCCATCTCTCTGCTGCTGTAAGAGACAGATCACCATCACT 60
Db 4 GAGCTCACCAGTCTCCATCTCTCTGCTGCTGTAAGAGACAGATCACCATCACT 63
Oy 1 TGCCGGGAGAGTCAAGATTAAGACCTATTAAATGGTATCAGACAGAAACCGGGAG 120
Db 64 TGCCGGGAGAGTCAAGATTAAGACCTATTAAATGGTATCAGACAGAAACCGGGAG 123
Oy 121 GCCCTAAGCTCTGATCTGTAGTGCATCCATTGCAAGTGGGTCCTCATCCAGTTC 180
Db 124 GCCCTAAGCTCTGATCTGTAGTGCATCCATTGCAAGTGGGTCCTCATCCAGTTC 183
Oy 181 AGTGCAGTGTATCTGGGACAGATTTCATCTCCACATCAGCAGTCTGCAACTGAAGAT 240
Db 184 AGTGCAGTGTATCTGGGACAGATTTCATCTCCACATCAGCAGTCTGCAACTGAAGAT 243
Oy 241 TTGCAAGTACTACTGTCAACAGATTACATCACTTATATACCTTGGCCCTGGGACC 300
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Db 244 TTGCAACTTACTACTGTCAACAGATTACATCACTTATATACCTTGGCCGAGACC 303
Oy 301 AAAGTGGAGATCAACAGA 318
Db 304 AAGCTGGAGATCAACAGA 321

RESULT 4
ACD45311
ID ACD45311 standard; DNA; 321 BP.
XX
XX ACD45311;
AC
XX
XX 12-SEP-2003 (first entry)
DT
XX
XX Anti-Rh(D) chain 102 DNA.
DE
XX
XX Human; de; gene; Rh(D) binding protein; blood typing; blood product;
KW magnetically activated cell sorting.
XX
XX Homo sapiens.
OS
XX US2003040605-A1.
PN
XX
XX 27-FEB-2003.
PD
XX
XX 04-MAY-2001; 2001US-00848798.
PF
XX
XX 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX
XX (TYPE-) UNIV PENNSYLVANIA.
PA
XX
XX Siegel DL;
PI
XX
XX WPI; 2003-512273/48.
DR P-PSDB; ABO27397.
XX
XX
XX New human Rh(D)-binding protein useful for various diagnostic and
XX therapeutic applications, including typing of blood or blood products.
XX
XX Claim 12; Page 39; 187pp; English.
XX
XX The invention relates to an isolated Rh(D) binding protein. The protein
XX can be used for magnetically activated cell sorting. The protein is
XX useful in various diagnostic and therapeutic applications in humans,
XX including typing of blood or blood products. The present sequence
XX represents DNA encoding a human anti-Rh(D) chain
XX
XX Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;
SQ
Query Match 86.9%; Score 276.4; DB 9; Length 321;
Best Local Similarity 91.8%; Pred. No. 1.1e-78;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Oy 1 GAGCTCACCAGTCTCCATCTCTCTGCTGCTGTAAGAGACAGATCACCATCACT 60
Db 4 GAGCTCACCAGTCTCCATCTCTCTGCTGCTGTAAGAGACAGATCACCATCACT 63
Oy 1 TGCCGGGAGAGTCAAGATTAAGACCTATTAAATGGTATCAGACAGAAACCGGGAG 120
Db 64 TGCCGGGAGAGTCAAGATTAAGACCTATTAAATGGTATCAGACAGAAACCGGGAG 123
Oy 121 GCCCTAAGCTCTGATCTGTAGTGCATCCATTGCAAGTGGGTCCTCATCCAGTTC 180
Db 124 GCCCTAAGCTCTGATCTGTAGTGCATCCATTGCAAGTGGGTCCTCATCCAGTTC 183
Oy 181 AGTGCAGTGTATCTGGGACAGATTTCATCTCCACATCAGCAGTCTGCAACTGAAGAT 240
Db 184 AGTGCAGTGTATCTGGGACAGATTTCATCTCCACATCAGCAGTCTGCAACTGAAGAT 243
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QY 241 TTTCAGATTACTACTGTCAACAGAGTTACCTTATATACCTTGGCCCTGGAGCC 300
    |||
DB 244 TTTCGAAGTTACTACTGTCAACAGAGTTACCTTATATACCTTGGCCCTGGAGCC 303
QY 301 AAAGTGGAGATCAACGA 318
    |||
DB 304 AAGGTGGAGATCAACGA 321

RESULT 5
ACD45365
ID ACD45365 standard; DNA; 321 BP.
XX
AC ACD45365;
XX
DT 12-SEP-2003 (first entry)
XX
DE Anti-Rh(D) light chain SH13 DNA.
XX
KW Human, dsi, gene; RH(D) binding protein; blood typing; blood product;
KW magnetically activated cell sorting.
XX
OS Homo sapiens.
XX
PN US2003040605-A1.
XX
PD 27-FEB-2003.
XX
PF 04-MAY-2001; 2001US-00848798.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2003-512273/48.
XX
P-PSDB; ABO27451.
XX
PT New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
XX
PS Claim 12; Page 57; 187pp; English.
XX
CC The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents DNA encoding a human anti-Rh(D) chain
XX
SQ Sequence 321 BP; 84 A; 89 C; 74 G; 74 T; 0 U; 0 Other;

Query Match 86.9%; Score 276.4; DB 9; Length 321;
Best Local Similarity 91.8%; Pred. No. 1.1e-78;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GAGTCAACCCAGTCTCCATCTCTGCTGCTGCTTGTAGAGACAGTCAACCTACT 60
    |||
DB 4 GAGTCAACCCAGTCTCCATCTCTGCTGCTGCTTGTAGAGACAGTCAACCTACT 63
QY 61 TGCCGGGAGCGTCAGAGATTAGACCTATTAAATGGTATCAGCAGAAACCGGGGAG 120
    |||
DB 64 TGCCGGGAGCGTCAGAGATTAGACCTATTAAATGGTATCAGCAGAAACCGGGGAA 123
QY 121 GCCCCTAAGCTCTGATCTGTAGTCATCAATTGCAAGTGGGTCCTCCAGGTTTC 180
    |||
DB 124 GCCCCTAAGCTCTGATCTGTAGTCATCAATTGCAAGTGGGTCCTCCAGGTTTC 183
QY 181 AGTGGAGTGGATCTGGAGCAGAGTTCACTCTCACCATCAGCATATCTGCAACCTGAAGAC 240
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```
DB 184 AGTGGAGTGGATCTGGAGCAGAGTTTACTCTCACTCAGCATCGACTCTGCAACCTGAAGAT 243
    |||
QY 241 TTTCGAAGTTACTACTGTCAACAGAGTTACCTTATATACCTTGGCCCTGGAGCC 300
    |||
DB 244 TTTCGAAGTTACTACTGTCAACAGAGTTACCTTATATACCTTGGCCCTGGAGCC 303
QY 301 AAAGTGGAGATCAACGA 318
    |||
DB 304 AAGGTGGAGATCAACGA 321

RESULT 6
AAV19761
ID AAV19761 standard; DNA; 315 BP.
XX
AC AAV19761;
XX
DT 12-JUN-1998 (first entry)
XX
DE Antibody LD2-20-VL chain coding sequence.
XX
DE Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
XX Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
KW idiopathic thrombocytopenic purpura; haemolytic disease of the newborn;
KW ss.
XX
OS Homo sapiens.
XX
PN WO9749809-A1.
XX
PD 31-DEC-1997.
XX
PF 20-JUN-1997; 97WO-EP003253.
XX
PR 24-JUN-1996; 96EP-00810421.
XX
PA (ROTK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
XX
PI Miescher S, Vogel M, Stadler B, Morell A, Imboden M, Amstutz H;
XX
DR WPI; 1998-077173/07.
XX
P-PSDB; AAM52237.
XX
PT New Rhesus D antigen binding polypeptide(s) - used to neutralise Rhesus
PT D antigen in therapy, e.g. for treating idiopathic thrombocytopenic
PT purpura.
XX
PS Claim 6; Fig 13B; 68pp; English.
XX
CC This sequence encodes the antibody LD2-20-VL chain sequence, which is a
CC polypeptide of the invention. The polypeptides are capable of forming
CC antigen binding structures with specificity for Rhesus D antigens which
CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
CC variable heavy (VH) and variable light (VL) chain sequences. The
CC antibodies are active against the Rhesus D antigen. They can be used for
CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
CC protection of Rhesus negative women before or immediately after the birth
CC of a Rhesus positive child to prevent haemolytic disease of the newborn
CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
CC to Rhesus negative recipients in order to prevent sensitisation to the
CC Rhesus D antigen. The products can also be used as diagnostic reagents
XX
SQ Sequence 315 BP; 84 A; 83 C; 71 G; 77 T; 0 U; 0 Other;

Query Match 86.0%; Score 273.4; DB 2; Length 315;
Best Local Similarity 91.7%; Pred. No. 9.9e-78;
Matches 289; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GAGTCAACCCAGTCTCCATCTCTGCTGCTGCTTGTAGAGACAGTCAACCTACT 60
    |||
```

Db 1 GTGATGACCCAGTCTCCATCCCTCTGTCGATCTGTAGAGACAGAGTCACCATCACT 60
 QY 61 TGCCGGGACAGTCTGAGATTAATTAAGCTATTAATGATGATGACGAGAAACCGGGAAG 120
 Db 61 TGCCGGGACAGTCTGAGATTAATTAAGCTATTAATGATGATGACGAGAAACCGGGAAG 120
 QY 121 GCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAATGGGGTCCCATCAAGTTC 180
 Db 121 GCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAATGGGGTCCCATCAAGTTC 180
 QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACATCTGCAACCTGGAAGAC 240
 Db 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACATCTGCAACCTGGAAGAT 240
 QY 241 TTTCGAACTTACTACTGTCACAGAGTTACACTTATATACCTTCGGCCCTGGAGCC 300
 Db 241 TTTCGAACTTACTACTGTCACAGAGTTACACTTATATACCTTCGGCCCTGGAGCC 300
 QY 301 AAAGCTGAGATCAAA 315
 Db 301 AAAGCTGATATCAAA 315
 RESULT 7
 AAH68720
 ID AAH68720 standard; DNA; 321 BP.
 AC AAH68720;
 DT 14-SEP-2001 (first entry)
 DE Human anti-Rh(D) antibody clone SH49 nucleotide sequence.
 XX Human: anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KM red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
 XX Homo sapiens.
 OS US6255455-B1.
 PN 03-JUL-2001.
 XX 29-JAN-1999; 99US-00240274.
 PF 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 XX (TYPE-) UNIV PENNSYLVANIA.
 PA Siegel DL;
 PI WPI; 2001-388931/41.
 DR P-PSDB; AAG93663.
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX Example 3; Col 79; 162pp; English.
 XX The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68658 to AAH68726 represent the nucleotide sequence which encode
 CC AAH93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention

SQ Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;
 Query Match 85.9%; Score 273.2; DB 5; Length 321;
 Best Local Similarity 91.2%; Pred. No. 1.2e-77;
 Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
 QY 1 GAGTCAACCCAGTCTCCATCCCTCTGTCGATCTGTAGAGACAGAGTCACCATCACT 60
 Db 4 GAGTCAACCCAGTCTCCATCCCTCTGTCGATCTGTAGAGACAGAGTCACCATCACT 63
 QY 61 TGCCGGGACAGTCTGAGATTAATTAAGCTATTAATGATGATGACGAGAAACCGGGAAG 120
 Db 64 TGCCGGGACAGTCTGAGATTAATTAAGCTATTAATGATGATGACGAGAAACCGGGAAG 123
 QY 121 GCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAATGGGGTCCCATCAAGTTC 180
 Db 124 GCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAATGGGGTCCCATCAAGTTC 183
 QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACATCTGCAACCTGGAAGAC 240
 Db 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACATCTGCAACCTGGAAGAT 243
 QY 241 TTTCGAACTTACTACTGTCACAGAGTTACACTTATATACCTTCGGCCCTGGAGCC 300
 Db 244 TTTCGAACTTACTACTGTCACAGAGTTACACTTATATACCTTCGGCCCTGGAGCC 303
 QY 301 AAAGCTGAGATCAAA 318
 Db 304 AAAGCTGAAATCAAA 321
 RESULT 8
 AAH68658
 ID AAH68658 standard; DNA; 321 BP.
 AC AAH68658;
 DT 14-SEP-2001 (first entry)
 DE Human anti-Rh(D) chain I13 nucleotide sequence.
 XX Human: anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KM red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
 XX Homo sapiens.
 OS US6255455-B1.
 PN 03-JUL-2001.
 XX 29-JAN-1999; 99US-00240274.
 PF 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 XX (TYPE-) UNIV PENNSYLVANIA.
 PA Siegel DL;
 PI WPI; 2001-388931/41.
 DR P-PSDB; AAG93601.
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX Example 2; Col 57; 162pp; English.
 XX The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.

CC	(1) can be used in diagnostic and therapeutic medicine. The antibodies
CC	are used in diagnostics that require human antibodies instead of animal
CC	antibodies, such as determine the Rh phenotype of human red blood cells.
CC	AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC	AAH68558 to AAH693669. AAH693670 to AAH693697 represent anti-Rh(D) heavy
CC	chain CDR3 amino acid sequences which are given in the exemplification of
CC	the present invention
XX	
XX	Sequence 321 BP, 82 A, 88 C, 77 G, 74 T, 0 U, 0 Other;
XX	
XX	Query Match 85.9%; Score 273.2; DB 5; Length 321;
XX	Best Local Similarity 91.2%; Pred.No.1,2e-77;
XX	Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
OY	1 GAGCTCACCCAGTCTCCATCCCTCCCTGTCGCTGTAGAGAGACAGATCACCATCACT 60
DB	4 GAGCTCACCCAGTCTCCATCCCTCCCTGTCGCTGTAGAGAGACAGATCACCATCACT 63
OY	61 TGGCGGGACGTCANAGATTAGACCCATTAAATTGGTATCAGACAACCCGGGAG 120
DB	64 TGGCGGGACGTCANAGATTAGACGGATTAAATTGGTATCAGACAACCCGGGAAA 123
OY	121 GCCCCTAAGCTCCTCATCTGTATGATCATCAATTTGGCAAAGGGGGTCCCATCCAGTTTC 180
DB	124 GCCCCTAAGCTCCTCATCTGTATGATCATCAATTTGGCAAAGGGGGTCCCATCAAGTTTC 183
OY	181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTGAAGAC 240
DB	184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAAGTCTGCAACTGAAGAT 243
OY	241 TTTGGAAATTACTGTCTCAACAGGTTTAACTACTTATATCTTGGGCGCTGGGACC 300
DB	244 TTTGGAAATTACTGTCTCAACAGGTTTAACTACTTATATCTTGGGCGGCGGAGAC 303
OY	301 AAACCTGAGATCAACGCA 318
DB	304 AAGCTGGAGATCAACGCA 321
XX	
XX	RESULT 9
XX	AAH68652
XX	ID AAH68652 standard; DNA, 321 BP.
XX	AC AAH68652;
XX	DT 14-SEP-2001 (first entry)
XX	DE Human anti-Rh(D) chain I07 nucleotide sequence.
XX	XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
XX	KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX	OS Homo sapiens.
XX	XX US6255455-B1.
XX	XX 03-JUL-2001.
XX	XX 29-JAN-1999; 99US-00240274.
XX	XX 11-OCT-1996; 96US-0028550P.
XX	XX 27-JUN-1997; 97US-00884045.
XX	XX 10-APR-1998; 98US-0081380P.
XX	XX (TYPE-) UNIV PENNSYLVANIA.
XX	XX Siegel DL;
XX	XX MPI, 2001-388931/41.
XX	XX P-PsDB; AAG93595.
XX	XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
XX	XX diagnostics requiring a human instead of an animal antibody and in
XX	XX

Query Match	85.9%;	Score 273.2;	DB 5;	Length 321;
Best Local Similarity	91.2%;	Pred. No. 1,2e-77;		
Matches 290;	Conservative 0;	Mismatches 28;	Indels 0;	Gaps 0
QY	1	GAGCTCACCCAGTCCCAATCCCTCCCTGCTGCTGCTGTGAGAGACAGATCCACATCACT	60	
Db	4	GAGCTCACCCAGTCCCAATCCCTCCCTGCTGCTGCTGTGAGAGACAGATCCACATCACT	63	
QY	61	TGCCGGGACGTCAGAGTATTAGACCTATTATTAATTTGGTATCAGCAGAAACCGGGAA	120	
Db	64	TGCCGGGACGTCAGAGTATTAGACCTATTATTAATTTGGTATCAGCAGAAACCGGGAA	123	
QY	121	GCCCCAAGCTTCCTGATCTGTAGTCATTCCAATTGGCAAAAGTGGGGTCCCATCCAGTTC	180	
Db	124	GCCCCAAGCTTCCTGATCTGTAGTCATTCCAATTGGCAAAAGTGGGGTCCCATCCAGTTC	183	
QY	181	AGTGCAGTGGATCTGGGACAGATTCACCTCACCATCAGCAATCTGCACCTGAAGAC	240	
Db	184	AGTGCAGTGGATCTGGGACAGATTCACCTCACCATCAGCAATCTGCACCTGAAGAT	243	
QY	241	TTTGCAGATTCTACTGTCTCAACAGAGTTACACTACTTATATACCTTCGCGCCCTGGGACC	300	
Db	244	TTTGCAGATTCTACTGTCTCAACAGAGTTACACTACTTATATACCTTCGCGCGGAGGACC	303	
QY	301	AAACTGGAGATCAAAACA 318		
Db	304	AAAGTGGAGATCAAAACA 321		
RESULT 10				
AAH68713				
ID	AAH68713 standard; DNA; 321 BP.			
XX				
AC	AAH68713;			
XX				
DT	14-SEP-2001 (first entry)			
XX				
DE	Human anti-Rh(D) antibody clone SH36 nucleotide sequence.			
XX				
KW	Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;			
XX				
OS	Homo sapiens.			
XX				
PN	US625455-B1.			
XX				
PD	03-JUL-2001.			
XX				
PF	29-JAN-1999; 99US-00240274.			
XX				
PR	11-OCT-1996; 96US-0028550P.			
XX				
PR	27-JUN-1997; 97US-0088404S.			
XX				
PR	10-APR-1996; 98US-0081380P.			
XX				
PA	(TYPE-) UNIV PENNSYLVANIA.			

```

XX Siegel DL;
XX WPI; 2001-388931/41.
DR P-PSDB; AAG93656.
XX
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
PS Example 3; Col 77; 162pp; English.
XX
CC The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93659. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93659. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 321 BP; 83 A; 89 C; 72 G; 77 T; 0 U; 0 Other;
Query Match 85.9%; Score 273.2; DB 5; Length 321;
Best Local Similarity 91.2%; Pred. No. 1.2e-77;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 1 GAGCTACCCAGTCTCCATCTCCCTGTCTGCTGTAGAGACAGAGTCAATCACT 60
DB 4 GAGCTCACTAGTCTCCATCTCCCTGTCTGCTGTAGAGACAGAGTCAATCACT 63
QY 61 TGCCTGGGACGTCAGAGTATTAGACCTATTAAATTGTTATCAGCAGAAACCGGGAG 120
DB 64 TGCCTGGGACGTCAGAGTATTAGACCTATTAAATTGTTATCAGCAGAAACCGGGAA 123
QY 121 GCCCTTAAGCTCTGATCTGTAGTGCATCCAAATTGCAAGTGGGGTCCCATCAAGTTC 180
DB 124 TCCCTTAAGCTCTGATCTGTAGTGCATCCAAATTGCAAGTGGGGTCCCATCAAGTTC 183
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCAACTGAAGAC 240
DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCAACTGAAGAT 243
QY 241 TTTCGAAGTTACTACTGTGCAAGAGTTACACTACTATATACCTTGCGCCCTGGGACC 300
DB 244 TTTCGAAGTTACTACTGTGCAAGAGTTACACTACTATATACCTTGCGCCCTGGGACC 303
QY 301 AAAGTGGAGATCAACGA 318
DB 304 AAAGTGGAGATCAACGA 321

```

RESULT 11
AAH68703 standard; DNA; 321 BP.

```

XX AAH68703;
XX
DT 14-SEP-2001 (first entry)
XX
DE Human anti-Rh(D) antibody clone SH16 nucleotide sequence.
XX
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
XX red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
OS Homo sapiens.
XX
XX US6255455-B1.
XX
PD 03-JUL-2001.

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XX 29-JAN-1999; 99US-00240274.
XX
XX 11-OCT-1996; 96US-0028550P.
XX
XX 27-JUN-1997; 97US-00884045.
XX
XX 10-APR-1998; 98US-0081380P.
XX
XX (UVE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
XX
XX WPI; 2001-388931/41.
XX
XX P-PSDB; AAG93646.
XX
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
PS Example 3; Col 75; 162pp; English.
XX
CC The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93659. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93659. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 321 BP; 85 A; 89 C; 74 G; 73 T; 0 U; 0 Other;
Query Match 85.9%; Score 273.2; DB 5; Length 321;
Best Local Similarity 91.2%; Pred. No. 1.2e-77;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 1 GAGCTACCCAGTCTCCATCTCCCTGTCTGCTGTAGAGACAGAGTCAATCACT 60
DB 4 GAGCTCACTAGTCTCCATCTCCCTGTCTGCTGTAGAGACAGAGTCAATCACT 63
QY 61 TGCCTGGGACGTCAGAGTATTAGACCTATTAAATTGTTATCAGCAGAAACCGGGAG 120
DB 64 TGCCTGGGACGTCAGAGTATTAGACCTATTAAATTGTTATCAGCAGAAACCGGGAA 123
QY 121 GCCCTTAAGCTCTGATCTGTAGTGCATCCAAATTGCAAGTGGGGTCCCATCAAGTTC 180
DB 124 GCCCTTAAGCTCTGATCTGTAGTGCATCCAAATTGCAAGTGGGGTCCCATCAAGTTC 183
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCAACTGAAGAC 240
DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCAACTGAAGAT 243
QY 241 TTTCGAAGTTACTACTGTGCAAGAGTTACACTACTATATACCTTGCGCCCTGGGACC 300
DB 244 TTTCGAAGTTACTACTGTGCAAGAGTTACACTACTATATACCTTGCGCCCTGGGACC 303
QY 301 AAAGTGGAGATCAACGA 318
DB 304 AAAGTGGAGATCAACGA 321

```

RESULT 12
ACD45377 standard; DNA; 321 BP.

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XX ACD45377;
XX
DT 12-SEP-2003 (first entry)
XX
DE Anti-Rh(D) light chain SH36 DNA.
XX

```

KM Human; ds; gene; RH(D) binding protein; blood typing; blood product;
KW magnetically activated cell sorting.
XX Homo sapiens.
XX US2003040605-A1.
XX PD 27-FEB-2003.
XX PF 04-MAY-2001; 2001US-00848798.
XX PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX PA (UYPE-) UNIV PENNSYLVANIA.
XX PI Siegel DL;
XX DR WPI; 2003-512273/48.
DR P-PSDB; ABO27463.
XX PT New human Rh(D)-binding protein useful for various diagnostic and
XX therapeutic applications, including typing of blood or blood products.
PS Claim 12; Page 60; 187P; English.
XX CC The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents DNA encoding a human anti-Rh(D) chain
XX SQ Sequence 321 BP; 83 A; 89 C; 72 G; 77 T; 0 U; 0 Other;
Query Match 85.9%; Score 273.2; DB 9; Length 321;
Best Local Similarity 91.2%; Pred. No. 1.2e-77;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 1 GAGCTACCCAGTCTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCCATCACT 60
Db 4 GAGCTACTAGTCTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCCATCACT 63
QY 61 TGGCGGCAAGTCTAGATTTAGCACTATTAAATTGTATCAGAGAAACGGGGAAG 120
Db 64 TGGCGGCAAGTCTAGATTTAGCACTATTAAATTGTATCAGAGAAACGGGGAAG 123
QY 121 GCCCTTAAGTCTGATCTGTAGTCATCCAAATTGCAAAAGTGGGTCCCATCAAGTTC 180
Db 124 TCCCTTAAGTCTGATCTGTAGTCATCCAAATTGCAAAAGTGGGTCCCATCAAGTTC 183
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTTCAACATCAGCAATCTGCAACTGGAAGAC 240
Db 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTTCAACATCAGCAATCTGCAACTGGAAGAT 243
QY 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTTATATACCTTTCGGCCCTGGAGCC 300
Db 244 TTTCGAAGTTACTACTGTCAACAGAGTTACACTTATATACCTTTCGGCCCTGGAGCC 303
QY 301 AAATCGAGATCAACGA 318
Db 304 AAAGTGAGATCAACGA 321

RESULT 13
ACD45367
ID ACD45367 standard; DNA; 321 BP.
XX ACD45367;
XX 12-SEP-2003 (first entry)

DE Anti-Rh(D) light chain SH16 DNA.
XX Human; ds; gene; RH(D) binding protein; blood typing; blood product;
KW magnetically activated cell sorting.
XX Homo sapiens.
XX US2003040605-A1.
XX PD 27-FEB-2003.
XX PF 04-MAY-2001; 2001US-00848798.
XX PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX PA (UYPE-) UNIV PENNSYLVANIA.
XX PI Siegel DL;
XX DR WPI; 2003-512273/48.
DR P-PSDB; ABO27453.
XX PT New human Rh(D)-binding protein useful for various diagnostic and
XX therapeutic applications, including typing of blood or blood products.
PS Claim 12; Page 57; 187P; English.
XX CC The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents DNA encoding a human anti-Rh(D) chain
XX SQ Sequence 321 BP; 85 A; 89 C; 74 G; 73 T; 0 U; 0 Other;
Query Match 85.9%; Score 273.2; DB 9; Length 321;
Best Local Similarity 91.2%; Pred. No. 1.2e-77;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 1 GAGCTACCCAGTCTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCCATCACT 60
Db 4 GAGCTACCCAGTCTCCATCTCCCTGCTGCTCTGTAGAGACAGAGTCCATCACT 63
QY 61 TGGCGGCAAGTCTAGATTTAGCACTATTAAATTGTATCAGAGAAACGGGGAAG 120
Db 64 TGGCGGCAAGTCTAGATTTAGCACTATTAAATTGTATCAGAGAAACGGGGAAG 123
QY 121 GCCCTTAAGTCTGATCTGTAGTCATCCAAATTGCAAAAGTGGGTCCCATCAAGTTC 180
Db 124 GCCCTTAAGTCTGATCTGTAGTCATCCAAATTGCAAAAGTGGGTCCCATCAAGTTC 183
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTTCAACATCAGCAATCTGCAACTGGAAGAC 240
Db 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTTCAACATCAGCAATCTGCAACTGGAAGAT 243
QY 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTTATATACCTTTCGGCCCTGGAGCC 300
Db 244 TTTCGAAGTTACTACTGTCAACAGAGTTACACTTATATACCTTTCGGCCCTGGAGCC 303
QY 301 AAATCGAGATCAACGA 318
Db 304 AAAGTGAGATCAACGA 321

RESULT 14
ACD45384
ID ACD45384 standard; DNA; 321 BP.
XX ACD45384;
XX

DT	12-SEP-2003	(first entry)
XX		
DE	Anti-Rh(D) light chain SH49 DNA.	
KM	Human; de; gene; RH(D) binding protein; blood typing; blood product;	
XX	magnetically activated cell sorting.	
OS	Homo sapiens.	
XX		
PN	US2003040605-A1.	
XX		
PD	27-FEB-2003.	
PF	04-MAY-2001; 2001US-00848798.	
XX		
PR	11-OCT-1996; 96US-0028550P.	
PR	27-JUN-1997; 97US-0088404S.	
PR	10-APR-1998; 98US-0081380P.	
PR	29-JAN-1999; 99US-00240274.	
XX		
PA	(TYPE-) UNIV PENNSYLVANIA.	
P1	Siegel DL;	
DR	WPI; 2003-512273/48.	
XX	P-PSDB; ABO27470.	
PT	New human Rh(D)-binding protein useful for various diagnostic and	
XX	therapeutic applications, including typing of blood or blood products.	
PS	Claim 12; Page 61; 187pp; English.	
XX		
CC	The invention relates to an isolated Rh(D) binding protein. The protein	
CC	can be used for magnetically activated cell sorting. The protein is	
CC	useful in various diagnostic and therapeutic applications in humans,	
CC	including typing of blood or blood products. The present sequence	
CC	represents DNA encoding a human anti-Rh(D) chain	
XX		
SQ	Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;	
Query Match	85.9%; Score 273.2; DB 9; Length 321;	
Best Local Similarity	91.2%; Pred. No. 1.2e-77;	
Matches 290; Conservative	0; Mismatches 28; Indels 0; Gaps 0	
QY	1 GAGGTCAACCGAGTGCATCCTCCCTGTCGCTGTGAAGAGACAGAGTCAACCATCTACT	60
Db	4 GAGGTCAACCGAGTGCATCCTCCCTGTCGCTGTGAAGAGACAGAGTCAACCATCTACT	63
QY	61 TGCCGGGACGTCAGATTATGACACTAATTTAAATGGTATCAGCAGAACAACCGGGGAAG	120
Db	64 TGCCGGGACGTCAGATTATGACACTAATTTAAATGGTATCAGCAGAACAACCGGGGAAG	123
QY	121 GCCCTTAAGTCTCCGATCTGTAGTAGTCATTCGAATTGGCAAAGTGGGGTCCCATTCCAGTTTC	180
Db	124 GCCCTTAAGTCTCCGATCTGTAGTAGTCATTCGAATTGGCAAAGTGGGGTCCCATTCCAGTTTC	183
QY	181 AGTGCACTGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTGAAGAC	240
Db	184 AGTGCACTGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTGAAGAT	243
QY	241 TTGCAAGTACTACTGTCAACAGAGTTACACTAACCTTAATATCTTGGGCCCTGGGACC	300
Db	244 TTGCAAGTACTACTGTCAACAGAGTTACAGTACCCCGTGAAGCTTGGCCAAGGACC	303
QY	301 AAACGTGAGATCAACGA 318	
Db	304 AAAGTGAAATCAACGA 321	
RESULT 15		
ACD45316		
ID	ACD45316 standard; DNA; 321 BP.	
XX		

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AC ACD45316;
XX
XX 12-SEP-2003 (first entry)
XX
XX Anti-Rh(D) chain I07 DNA.
XX
XX Human; ds; gene; RH(D) binding protein; blood typing; blood product;
XX magnetically activated cell sorting.
XX
XX Homo sapiens.
XX
XX US2003040605-A1.
XX
XX 27-FEB-2003.
XX
XX
XX PF 04-MAY-2001; 2001US-00848798.
XX
XX PR 11-OCT-1996; 96US-0028550P.
XX PR 27-JUN-1997; 97US-00884045.
XX PR 10-APR-1998; 98US-0081380P.
XX PR 29-JAN-1999; 99US-00240274.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX PA
XX
XX P1 Siegel DL;
XX
XX DR WP1; 2003-512273/48.
XX DR P-PSDB; ABO27402.
XX
XX PT New human Rh(D)-binding protein useful for various diagnostic and
XX therapeutic applications, including typing of blood or blood products.
XX
XX Claim 12; Page 40; 187pp; English.
XX
XX
XX The invention relates to an isolated Rh(D) binding protein. The protein
XX can be used for magnetically activated cell sorting. The protein is
XX useful in various diagnostic and therapeutic applications in humans,
XX including typing of blood or blood products. The present sequence
XX represents DNA encoding a human anti-Rh(D) chain
XX
XX
XX
XX
XX Sequence 321 BP; 85 A; 87 C; 76 G; 73 T; 0 U; 0 Other;
XX
XX
XX Query Match 85.9%; Score 273.2; DB 9; Length 321;
XX Best Local Similarity 91.2%; Pred. No. 1.2e-77;
XX Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
XX
XX
XX 1 GAGGTCAACCCAGTCTCCATCTCCCTGCTGTCGCTCTGTAGGAGACAGAGTCACATCACT 60
XX 4 GAGGTCAACCCAGTCTCCATCTCCCTGCTGTCGCTCTGTAGGAGACAGAGTCACATCACT 63
XX
XX 61 TGCCGGGACGTCAGAGTATTAGACACCTAATTAATTGGTATTCAGACAGAAACGGGGAG 120
XX 64 TGCCGGGACGTCAGAGTATTAGACACCTAATTAATTGGTATTCAGACAGAAACGGGGAG 123
XX
XX 121 GCCCTTAAGTCTGTATCTGTAGTCATCAATTGGCAAAAGTGCGGTCCATCAAGTTTC 180
XX 124 GCCCTTAAGTCTGTATCTGTAGTCATCAATTGGCAAAAGTGCGGTCCATCAAGTTTC 183
XX
XX 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGACATCTGCACCTGGAAGC 240
XX 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGACAGTCTGCAACCTGGAAT 243
XX
XX 241 TTGTGAATTAATCTGTCTGTCAACAGAGTTACACTTAATATCTTGCGGCGCTGGAGAC 300
XX 244 TTGTGAATTAATCTGTCTGTCAACAGAGTTACACTTAATATCTTGCGGCGGAGGAGAC 303
XX
XX 301 AAATGAGATCAACGA 318
XX |||
XX |||
XX 304 AAGGTGAGATCAACGA 321
XX |||

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Db 61 TGGCGGAGAGTGAAGATATTAGACCTATTAAATTGATATGACAGAAAACGGGGAG 120
QY 121 GCCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAAGGGGTCCTCCATCCAGGTTTC 180
Db 121 GCCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAAGGGGTCCTCCATCCAGGTTTC 180
QY 181 AGTGGCAGTGGATCTGGAGACAGAGTTCACTCTCCATCCAGCATCTGGCAACCTGAAGAC 240
Db 181 AGTGGCAGTGGATCTGGAGACAGAGTTCACTCTCCATCCAGCATCTGGCAACCTGAAGAC 240
QY 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTCGGCCCTGGGACC 300
Db 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTCGGCCCTGGGACC 300
QY 301 AAATCGAGATCAAAACA 318
Db 301 AAATCGAGATCAAAACA 318

RESULT 2
US-09-848-798-102
; Sequence 102, Application US/09848798
; Publication No. US2003040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 102
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-848-798-102

Query Match 86.9%; Score 276.4; DB 10; Length 321;
Best Local Similarity 91.8%; Pred. No. 3.4e-84;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GAGGTACCCAGTCTCATCTCCCTGTCGCTCTGTAGAGACAGAGTCCATCATCACT 60
Db 4 GAGGTACCCAGTCTCATCTCCCTGTCGCTCTGTAGAGACAGAGTCCATCATCACT 63
QY 61 TGGCGGAGAGTGAAGATATTAGACCTATTAAATTGATATGACAGAAAACGGGGAG 120
Db 64 TGGCGGAGAGTGAAGATATTAGACCTATTAAATTGATATGACAGAAAACGGGGAG 123
QY 121 GCCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAAGGGGTCCTCCATCCAGGTTTC 180
Db 124 GCCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAAGGGGTCCTCCATCCAGGTTTC 183
QY 181 AGTGGCAGTGGATCTGGAGACAGAGTTCACTCTCCATCCAGCATCTGGCAACCTGAAGAC 240
Db 184 AGTGGCAGTGGATCTGGAGACAGAGTTCACTCTCCATCCAGCATCTGGCAACCTGAAGAT 243
QY 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTCGGCCCTGGGACC 300
Db 244 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTCGGCCCTGGGACC 303
QY 301 AAATCGAGATCAAAACA 318
Db 304 AAATCGAGATCAAAACA 321

RESULT 3
US-09-848-798-199
; Sequence 199, Application US/09848798
; Publication No. US2003040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 199
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-848-798-199

Query Match 86.9%; Score 276.4; DB 10; Length 321;
Best Local Similarity 91.8%; Pred. No. 3.4e-84;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GAGGTACCCAGTCTCATCTCCCTGTCGCTCTGTAGAGACAGAGTCCATCATCACT 60
Db 4 GAGGTACCCAGTCTCATCTCCCTGTCGCTCTGTAGAGACAGAGTCCATCATCACT 63
QY 61 TGGCGGAGAGTGAAGATATTAGACCTATTAAATTGATATGACAGAAAACGGGGAG 120
Db 64 TGGCGGAGAGTGAAGATATTAGACCTATTAAATTGATATGACAGAAAACGGGGAG 123
QY 121 GCCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAAGGGGTCCTCCATCCAGGTTTC 180
Db 124 GCCCCTTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAAAGGGGTCCTCCATCCAGGTTTC 183
QY 181 AGTGGCAGTGGATCTGGAGACAGAGTTCACTCTCCATCCAGCATCTGGCAACCTGAAGAC 240
Db 184 AGTGGCAGTGGATCTGGAGACAGAGTTCACTCTCCATCCAGCATCTGGCAACCTGAAGAT 243
QY 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTCGGCCCTGGGACC 300
Db 244 TTTCGAAGTTACTACTGTCAACAGAGTTACACTACTTATATACCTTCGGCCCTGGGACC 303
QY 301 AAATCGAGATCAAAACA 318
Db 304 AAATCGAGATCAAAACA 321

RESULT 4
US-09-848-798-107
; Sequence 107, Application US/09848798
; Publication No. US2003040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 107
; LENGTH: 321

```

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I07
US-09-848-758-107

```

Query Match	85.9%	Score 273.2;	DB 10;	Length 321;
Best Local Similarity	91.2%;	Pred. No. 4.2e-83;		
Matches 290; Conservative	0;	Mismatches 28;	Indels 0;	Gaps 0;

Qy	1	GAGCTCACCCAGTCTCCATCTCCCTGATCTGCTCTGTAGAGAGACAGAGTATCACTCACT	60
Db	4	GAGCTCACCCAGTCTTCCATCTCTCCCTGTCTGTGCATCTGTAGAGACAGAGTATCACTCACT	63
Qy	61	TGCCGGGACGTCAGAGTATTAGACCTATTAAATTTGATATCAGCAAAACGGGGAAG	120
Db	64	TGCCGGGACGTCAGAGCTTAGAGCATTTTAAATTTGATATCAGCAAAACGGGGAAG	123
Qy	121	GCCCCTAAGTCTCTGATCTGTAGTGCATCAAATTGGCAAAGTGGGGTCCCATTCAGGTTTC	180
Db	124	GCCCCTAAGTCTCTGATCTGTAGTGCATCAAAGTTTGGCAAAGTGGGGTCCCATTCAGGTTTC	183
Qy	181	AGTGGCAATGGATCTTGGGACAGAGTTCACTCTTCACCATCAGCAATTTGCAACTTGAAGAC	240
Db	184	AGTGGCAATGGATCTTGGGACAGAGTTCACTCTTCACCATCAGCAGTCTGCAAACTTGAAGAT	243
Qy	241	TTTGGAAATTACTACTGTCCAAAGAGTTACACTACCTTATATACCTTGGGCCCTGGAGAC	300
Db	244	TTTGGAAATTACTACTGTCCAAAGAGTTACAGTACCCCTCGAACTTTTGGCGGAGGAGACC	303
Qy	301	AAACTGGAGATCAAAACGA	318
Db	304	AAAGTGGAGATCAAAACGA	321

```

RESULT 5
US-09-848-798-113
; Sequence 113, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:

```

```

1 TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS
2
3 TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
4
5 FILE REFERENCE: 09596-4202
6
7 CURRENT APPLICATION NUMBER: US/09/848,798
8
9 CURRENT FILING DATE: 2001-05-04
10
11 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
12
13 PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
14
15 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
16
17 PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
18
19 NUMBER OF SEQ ID NOS: 224
20
21 SOFTWARE: PatentIn Ver. 2.0
22
23 SEQ ID NO 113
24
25 LENGTH: 321
26
27 TYPE: DNA
28
29 ORGANISM: Homo sapiens
30
31 FEATURE:
32
33 OTHER INFORMATION: anti-Rh(D) chain 113
34
35 US-09-848-798-113

```

Query Match	85.9%	Score 273.2	DB 10	Length 321
Best Local Similarity	91.2%	Pred No. 4.2e-83		
Matches	290	Conservative	0	Mismatches 28; Indels 0; Gaps 0
QY	1	GAGCTCACCCACTCTCCATTCCTCCTCTGCTCTGTAGAGACAGATCCATCACT	60	
Db	4	GAGCTCACCCACTCTCCATTCCTCCTCTGCTCTGTAGAGACAGATCCATCACT	63	
QY	61	TGCCGGGCACTCAGAGATTAGACCTATTTTAAATTGGTATCAGCAGAAACGGGGAG	120	
Db	64	TGCCGGGCACTCAGAGATTAGACAGATTATTTAAATTGGTATCAGCAGAAACGAGGANA	123	
QY	121	GCCCTAAAGCTCTGATCTGTATGTATGATCAATTTGCAGAAAGTGGGGTCCCATTCACGTTTC	180	

Db 124 GCCCTTAAGCTCCGTATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGTTT 183

Qy 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTTCACCATCAGCAATCTGCAACTGAAGAC 240

Db 184 AGTGGCAGTGGATCTGGGACAGAGTTTCACTTCACCATCAGCAGTTCGCAACTGAAGAT 243

Qy 241 TTTCGAAGTACTACTGTCAACAGAGTTACACTACTTATATATACCTTCGGCCCTGGGACC 300

Db 244 TTTCGAAGTACTACTGTCAACAGAGTTACGGTATCCCTCACAGTTTTCGCGGGGACC 303

Qy 301 AAACGTGAGATCAACGA 318

Db 304 AAGCTGAGATCAACGA 321

RESULT 6
US-09-848-798-201
; Sequence 201, Application US/09848798
; Publication No. US20030040605A1
GENERAL INFORMATION.

```

? APPLICANT: Siegel, Donald L.
? TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELLS
? TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
? FILE REFERENCE: 09596-4202
? CURRENT APPLICATION NUMBER: US/09/848,798
? PRIOR FILING DATE: 2001-05-04
? PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
? PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
? PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
? PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
? NUMBER OF SEQ ID NOS: 224
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 201
? LENGTH: 321
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: anti-Rh(D) antibody clone SH16
? US-09-848-798-201

```

Query Match	85.9%;	Score 273.2;	DB 10;	Length 321;
Best Local Similarity	91.2%;	Pred. No. 4.2e-83;		
Matches 290; Conservative	0;	Mismatches 28;	Indels 0;	Gaps 0

QY	1	GAGCTCACCACGTCCTCCATCTCCCTGTCGCTCTGTAGGAGACAGAGATCAACATCACT	60
Db	4	GAGCTCACCCAGTCTCCATCTCCTCTGCTCTGTAGGAGACAGAGTCAACATCACT	63
QY	61	TGCGGGGACGTCAGAGTATTAGACCTATTAAATGGTGATCAGAGAAACCGGGGAAG	120
Db	64	TGCGGGGACGTCAGAGCATTAGACGCTATTAAATGGTGATCAGAGAAACCGGGAAA	123
QY	121	GCCCCTAAGTCTCTATCTGTAGTCATCCAAATTTGGCAAGTGGGTCCATCAAGTTTC	180
Db	124	GCCCCTAAGCTCTCATCTATGCTCATGATCCAACTTTGGCAAGTGGGTTCCATCAAGTTTC	183
QY	181	AGTGCAGTGGATCTGGGACAGAGTTCACTTCACCATCAGCAATCTGCACCTGAAAGAC	240
Db	184	AGTGCAGTGGATCTGGGACAGATTTCACTTCACCATCAGCAGTCTGCACCACTGAAGAT	243
QY	241	TTTGGCAAGTACTACTGTCAACAGAGTTACACTACTTATATACCTTTGGGCCCTGGGACC	300
Db	244	TTTGGCAAGTACTACTGTCAACAGAGTTACAGATCCCTCCAACTTTGGCGGAGGGACC	303
QY	301	AAACTGGAGATCAAAACGA	318
Db	304	AAAGTGGAGATCAAAACGA	321

RESULT 7
US-09-848-798-211
; Sequence 211, Application US/09848798

```
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH36
US-09-848-798-211
```

```
Query Match      85.9%; Score 273.2; DB 10; Length 321;
Best Local Similarity 91.2%; Pred. No. 4.2e-83;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
```

```
QY 1 GAGCTACCCAGTCTCCATCTCCCTGTGTGCTCTGTAGAGACAGAGTCACCATCACT 60
DB 4 GAGCTCACTCAGTCTCCATCTCCCTGTGTGCTCTGTAGAGACAGAGTCACCATCACT 63
QY 61 TGCCGGGACAGTCAAGATATTAGACACCTTAATTGATGATCAAGCAAAACCGGGAG 120
DB 64 TGCCGGGACAGTCAAGATATTAGACACCTTAATTGATGATCAAGCAAAACCGGGAG 123
QY 121 GCCCCTAAGCTCTGATCTGTAGTGCATCCATTTGCAAGTGGGTCCTCCATCCAGTTC 180
DB 124 TCCCTTAAGCTCTGATCTGTAGTGCATCCATTTGCAAGTGGGTCCTCCATCCAGTTC 183
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCAACCTGAAGAC 240
DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCAACCTGAAGAT 243
QY 241 TTGGCAAGTTACTACTGTGCACAGAGTTACCTTACTTACTTGGCCCTGGGACC 300
DB 244 TTGGCAAGTTACTACTGTGCACAGAGTTACCTTACTTACTTGGCCCTGGGACC 303
QY 301 AAAGTGGAGATCAACGA 318
DB 304 AAAGTGGAGATCAACGA 321
```

```
RESULT 8
US-09-848-798-218
; Sequence 218, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 218
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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```
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-218
```

```
Query Match      85.9%; Score 273.2; DB 10; Length 321;
Best Local Similarity 91.2%; Pred. No. 4.2e-83;
Matches 290; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
```

```
QY 1 GAGCTACCCAGTCTCCATCTCCCTGTGTGCTCTGTAGAGACAGAGTCACCATCACT 60
DB 4 GAGCTCACTCAGTCTCCATCTCCCTGTGTGCTCTGTAGAGACAGAGTCACCATCACT 63
QY 61 TGCCGGGACAGTCAAGATATTAGACACCTTAATTGATGATCAAGCAAAACCGGGAG 120
DB 64 TGCCGGGACAGTCAAGATATTAGACACCTTAATTGATGATCAAGCAAAACCGGGAG 123
QY 121 GCCCCTAAGCTCTGATCTGTAGTGCATCCATTTGCAAGTGGGTCCTCCATCCAGTTC 180
DB 124 TCCCTTAAGCTCTGATCTGTAGTGCATCCATTTGCAAGTGGGTCCTCCATCCAGTTC 183
QY 181 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCAACCTGAAGAC 240
DB 184 AGTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCAACCTGAAGAT 243
QY 241 TTGGCAAGTTACTACTGTGCACAGAGTTACCTTACTTACTTGGCCCTGGGACC 300
DB 244 TTGGCAAGTTACTACTGTGCACAGAGTTACCTTACTTACTTGGCCCTGGGACC 303
QY 301 AAAGTGGAGATCAACGA 318
DB 304 AAAGTGGAGATCAACGA 321
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```
RESULT 9
US-10-309-762-115
; Sequence 115, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Folitz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX. 027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-115
```

```
Query Match      85.6%; Score 272.2; DB 17; Length 384;
Best Local Similarity 91.2%; Pred. No. 1e-82;
Matches 289; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
```

```
QY 2 AGCTACCCAGTCTCCATCTCCCTGTGTGCTCTGTAGAGACAGAGTCACCATCACT 61
DB 68 AGATGACCCAGTCTCCATCTCCCTGTGTGCTCTGTAGAGACAGAGTCACCATCACT 127
QY 62 GCCGGGACAGTCAAGATATTAGACACCTTAATTGATGATCAAGCAAAACCGGGAGG 121
DB 128 GCCGGGACAGTCAAGATATTAGACACCTTAATTGATGATCAAGCAAAACCGGGAGG 187
QY 122 CCCCTAAGCTCTGATCTGTAGTGCATCCATTTGCAAGTGGGTCCTCCATCCAGTTC 181
DB 188 CCCCTAAGCTCTGATCTGTAGTGCATCCATTTGCAAGTGGGTCCTCCATCCAGTTC 247
QY 182 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCAACCATCAGCAATCTGCAACCTGAAGACT 241
```

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Db 248 GTGGCAGAGATCTGGGACAGATTTCACCTCCACCATAGCGGCTCTGCAACCTGAAGATT 307
Qy 242 TTGCAAGTACTACTGTCAACAGAGTTACACTTATATACCTTGGCCCTGGAGCA 301
Db 308 TTGCACTTACTACTGTCAACAGAGTTACAGTTCCCTTATTCATTTCGGCCCTGGAGCA 367
Qy 302 AACTGAGATCAACGA 318
Db 368 AAGTGATATCAACGA 384

RESULT 10
US-09-848-798-106
; Sequence 106, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 106
US-09-848-798-106

Query Match      85.4%; Score 271.6; DB 10; Length 321;
Best Local Similarity 90.9%; Pred. No. 1.5e-82;
Matches 289; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 1 GAGCTCACCCAGTCTCCATCTCCTGTGCTGTGAGAGACAGATCAATCACT 60
Db 4 GAGCTCACCCAGTCTCCATCTCCTGTGCTGTGAGAGACAGATCAATCACT 63
Qy 61 TGGCGGGAGCTGAGATTTAGACCTTAAATGGTATCAGCAAAACCGGGAG 120
Db 64 TGGCGGGAGCTGAGATTTAGACCTTAAATGGTATCAGCAAAACCGGGAG 123
Qy 121 GCCCTTAAGCTCTGATCTGTAGTACCAATTGGCAAGTGGGGTCCATCCAGTTC 180
Db 124 GCCCTTAAGCTCTGATCTGTAGTACCAATTGGCAAGTGGGGTCCATCCAGTTC 183
Qy 181 AGTGGCAGTGTATGGAGACAGATTCTCACTCAACATCAGAGATCTCAAGAC 240
Db 184 AGTGGCAGTGTATGGAGACAGATTCTCACTCAACATCAGAGATCTCAAGAT 243
Qy 241 TTGCAAGTACTACTGTCAACAGAGTTACACTTATATACCTTGGCCCTGGAGCC 300
Db 244 TTGCAAGTACTACTGTCAACAGAGTTACACTTATATACCTTGGCCCTGGAGCC 303
Qy 301 AAAGTGAGATCAACGA 318
Db 304 GAAGTGAGATCAACGA 321

RESULT 11
US-09-848-798-205
; Sequence 205, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
```

```
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 205
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH24
US-09-848-798-205

Query Match      85.4%; Score 271.6; DB 10; Length 321;
Best Local Similarity 90.9%; Pred. No. 1.5e-82;
Matches 289; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 1 GAGCTCACCCAGTCTCCATCTCCTGTGCTGTGAGAGACAGATCAATCACT 60
Db 4 GAGCTCACCCAGTCTCCATCTCCTGTGCTGTGAGAGACAGATCAATCACT 63
Qy 61 TGGCGGGAGCTGAGATTTAGACCTTAAATGGTATCAGCAAAACCGGGAG 120
Db 64 TGGCGGGAGCTGAGATTTAGACCTTAAATGGTATCAGCAAAACCGGGAG 123
Qy 121 GCCCTTAAGCTCTGATCTGTAGTACCAATTGGCAAGTGGGGTCCATCCAGTTC 180
Db 124 GCCCTTAAGCTCTGATCTGTAGTACCAATTGGCAAGTGGGGTCCATCCAGTTC 183
Qy 181 AGTGGCAGTGTATGGAGACAGATTCTCACTCAACATCAGAGATCTCAAGAC 240
Db 184 AGTGGCAGTGTATGGAGACAGATTCTCACTCAACATCAGAGATCTCAAGAT 243
Qy 241 TTGCAAGTACTACTGTCAACAGAGTTACACTTATATACCTTGGCCCTGGAGCC 300
Db 244 TTGCAAGTACTACTGTCAACAGAGTTACACTTATATACCTTGGCCCTGGAGCC 303
Qy 301 AAAGTGAGATCAACGA 318
Db 304 GAAGTGAGATCAACGA 321

RESULT 12
US-09-848-798-221
; Sequence 221, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-848-798-221

Query Match      85.4%; Score 271.6; DB 10; Length 321;
```

Best Local Similarity 90.9%; Pred. No. 1.5e-82;
Matches 289; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 GAGCTCACCAGTCTCCATCTCCCTGTCTGCTCTGTAGAGACAGAGTCAACCATCACT 60
Db 4 GAGCTCACCAGTCTCCATCTCCCTGTCTGCTCTGTAGAGACAGAGTCAACCATCACT 63
QY 61 TGCCTGGGACAGTCTGAGTATTAGCACTATTAAATTGGTATCAGCAGAAACCGGGAG 120
Db 64 TGCCTGGGACAGTCTGAGCATTGGCACTTAATTAATTGGTATCAGCAGAAACCGGGAAA 123
QY 121 GCCCCTAAGCTCCGATCTGTAGTCACTCAATTGGCAAGTGGGGTCCCATCAAGGTTC 180
Db 124 GCCCCTAAGCTCCGATCTGTAGTCACTCAATTGGCAAGTGGGGTCCCATCAAGGTTC 183
QY 181 AGTGGCAGTGGATCTGGAGACAGAGTCACTCTCAACCAATCTGCAACTGGAAGAC 240
Db 184 AGTGGCAGTGGATCTGGAGACAGATTTCACTCTCAACCAATCTGCAACTGGAAGAT 243
QY 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTAATCTTATATACCTTGGCCCTGGGACC 300
Db 244 TTTCGAAGTTACTACTGTCAACAGAGTTACAGTACCCCGTGGACGTTGGCCAAAGGACC 303
QY 301 AAATGGAGATCAACGA 318
Db 304 AAGGTGAATCAACGA 321

RESULT 13

US-09-848-798-222
; Sequence 222, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 222
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-222

Query Match 85.4%; Score 271.6; DB 10; Length 321;

Best Local Similarity 90.9%; Pred. No. 1.5e-82;
Matches 289; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 GAGCTCACCAGTCTCCATCTCCCTGTCTGCTCTGTAGAGACAGAGTCAACCATCACT 60
Db 4 GAGCTCACCAGTCTCCATCTCCCTGTCTGCTCTGTAGAGACAGAGTCAACCATCACT 63
QY 61 TGCCTGGGACAGTCTGAGTATTAGCACTATTAAATTGGTATCAGCAGAAACCGGGAG 120
Db 64 TGCCTGGGACAGTCTGAGCATTGGCACTTAATTAATTGGTATCAGCAGAAACCGGGAAA 123
QY 121 GCCCCTAAGCTCCGATCTGTAGTCACTCAATTGGCAAGTGGGGTCCCATCAAGGTTC 180
Db 124 GCCCCTAAGCTCCGATCTGTAGTCACTCAAGTGGGGTCCCATCAAGGTTC 183
QY 181 AGTGGCAGTGGATCTGGAGACAGAGTCACTCTCAACCAATCTGCAACTGGAAGAC 240
Db 184 AGTGGCAGTGGATCTGGAGACAGATTTCACTCTCAACCAATCTGCAACTGGAAGAT 243

QY 241 TTTCGAAGTTACTACTGTCAACAGAGTTACACTTATATACCTTGGCCCTGGGACC 300
Db 244 TTTCGAAGTTACTACTGTCAACAGAGTTACAGTACCCCGTGGACGTTGGCCAAAGGACC 303
QY 301 AAATGGAGATCAACGA 318
Db 304 AAGGTGAATCAACGA 321

RESULT 14

US-09-192-854-1
; Sequence 1, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-192-854-1

Query Match 85.3%; Score 271.2; DB 9; Length 720;
Best Local Similarity 91.1%; Pred. No. 2.7e-82;
Matches 288; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 2 AGCTCACCAGTCTCCATCTCCCTGTCTGCTCTGTAGAGACAGAGTCAACCATCACT 61
Db 404 AGATGACCCAGTCTCCATCTCCCTGTCTGCTCTGTAGAGACAGAGTCAACCATCACT 463
QY 62 GCCCGGACAGTCTGAGTATTAGCACTATTAAATTGGTATCAGCAGAAACCGGGAGAG 121
Db 464 GCCCGGACAGTCTGAGCATTAGAGCATTAAATTGGTATCAGCAGAAACCGGGAGAG 523
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Db 524 CCCTTAAGCTCTGATCTGTAGTCACTCAATTGGCAAGTGGGGTCCCATCCAGTTCA 583
QY 182 GTGGCAGTGGATCTGGAGACAGAGTTCACTCTCAACCAATCTGCAACTGGAAGACT 241
Db 584 GTGGCAGTGGATCTGGAGACAGATTTCACTCTCAACCAATCTGCAACTGGAAGATT 643
QY 242 TTTCGAAGTTACTACTGTCAACAGAGTTACACTTATATACCTTGGCCCTGGGACCA 301
Db 644 TTTCGAAGTTACTACTGTCAACAGAGTTACAGTACCCCGTGGACGTTGGCCAAAGGACCA 703
QY 302 AACTGGAGATCAACG 317
Db 704 AAGTGAATCAACG 719

RESULT 15

US-09-968-561A-1
; Sequence 1, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248

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? PRIOR FILING DATE: 1997-11-13
? PRIOR APPLICATION NUMBER: US 60/066,729
? PRIOR FILING DATE: 1997-11-21
? PRIOR APPLICATION NUMBER: PCT/GB98/03135
? PRIOR FILING DATE: 1998-10-20
? PRIOR APPLICATION NUMBER: US 09/511,939
? PRIOR FILING DATE: 2000-02-24
? NUMBER OF SEQ ID NOS: 350
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 1
? LENGTH: 720
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-968-561A-1

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Db	464	GCCGGGCAAGTCAGGCAATTACCACTATTATAATTGTATCAGCAAAAAACGAGGAAG	523
OY	122	CCCCTAAGCTCCTGATCTGTAGTGATCCCAATTGCAAAAGTGGGGTCCCATCAGGTCCA	181
Db	524	CCCCTAAGCTCCTGATCTGTATGTGTGATCCAGTTTGGAAAGTGGGGTCCCATCAAGTTCA	583
OY	182	GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTTGCAA CTTGAAGACT	241
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Job time : 476.839 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:09:06 ; Search time 1819.51 Seconds

(without alignments)
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Perfect score: 318
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Searched: 4708233 seqs, 2422767955 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	316.4	99.5	318	9	HS458380 Homo sapi
2	281.2	88.4	321	9	HS16VX110
3	278	87.4	322	9	HUMIGHG
4	278	87.4	326	9	HUMIGHG
5	277	87.1	830	9	AB064095 Homo sapi
6	276.4	86.9	321	6	AR160973 Sequence
7	276.4	86.9	321	6	AR161027 Sequence
8	276.4	86.9	328	9	HUMIGHG
9	275.8	86.1	324	9	AB063929
10	275.8	86.1	324	9	AR107245
11	275.8	86.1	390	9	HS043773
12	273.8	86.1	828	9	AB064098 Homo sapi
13	273.4	86.0	315	6	A68535
14	273.4	86.0	315	9	HS16220V
15	273.4	86.0	318	12	AF044451
16	273.2	85.9	321	6	AR160978
17	273.2	85.9	321	6	AR160984
18	273.2	85.9	321	6	AR161029
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22	273.2	85.9	796	9	AB064138	AB064138 Homo sapi
23	272.6	85.7	311	9	HSX98989	X98989 H. sapiens r
24	272.2	85.6	387	12	AF453148	AF453148 Synthetic
25	272.2	85.6	429	9	HUMIGHG	M74019 Homo sapien
26	272.2	85.6	735	6	CQ849413	CQ849413 Sequence
27	272.2	85.6	735	6	CQ849425	CQ849425 Sequence
28	272.2	85.6	735	6	CQ849427	CQ849427 Sequence
29	272.2	85.6	736	6	CQ758827	CQ758827 Sequence
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35	271.6	85.4	321	6	AR161033	AR161033 Sequence
36	271.6	85.4	321	6	AR161049	AR161049 Sequence
37	271.6	85.4	321	6	AR161050	AR161050 Sequence
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DEFINITION	Homo sapiens partial mRNA for immunoglobulin kappa light chain				
ACCESSION	AF458380				
VERSION	AF458380.1	GI:20387059			
KEYWORDS	IGKV gene; immunoglobulin kappa; light chain; variable region.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1				
AUTHORS	Flicker, S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y.,				
TITLE	Valent, P., Kraft, D. and Valenta, R.				
JOURNAL	Conversion of grass allergen-specific human IgE into a protective				
REFERENCE	2 (bases 1 to 318)				
AUTHORS	Unpublished				
TITLE	Flicker, S.				
JOURNAL	Direct Submission				
FEATURES	Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,				
source	General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090				
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Best Local Similarity 92.1%; Pred. No. 1.1e-77;
Matches 293; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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QY 121 GCCCCTAAGCTCTGATCTGTAGTCATCCAAATTTGCAAGTGGGGTCCCATCAAGTTC 180
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DB 301 AAAGCTGAGATCAACGCA 318

RESULT 4
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DEFINITION Homo sapiens cell-type T-cell immunoglobulin gamma-chain, V region
(GIGHV) mRNA, partial cds.
ACCESSION L03160
VERSION L03160.1 GI:185395
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 326)
Collier,T.A., Roben,P., O'Kennedy,R., Barbae,C.F. III, Burton,D.R.
and Lerner,R.A.
A binary plasmid system for shuffling combinatorial antibody
libraries
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
MEDLINE 93066172
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Best Local Similarity 92.1%; Pred. No. 1.1e-77;
Matches 293; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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    |||
DB 1 GAGCTCACCAGTCCATCTCCCTGTCGCTCTGTAGAGACAGATCAATCACT 60

QY 61 TGCCGGGACAGTCAGATTTAGACACCTATTAAATTGATACGAGAAACCGGGGAAG 120
    |||
DB 61 TGCCGGGACAGTCAGATTTAGACACCTATTAAATTGATACGAGAAACCGGGGAAG 120

QY 121 GCCCCTAAGCTCTGATCTGTAGTCATCCAAATTTGCAAGTGGGGTCCCATCAAGTTC 180
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DB 121 GCCCCTAAGCTCTGATCTGTAGTCATCCAAATTTGCAAGTGGGGTCCCATCAAGTTC 180

QY 181 AGTGGCAGTGGATTTGGAGACAGATTCATCTCAACCATCAGCAATCTGCAACTGGAAGAC 240
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DB 301 AAAGCTGAGATCAACGCA 318

RESULT 5
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LOCUS
DEFINITION Homo sapiens IGH mRNA for immunoglobulin kappa light chain VLJ
region, partial cds, clone:K54.
ACCESSION AB064095
VERSION AB064095.1 GI:21669396
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
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Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,U.,
Miura,K. and Kurosawa,Y.
Construction and characterization of antibody libraries: isolation
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JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (25-JUN-2001) Yoshihazu Kurosawa, Institute for
Direct Submission
Kurosawa, Y
Unpublished
2 (bases 1 to 830)
genomics
of therapeutic human antibodies and application to functional

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Db	194	CCCTTAAGCTCTGATCTATGCTGTGATCCAGTTTGCAAAAGTGGGTTCCCATTCAGATTCA	253
QY	182	GTGGCAGTGGATTCTGGGACAGAGTTCACTCTCACCATTAGCAATTTGCAACTGGAAGCT	241
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QY	242	TTGCAAGTTACATCTGTCAACAGAGATTACACTTATATACCTTGGGCGCTGGGACCA	301
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QY	302	AACTGGAGATCAAAACA 318	
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DEFINITION	Sequence 102 from patent US 6255455.	linear PAT 17-OCT-2001

ACCESSION	AR160973	
VERSION	AR160973.1	GI:16226189
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 321)	
TITLE	Siegel, D.L.	
	Rh(D)-binding proteins and magnetically activated cell sorting	
	method for production thereof	
JOURNAL	Patent: US 6256455-A 102 03-JUL-2001;	
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QY	181	AGTGGCAGTGGATCTGGGACAGAGTTTACCTCACTCAACATCGACATCTGCAACTCGAAGAC	240
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Db	244	TTTTCGAATTACTACTGTCAACAGAGTTTACAGTACCTCTGTGAGAGTTTCGGCCAAAGGACC	303
QY	301	AAACTGAGATCAACAAGA 318	
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DEFINITION	Sequence 199 from patent US 6255455.				
ACCESSION	ARI61027				
VERSION	ARI61027.1	GI:16226382			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	I (bases 1 to 321)				
TITLE	Siegel,D.L.				
JOURNAL	Rh(D)-binding proteins and magnetically activated cell sorting				
FEATURES	method for production thereof				
source	Patent: US 6255455-A 199 03-JUL-2001;				
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Query Match	86.9%	Score 276.4	DB 6	Length 321
Best Local Similarity	91.8%	Pred. No. 3.6e-77		
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Db 4 GAGCTCACCCAGTCTCCATCTCCCTGTCTGATCTGTAGAGACAGAGTCAACCATCACT 63
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Qy 301 AAAGCTGAGATCAACGA 318
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RESULT 8
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DEFINITION (IGHV6) mRNA, partial cds.
ACCESSION L03164
VERSION L03164.1 GI:185399
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Collier,T.A., Roben,P., O'Kennedy,R., Barbas,C.F. III, Burton,D.R.
and Lerner,R.A.
TITLE A binary plasmid system for shuffling combinatorial antibody
libraries
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
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PUBMED 1438192
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Query Match 86.9%; Score 276.4; DB 9; Length 328;
Best Local Similarity 91.8%; Pred. No. 3,6e-77;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Db 1 GAGCTCACCCAGTCTCCATCTCCCTGTCTGATCTGTAGAGACAGAGTCAACCATCACT 60
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Qy 301 AAAGCTGAGATCAACGA 318
Db 301 AAGCTGAGATCAACGA 318

RESULT 9
AB063929 324 bp mRNA linear PRI 02-JUL-2002
LOCUS Homo sapiens IGH mRNA for immunoglobulin kappa light chain VLJ
DEFINITION region, partial cds, clone:K102.
ACCESSION AB063929
VERSION AB063929.1 GI:21669064
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hiroo,Y., Kakita,M.,
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsuni,H., Okada,T.,
Mura,K. and Kurosawa,Y.
TITLE Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 324)
AUTHORS Kurosawa,Y.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kurosawa-cho, Toyoake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp; Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.

COMMENT
Location/Qualifiers
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VERSION A68535.1 GI:4759587
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ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 315)
AUTHORS Miescher, S., Vogel, M., Stadler, B., Morell, A., Imboden, M. and Amstutz, H.
TITLE POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING STRUCTURES WITH SPECIFICITY FOR THE RHESUS D ANTIGENS, THE DNA ENCODING THEM AND THE PROCESS FOR THEIR PREPARATION AND USE
JOURNAL Patent: WO 9749809-A 51 31-DEC-1997;
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QY 301 AAACGTGAGATCAAA 315
DB 301 AAACGTGAGATCAAA 315
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LOCUS H.sapiens mRNA for variable region of immunoglobulin kappa light
DEFINITION chain, clone LD2-20-VL.
ACCESSION Y08251
VERSION Y08251.1 GI:1561609

KEYWORDS Ig kappa chain; immunoglobulin; light chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Miescher, S.M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 315)
AUTHORS Miescher, S.M.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-1996) S.M. Miescher, Institute of Immunology and Allergy, University of Bern, Sahli Haus 2, Inselspital, CH-3010 Bern, SWITZERLAND
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Query Match 86.0%; Score 273.4; DB 9; Length 315;
Best Local Similarity 91.7%; Pred. No. 3.3e-76;
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DB 241 TTTCGAAGTTACTACTGTCACACAGAGTTACACTACTATATACCTTGCGGCTGGGAGC 300
QY 301 AAACGTGAGATCAAA 315
DB 301 AAACGTGAGATCAAA 315
RESULT 15
AF044451 318 bp mRNA linear SYN 31-OCT-2001
LOCUS AF044451
DEFINITION Synthetic construct from Homo sapiens clone 102 anti-Rh(D) antibody
V kappa segment mRNA, partial cds.
ACCESSION AF044451

VERSION AF044451.1 GI:3046473
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE
AUTHORS Siegel,D.L., Chang,T.Y., Russell,S.L. and Bunya,V.Y.
TITLE Isolation of cell surface-specific human monoclonal antibodies
using phage display and magnetically-activated cell sorting:
applications in immunohematology
J. Immunol. Methods 206 (1-2), 73-85 (1997)
JOURNAL
MEDLINE 97469098
PUBMED 9328570
REFERENCE
AUTHORS Chang,T.Y. and Siegel,D.L.
TITLE Genetic and immunological properties of phage-displayed human
anti-Rh(D) antibodies: implications for Rh(D) epitope topology
Blood 91 (8), 3066-3078 (1998)
JOURNAL
MEDLINE 96200617
PUBMED 9531621
REFERENCE
AUTHORS Chang,T.Y., Russell,S.L., Bunya,V.Y. and Siegel,D.L.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-1998) Path & Lab Med, University of Pennsylvania,
36th & Hamilton, Philadelphia, PA 19104, USA
location/Qualifiers
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Best Local Similarity 91.7%; Pred. No. 3.3e-76;
Matches 289; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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QY 241 TTTCGAAGTTACTACTGTCAACAGAGTTTACACTATTATATACCTTGCGCCTGGAGAC 300
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DB 304 AAAGTGGAGATCAAA 318

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Title: US-10-027-725A-4

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Searched: 1202784 seqs, 81813359 residues

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Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	287.6	90.4	321	US-09-240-274-199	Sequence 199, App
2	281.2	88.4	321	US-09-240-274-102	Sequence 102, App
3	281.2	88.4	321	US-09-240-274-109	Sequence 109, App
4	281.2	88.4	321	US-09-240-274-218	Sequence 218, App
5	279.6	87.9	321	US-09-240-274-107	Sequence 107, App
6	279.6	87.9	321	US-09-240-274-113	Sequence 113, App
7	279.6	87.9	321	US-09-240-274-221	Sequence 221, App
8	279.6	87.9	321	US-09-240-274-222	Sequence 222, App
9	276.4	86.9	321	US-09-240-274-201	Sequence 201, App
10	276.4	86.9	321	US-09-240-274-211	Sequence 211, App
11	276.2	86.9	324	US-09-240-274-101	Sequence 101, App
12	276.2	86.9	324	US-09-240-274-112	Sequence 112, App
13	276.2	86.9	324	US-09-240-274-210	Sequence 210, App
14	276	86.8	320	US-09-192-854-1	Sequence 1, App1
15	274.8	86.4	321	US-09-240-274-105	Sequence 105, App
16	274.8	86.4	321	US-09-240-274-216	Sequence 216, App
17	273.2	85.9	321	US-09-240-274-104	Sequence 104, App
18	273.2	85.9	321	US-09-240-274-106	Sequence 106, App
19	273.2	85.9	321	US-09-240-274-215	Sequence 215, App
20	273.2	85.9	321	US-09-240-274-217	Sequence 217, App
21	273	85.8	324	US-09-240-274-206	Sequence 206, App
22	271.4	85.3	324	US-09-240-274-110	Sequence 110, App
23	270.6	85.1	714	US-09-472-087-62	Sequence 62, App1
24	270	84.9	321	US-09-240-274-205	Sequence 205, App
25	270	84.9	321	US-09-240-274-207	Sequence 207, App
26	268.2	84.3	324	US-09-240-274-224	Sequence 224, App
27	266.8	83.9	321	US-09-240-274-108	Sequence 108, App

28	266.8	83.9	321	US-09-240-274-203	Sequence 203, App
29	265.2	83.4	321	US-09-240-274-103	Sequence 103, App
30	261.6	82.3	672	US-09-456-090A-47	Sequence 47, App1
31	261.6	82.3	672	US-09-453-234-47	Sequence 47, App1
32	261.4	82.2	417	US-09-472-087-48	Sequence 48, App1
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34	260.4	81.9	321	US-09-240-274-200	Sequence 200, App
35	260.4	81.9	321	US-09-240-274-213	Sequence 213, App
36	259.4	81.6	458	US-08-378-939-23	Sequence 23, App1
37	259.4	81.6	458	US-09-472-087-44	Sequence 44, App1
38	259.2	81.5	451	US-09-472-087-50	Sequence 50, App1
39	259	81.4	388	US-09-042-353-358	Sequence 358, App
40	259	81.4	388	US-08-758-417A-206	Sequence 206, App
41	258.8	81.4	321	US-09-240-274-212	Sequence 212, App
42	258.2	81.2	402	US-09-472-087-49	Sequence 49, App1
43	257.2	80.9	318	US-09-240-274-208	Sequence 208, App
44	256.4	80.6	318	US-08-844-215-20	Sequence 20, App1
45	255.6	80.4	321	US-09-240-274-114	Sequence 114, App

ALIGNMENTS

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RESULT 1
US-09-240-274-199
Sequence 199, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240, 274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 199
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-199
Query Match          90.4%; Score 287.6; DB 3; Length 321;
Best Local Similarity 94.0%; Pred. No. 9.2e-91;
Matches 299; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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Db      304 AAGCTGAGATCAACGA 321
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RESULT 2
US-09-240-274-102
; Sequence 102, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rn(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; OTHER INFORMATION: anti-Rh(D) chain I02
US-09-240-274-102

Query Match      88.4%; Score 281.2; DB 3; Length 321;
Best Local Similarity 92.8%; Pred. No. 1,6e-88;
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0

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Db      304 AAGGTGAGATCAACGA 321
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RESULT 3
US-09-240-274-109
; Sequence 109, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rn(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11

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Query Match	88.4%;	Score 281.2;	DB 3;	Length 321;
Best Local Similarity	92.8%;	Pred. No. 1.6e-88;		
Matches 295;	Conservative 0;	Mismatches 23;	Indels 0;	Gaps 0;
<p>US-09-240-274-109</p> <p>OTHER INFORMATION: anti-Rh(D) chain I09</p>				
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<p>RESULT 4</p> <p>US-09-240-274-218</p> <p>Sequence 218; Application us/09240274</p> <p>Patent No. 6255455</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Siegel, Donald L.</p> <p>TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL</p> <p>FILE REFERENCE: 09596-42U2</p> <p>CURRENT APPLICATION NUMBER: US/09/240,274</p> <p>CURRENT FILING DATE: 1999-01-29</p> <p>EARLIER APPLICATION NUMBER: 60/081,380</p> <p>EARLIER FILING DATE: 1998-04-10</p> <p>EARLIER APPLICATION NUMBER: 60/028,550</p> <p>EARLIER FILING DATE: 1996-10-11</p> <p>NUMBER OF SEQ ID NOS: 224</p> <p>SOFTWARE: PatentIn Ver. 2.0</p> <p>SEQ ID NO 218</p> <p>LENGTH: 321</p> <p>TYPE: DNA</p> <p>ORGANISM: Homo sapiens</p> <p>FEATURE:</p> <p>OTHER INFORMATION: anti-Rh(D) antibody clone SH49</p> <p>US-09-240-274-218</p>				
Query Match	88.4%;	Score 281.2;	DB 3;	Length 321;
Best Local Similarity	92.8%;	Pred. No. 1.6e-88;		
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Db	64	TGCCGGGCAAGTCAGAGATTAAGAGCTATTATTAATTGGTATCGACAGAAACAGGAAA	123	
Query	121	GCCCCTAAGTCTCTGATCTATGCTGATCCAGTTGGAAAAGTGGGATCCCATCAAGTTC	180	
Db	124	GCCCCTAAGTCTCTGATCTATGCTGATCCAGTTGGAAAAGTGGGATCCCATCAAGTTC	183	
Query	181	AGTGGCAGTGTGATTTGGGACAGACTTCACTTCCATCAGACATCTGACGCTTGAAAGAT	240	
Db	184	AGTGGCAGTGTGATTTGGGACAGACTTCACTTCCATCAGACATCTGACGCTTGAAAGAT	243	
Query	241	TTTSCAAGTTACTACTGTCAAGAGAGTCTGAGTCTCTGTAACCTTTTGGCAGGGAGC	300	
Db	244	TTTSCAAGTTACTACTGTCAAGAGAGTCTGAGTCTCTGTAACCTTTTGGCAGGGAGC	303	
Query	301	AAGGTGAGATCAACAGA 318		
Db	304	AAGGTGAGATCAACAGA 321		

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Db      64 TCCGGGCAAGTCAGAGATTGACGAGCTATTAAATGGTATCAGACAGAAACCGAGGGAAA 123
Qy      121 GCCCCTAAGCTCCGATCATATGTCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 180
Db      124 GCCCTTAAGCTCCGATCATATGTCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 183
Qy      181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGACAGTCTGACCTGAAGAT 240
Db      184 AGTGGCAGTGGATATGGGACAGATTTCATCTCTCAACATCAGACAGTCTGACCTGAAGAT 243
Qy      241 TTTCGAAGTTACTACTGTCAGAGAGAGTCTCAGTGCCTTGTAACCTTTTGGCCAGGGGACC 300
Db      244 TTTCGAAGTTACTACTGTCAGAGAGAGTTCAGTACAGTCCCGTGGAGCGTTCGCCAAGGGACC 303
Qy      301 AAGGTGAGATCAAAACGA 318
Db      304 AAGGTGAGATCAAAACGA 321

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RESULT 5

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US-09-240-274-107
; Sequence 107, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240, 274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 107
US-09-240-274-107

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Query Match 87.9%; Score 279.6; DB 3; Length 321;
 Best Local Similarity 92.5%; Pred. No. 6e-88;
 Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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Qy      1 GAGCTCACTCAGTCTCCATCTCCCTGTCGATCTGTGGGACAGAGTCACCATCAGT 60
Db      4 GAGCTCACTCAGTCTCCATCTCCCTGTCGATCTGTGGGACAGAGTCACCATCAGT 63
Qy      61 TCCGGGCAAGTCAGAGATTAAACATTAATTAATGGTATCAGCATTAACAGGGAAA 120
Db      64 TCCGGGCAAGTCAGAGATTAAACATTAATTAATGGTATCAGCATTAACAGGGAAA 123
Qy      121 GCCCCTAAGCTCCGATCATATGTCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 180
Db      124 GCCCCTAAGCTCCGATCATATGTCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 183
Qy      181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGACAGTCTGACCTGAAGAT 240
Db      184 AGTGGCAGTGGATATGGGACAGATTTCATCTCTCAACATCAGACAGTCTGACCTGAAGAT 243
Qy      241 TTTCGAAGTTACTACTGTCAGAGAGAGTCTCAGTGCCTTGTAACCTTTTGGCCAGGGGACC 300
Db      244 TTTCGAAGTTACTACTGTCAGAGAGAGTTCAGTACAGTCCCGTGGAGCGTTCGCCAAGGGACC 303
Qy      301 AAGGTGAGATCAAAACGA 318
Db      304 AAGGTGAGATCAAAACGA 321

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RESULT 6
 US-09-240-274-113
 ; Sequence 113, Application US/09240274
 ; Patent No. 6255455
 ; GENERAL INFORMATION:
 ; APPLICANT: Siegel, Donald L.
 ; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
 ; FILE REFERENCE: 09596-4202
 ; CURRENT APPLICATION NUMBER: US/09/240, 274
 ; EARLIER FILING DATE: 1999-01-29
 ; EARLIER APPLICATION NUMBER: 60/081,380
 ; EARLIER FILING DATE: 1998-04-10
 ; EARLIER APPLICATION NUMBER: 60/028,550
 ; EARLIER FILING DATE: 1996-10-11
 ; NUMBER OF SEQ ID NOS: 224
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 113
 ; LENGTH: 321
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: anti-Rh(D) chain 113
 US-09-240-274-113

Query Match 87.9%; Score 279.6; DB 3; Length 321;
 Best Local Similarity 92.5%; Pred. No. 6e-88;
 Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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Qy      1 GAGCTCACTCAGTCTCCATCTCCCTGTCGATCTGTGGGACAGAGTCACCATCAGT 60
Db      4 GAGCTCACTCAGTCTCCATCTCCCTGTCGATCTGTGGGACAGAGTCACCATCAGT 63
Qy      61 TCCGGGCAAGTCAGAGATTAAACATTAATTAATGGTATCAGCATTAACAGGGAAA 120
Db      64 TCCGGGCAAGTCAGAGATTAAACATTAATTAATGGTATCAGCATTAACAGGGAAA 123
Qy      121 GCCCCTAAGCTCCGATCATATGTCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 180
Db      124 GCCCCTAAGCTCCGATCATATGTCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 183
Qy      181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGACAGTCTGACCTGAAGAT 240
Db      184 AGTGGCAGTGGATATGGGACAGATTTCATCTCTCAACATCAGACAGTCTGACCTGAAGAT 243
Qy      241 TTTCGAAGTTACTACTGTCAGAGAGAGTCTCAGTGCCTTGTAACCTTTTGGCCAGGGGACC 300
Db      244 TTTCGAAGTTACTACTGTCAGAGAGAGTTCAGTACAGTCCCGTGGAGCGTTCGCCAAGGGACC 303
Qy      301 AAGGTGAGATCAAAACGA 318
Db      304 AAGGTGAGATCAAAACGA 321

```

RESULT 7

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US-09-240-274-221
; Sequence 221, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240, 274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221

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LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-240-274-221

Query Match 87.9%; Score 279.6; DB 3; Length 321;
Best Local Similarity 92.5%; Pred. No. 6e-88;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGTCACCTGCTGATCTCTCCCTGTCGATCTGTGGGAGACAGATCAATCAGT 60
DB 4 GAGTCACCTGCTGATCTCTCCCTGTCGATCTGTGGGAGACAGATCAATCAGT 63
QY 61 TGCCGGGCAAGTCAAGAAATTAACACCTATTAAATGGTATCAGCAAGAAACGAGGAAA 120
DB 64 TGCCGGGCAAGTCAAGAAATTAACACCTATTAAATGGTATCAGCAAGAAACGAGGAAA 123
QY 121 GCCCTTAAGCTCTGATCTATGTCGATCCAGTTTGCAAGTGGGTCCTCAAGGTTTC 180
DB 124 GCCCTTAAGCTCTGATCTATGTCGATCCAGTTTGCAAGTGGGTCCTCAAGGTTTC 183
QY 181 AGTGGCAGTGAATATGGAGACAGCTTCGCTCCACACAGAGTCTGAGCTGAAGAT 240
DB 184 AGTGGCAGTGAATATGGAGACAGCTTCGCTCCACACAGAGTCTGAGCTGAAGAT 243
QY 241 TTTCGAAGTTACTACTGTCAAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 300
DB 244 TTTCGAAGTTACTACTGTCAAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 303
QY 301 AAGGTGAGATCAAAACA 318
DB 304 AAGGTGAGATCAAAACA 321

RESULT 8

US-09-240-274-222
Sequence 222, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 222
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-222

Query Match 87.9%; Score 279.6; DB 3; Length 321;
Best Local Similarity 92.5%; Pred. No. 6e-88;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGTCACCTGCTGATCTCTCCCTGTCGATCTGTGGGAGACAGATCAATCAGT 60
DB 4 GAGTCACCTGCTGATCTCTCCCTGTCGATCTGTGGGAGACAGATCAATCAGT 63
QY 61 TGCCGGGCAAGTCAAGAAATTAACACCTATTAAATGGTATCAGCAAGAAACGAGGAAA 120
DB 64 TGCCGGGCAAGTCAAGAAATTAACACCTATTAAATGGTATCAGCAAGAAACGAGGAAA 123

QY 121 GCCCTTAAGCTCTGATCTATGTCGATCCAGTTTGCAAGTGGGTCCTCAAGGTTTC 180
DB 124 GCCCTTAAGCTCTGATCTATGTCGATCCAGTTTGCAAGTGGGTCCTCAAGGTTTC 183
QY 181 AGTGGCAGTGAATATGGAGACAGCTTCGCTCCACACAGAGTCTGAGCTGAAGAT 240
DB 184 AGTGGCAGTGAATATGGAGACAGCTTCGCTCCACACAGAGTCTGAGCTGAAGAT 243
QY 241 TTTCGAAGTTACTACTGTCAAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 300
DB 244 TTTCGAAGTTACTACTGTCAAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 303
QY 301 AAGGTGAGATCAAAACA 318
DB 304 AAGGTGAGATCAAAACA 321

RESULT 9

US-09-240-274-201
Sequence 201, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 201
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-09-240-274-201

Query Match 86.9%; Score 276.4; DB 3; Length 321;
Best Local Similarity 91.8%; Pred. No. 7.9e-87;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GAGTCACCTGCTGATCTCTCCCTGTCGATCTGTGGGAGACAGATCAATCAGT 60
DB 4 GAGTCACCTGCTGATCTCTCCCTGTCGATCTGTGGGAGACAGATCAATCAGT 63
QY 61 TGCCGGGCAAGTCAAGAAATTAACACCTATTAAATGGTATCAGCAAGAAACGAGGAAA 120
DB 64 TGCCGGGCAAGTCAAGAAATTAACACCTATTAAATGGTATCAGCAAGAAACGAGGAAA 123
QY 121 GCCCTTAAGCTCTGATCTATGTCGATCCAGTTTGCAAGTGGGTCCTCAAGGTTTC 180
DB 124 GCCCTTAAGCTCTGATCTATGTCGATCCAGTTTGCAAGTGGGTCCTCAAGGTTTC 183
QY 181 AGTGGCAGTGAATATGGAGACAGCTTCGCTCCACACAGAGTCTGAGCTGAAGAT 240
DB 184 AGTGGCAGTGAATATGGAGACAGCTTCGCTCCACACAGAGTCTGAGCTGAAGAT 243
QY 241 TTTCGAAGTTACTACTGTCAAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 300
DB 244 TTTCGAAGTTACTACTGTCAAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 303
QY 301 AAGGTGAGATCAAAACA 318
DB 304 AAGGTGAGATCAAAACA 321

RESULT 10
US-09-240-274-211

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; Sequence 211, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 211
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH36
US-09-240-274-211

Query Match      86.9%; Score 276.4; DB 3; Length 321;
Best Local Similarity 91.8%; Pred. No. 7.9e-87;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GAGCTCACTGATCTCCATCTCTCTGTCGATCTGGGAGACAGTCAACATCACT 60
DB 4 GAGCTCACTGATCTCCATCTCTCTGTCGATCTGGGAGACAGTCAACATCACT 63
QY 61 TCCCGGCAAGTCAAGATTAACACCTATTAAATGGTATCGACAAACCGAGGAAA 120
DB 64 TCCCGGCAAGTCAAGATTAACACCTATTAAATGGTATCGACAAACCGAGGAAA 123
QY 121 GCCCTTAAGCTCTGATCTATGTCGATCTGATTCAGATTGCAAGTGGGATTC 180
DB 124 TCCCTTAAGCTCTGATCTATGTCGATCTGATTCAGATTGCAAGTGGGATTC 183
QY 181 AGTGGCAGTGATGAGACAGATCTGATCTGATTCAGATGTCGACCTGAGAT 240
DB 184 AGTGGCAGTGATGAGACAGATCTGATCTGATTCAGATGTCGACCTGAGAT 243
QY 241 TTTCGAAGTACTGATCTGATCAAGAGTCTGATCTGATTCGACCTGAGAT 300
DB 244 TTTCGAAGTACTGATCTGATCAAGAGTCTGATCTGATTCGACCTGAGAT 303
QY 301 AAGGTGAGATCAACGA 318
DB 304 AAGGTGAGATCAACGA 321

RESULT 11
US-09-240-274-101
; Sequence 101, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 101
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 101
US-09-240-274-101

Query Match      86.9%; Score 276.2; DB 3; Length 324;
Best Local Similarity 93.5%; Pred. No. 9.3e-87;
Matches 300; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

QY 1 GAGCTCACTGATCTCCATCTCTCTGTCGATCTGGGAGACAGTCAACATCACT 60
DB 4 GAGCTCACTGATCTCCATCTCTCTGTCGATCTGGGAGACAGTCAACATCACT 63
QY 61 TCCCGGCAAGTCAAGATTAACACCTATTAAATGGTATCGACAAACCGAGGAAA 120
DB 64 TCCCGGCAAGTCAAGATTAACACCTATTAAATGGTATCGACAAACCGAGGAAA 123
QY 121 GCCCTTAAGCTCTGATCTATGTCGATCTGATTCAGATTGCAAGTGGGATTC 180
DB 124 GCCCTTAAGCTCTGATCTATGTCGATCTGATTCAGATTGCAAGTGGGATTC 183
QY 181 AGTGGCAGTGATGAGACAGATCTGATCTGATTCAGATGTCGACCTGAGAT 240
DB 184 AGTGGCAGTGATGAGACAGATCTGATCTGATTCAGATGTCGACCTGAGAT 243
QY 241 TTTCGAAGTACTGATCTGATCAAGAGTCTGATCTGATTCGACCTGAGAT 297
DB 244 TTTCGAAGTACTGATCTGATCAAGAGTCTGATCTGATTCGACCTGAGAT 303
QY 298 ACCAAGCTGAGATCAACGA 318
DB 304 ACCAAGCTGAGATCAACGA 324

RESULT 12
US-09-240-274-112
; Sequence 112, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 112
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 112
US-09-240-274-112

Query Match      86.9%; Score 276.2; DB 3; Length 324;
Best Local Similarity 93.5%; Pred. No. 9.3e-87;
Matches 300; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

QY 1 GAGCTCACTGATCTCCATCTCTCTGTCGATCTGGGAGACAGTCAACATCACT 60
DB 4 GAGCTCACTGATCTCCATCTCTCTGTCGATCTGGGAGACAGTCAACATCACT 63
QY 61 TCCCGGCAAGTCAAGATTAACACCTATTAAATGGTATCGACAAACCGAGGAAA 120
DB 64 TCCCGGCAAGTCAAGATTAACACCTATTAAATGGTATCGACAAACCGAGGAAA 123
QY 121 GCCCTTAAGCTCTGATCTATGTCGATCTGATTCAGATTGCAAGTGGGATTC 180
DB 124 GCCCTTAAGCTCTGATCTATGTCGATCTGATTCAGATTGCAAGTGGGATTC 183
```



```
QY 1 GAGCTCACTCACTCTCCATCTCCCTGTCTGCAATCTGTGGAGACAGAGTCACCATCAGT 60
   |||||
Db 4 GAGCTCAACCCAGTCTCCATCTCCCTGTCTGCAATCTGTAGGAGACAGAGTCACCATCAGT 63
   |||||
QY 61 TGGCGGGCAAGTCAGAGAAATTAAACACCTAATTAAATTGTAATCAGCAATAACCAAGGAAA 120
   |||||
Db 64 TGGCGGGCAAGTCAGAGCAATTAGAGGTATTTAAATTGTAATCAGCAATAACCAAGGAAA 123
   |||||
QY 121 GCCCCTAAGCTCTGATCTATGCTGCAATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTT 180
   |||||
Db 124 GCCCCTAAGCTCTGATCTTTGCTGCAATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTT 183
   |||||
QY 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAAGCTGAAGAT 240
   |||||
Db 184 ACTGGCAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGTCTGCAAGCTGAAGAT 243
   |||||
QY 241 TTTCGAAGTCTACTGTCAGAGAGTCTCAGTGCTCTGTACACTTTTGGCCAGGGGACC 300
   |||||
Db 244 TTTCGAAGTCTACTGTCAGAGAGTCTCAGTGCTCTGTACACTTTTGGCCAGGGGACC 303
   |||||
QY 301 AAGGTGAGATCAACGA 318
   |||||
Db 304 AAGGTGAGATCAACGA 321
   |||||
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:42:26 ; Search time 95.3455 Seconds
(without alignments)
5869.253 Million cell updates/sec

Title: US-10-027-725A-3

Perfect score: 342
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	267.2	78.1	516	4	US-09-472-087-33 Sequence 33, Appl
2	263.6	77.1	357	1	US-08-360-125-3 Sequence 3, Appl
3	263.6	77.1	357	2	US-08-450-578-3 Sequence 3, Appl
4	263.6	77.1	357	2	US-09-017-628-3 Sequence 3, Appl
5	263.6	77.1	357	2	US-09-014-880-3 Sequence 3, Appl
6	263.6	77.1	357	2	US-08-450-363-3 Sequence 3, Appl
7	263.6	77.1	357	4	US-09-467-903-3 Sequence 3, Appl
8	257	75.1	631	3	US-08-545-809A-31 Sequence 31, Appl
9	255.8	74.8	450	4	US-09-583-337-13 Sequence 13, Appl
10	251.8	73.6	1567	3	US-09-048-672A-17 Sequence 17, Appl
11	246.2	72.0	351	4	US-09-720-493-1 Sequence 1, Appl
12	246.2	72.0	351	4	US-09-720-493-21 Sequence 21, Appl
13	246.2	71.9	1543	4	US-09-800-729-74 Sequence 74, Appl
14	244.8	71.6	504	4	US-09-471-276-100 Sequence 100, App
15	244.2	71.4	466	4	US-09-471-276-51 Sequence 51, Appl
16	241.8	70.7	366	1	US-08-360-125-9 Sequence 9, Appl
17	241.8	70.7	366	2	US-08-450-578-9 Sequence 9, Appl
18	241.8	70.7	366	2	US-09-017-628-9 Sequence 9, Appl
19	241.8	70.7	366	2	US-09-014-880-9 Sequence 9, Appl
20	241.8	70.7	366	3	US-08-450-363-9 Sequence 9, Appl
21	241.8	70.7	366	4	US-09-467-903-9 Sequence 9, Appl
22	237.8	69.5	1212	3	US-08-545-809A-61 Sequence 61, Appl
23	233	68.1	800	3	US-08-545-809A-39 Sequence 39, Appl
24	226.2	66.1	840	3	US-09-260-527-4 Sequence 4, Appl
25	224.8	65.7	403	3	US-09-042-353-357 Sequence 357, App
26	224.8	65.7	403	3	US-08-758-417A-205 Sequence 205, App
27	220.8	64.6	288	3	US-08-851-362D-7 Sequence 7, Appl

28	218.8	64.0	417	4	US-09-203-768A-1 Sequence 1, Appl
29	217.8	63.7	357	2	US-08-652-816A-20 Sequence 58, Appl
30	217.2	63.5	469	4	US-09-471-276-58 Sequence 419, App
31	216.8	63.4	524	3	US-09-042-353-419 Sequence 219, App
32	216.8	63.4	524	3	US-08-758-417A-219 Sequence 418, App
33	216.8	63.4	4926	3	US-09-042-353-418 Sequence 268, App
34	216.8	63.4	4926	3	US-08-758-417A-268 Sequence 11, Appl
35	216.2	63.2	291	3	US-08-851-362D-11 Sequence 59, Appl
36	215.8	63.1	622	3	US-08-545-809A-59 Sequence 28, Appl
37	215.4	63.0	624	3	US-08-545-809A-28 Sequence 355, App
38	214.2	62.6	404	3	US-09-042-353-355 Sequence 203, App
39	214.2	62.6	404	3	US-08-758-417A-203 Sequence 19, Appl
40	213.2	62.6	360	4	US-09-424-840B-19 Sequence 3, Appl
41	212.8	62.2	294	3	US-08-851-362D-3 Sequence 4, Appl
42	212.6	62.2	650	3	US-08-545-809A-4 Sequence 49, Appl
43	212.2	62.0	456	4	US-09-471-276-49 Sequence 52, Appl
44	211.4	61.8	392	4	US-09-471-276-52 Sequence 5, Appl
45	211.4	61.8	402	1	US-08-259-372A-5

ALIGNMENTS

RESULT 1
US-09-472-087-33
Sequence 33, Application US/09472087

Patent No. 6682736

GENERAL INFORMATION:

APPLICANT: HANSON, DOUGLAS C.

APPLICANT: NEVEU, MARK J.

APPLICANT: MUELLER, EILEEN B.

APPLICANT: HANKE, JEFFREY H.

APPLICANT: GILMAN, STEVEN C.

APPLICANT: DAVIS, C. GREGORY

APPLICANT: CORVALAN, JOSE R.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

FILE REFERENCE: ABX-PFI

CURRENT APPLICATION NUMBER: US/09/472,087

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 60/113,647

NUMBER OF SEQ ID NOS: 147

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 33

LENGTH: 516

TYPE: DNA

ORGANISM: Homo sapiens

US-09-472-087-33

Query Match
Best Locality 78.1%; Score 267.2; DB 4; Length 516;
Matches 303; Conservative 0; Mismatches 33; Indels 6; Gaps 1;

QY	7	TCGAGCCAGGACGCGTGAACCTTCAAGACCTGTCCTGACCTGCTCTCTGT	66
DB	1	TCGGGCCAGGACGCGTGAACCTTCAAGACCTGTCCTGACCTGCTCTCTGT	60
QY	67	GCTTCATCCGACGCGTGTGTTATTAATGAGTTGATCCGACGCTCCAGGAGGC	126
DB	61	GCTTCATCCGACGCGTGTGTTATTAATGAGTTGATCCGACGCTCCAGGAGGC	120
QY	127	CTGAGTGGATCGGTTATTAATGAGTTGATCCGACGCTCCAGGAGGC	186
DB	121	CTGAGTGGATCGGTTATTAATGAGTTGATCCGACGCTCCAGGAGGC	180
QY	187	AGTGAAGTTACCATGATGAGACGCTTAAGACCACTTCTCCAGGAGTGAAGCT	246
DB	181	AGTGAAGTTACCATGATGAGACGCTTAAGACCACTTCTCCAGGAGTGAAGCT	240
QY	247	GTGACTGCGCGGACGACGCGCTGTATTAATGAGTTGATCCGACGCTCCAGG	300
DB	241	GTGACTGCGCGGACGACGCGCTGTATTAATGAGTTGATGAGTGAAGTGAAGCT	300

QY 301 TTGACACACTGGGGCCAGGAAACCTGTGACCGTCTCCCTCA 342
DB 301 ATAGACGTCTGGGGCCAGGAAACCGTCAACCGTCTCTCTCA 342

RESULT 2
US-08-360-125-3
Sequence 3, Application US/08360125
Patent No. 5767246
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246ihiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360.125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905.534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL LINE: antibody G4H
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:

CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-3

Query Match 77.1%; Score 263.6; DB 1; Length 357;
Best Local Similarity 87.7%; Pred. No. 5.4e-75;
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCGACGACTGTGAAGCCTTCAACAGACCTGTGCTACCTGCATCTCTCT 63
DB 16 GAGTCGGGGCCCAAGGACTGTGAAGCCTTCAACAGACCTGTGCTACCTGCATCTCTCT 75
QY 64 GGTGGCTCCATCCGCAGTGTGTTATTACTGAGTTGATCCGCCAGCGCTCCAGGGAG 123
DB 76 GGTGGCTCCATCAGCACTGTGTTTCTACTGGAATCGCCAGCAACCCAGGGAG 135
QY 124 GGCTGGAGTGAATCGGATCATCTATCAAGTGGCAACACTTAACAACCCGCTCC 183
DB 136 GGCTGGAGTGAATCGGATCATCTATCAAGTGGCAACACTTAACAACCCGCTCC 195
QY 184 AAGAGTCGAGTTACCATGTGACAGACAGCGTTAAGAACCACTTCTCCAGGCTGAGC 243
DB 196 AAGAGTCGAGTTACCATGTGACAGACAGCGTTAAGAACCACTTCTCCAGGCTGAGC 255
QY 244 TCTGTACTGCCCGGACACGGCCGTATTATTAATGTCGAGGATCAAGTGGTACACTTGG 303
DB 256 TCTGTACTGCCCGGACACGGCCGTATTATTAATGTCGAGGATCAAGTGGTACACTTGG 315
QY 304 ---GACAACTGGGGCCAGGAAACCTGTGACCGTCTCTCTCA 342
DB 316 GCTGACTACTGGGGCCAGGAAACCAATGTGACCGTCTCTCTCA 357

RESULT 3
US-08-450-578-3
Sequence 3, Application US/08450578
Patent No. 5837845
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845ihiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL LINE: antibody GAH
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-3

Query Match 77.1%; Score 263.6; DB 2; Length 357;
Best Local Similarity 87.7%; Pred. No. 5.4e-75;
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCCAGGACTGTGTGAACCTTACAGACCCTGTCTTCACTGCTGTCT 63
DB 16 GAGTCGGGCCCAAGAGACTGTGAACCTTACAGACCCTGTCTTCACTGCTGTCT 75
QY 64 GGTGGCTTCATCCGCACTGGTGGTTTATTACTGAGTTGATCCGCCAGCGTCCAGGAAG 123
DB 76 GTGGCTTCATCCAGCACTGGTGGTTTATTACTGAGTTGATCCGCCAGCGTCCAGGAAG 135
QY 124 GGCCTGAGTGGATCGGGTACATCTATCAACAGTGGCAACCTTCAACAAACCGTCCCTC 183
DB 136 GGCCTGAGTGGATCGGGTACATCTATCAACAGTGGCAACCTTCAACAAACCGTCCCTC 195
QY 184 AAGAGTCAGTTTACATGTCAGTAGACAGTCTAAGAACCTTCTCCCTGAGGCTGAGC 243
DB 196 AAGAGTCAGTTTACATGTCAGTAGACAGTCTAAGAACCTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACCGCGTGTATTACTGTGCGAGGTCAAGTGGTACACTTTG 303
DB 256 TCTGTGACTGCGCGGACACCGCGTGTATTACTGTGCGAGGTCAAGTGGTACACTTTG 315
QY 304 ---GACAACTGGGGCGAGGGAACCGTGTCAACGCTTCTCTCA 342
DB 316 GCTGACTGAGGGCGAGGGAACATGGTCAACGCTTCTCTCA 357

RESULT 4
US-09-017-628-3
Sequence 3, Application US/09017628
Patent No. 5990287
GENERAL INFORMATION:
APPLICANT: HOSOKAWA, Saiko
APPLICANT: TAGAWA, Toshiaki
APPLICANT: HIRAKAWA, Yoko
APPLICANT: ITO, No. 5990287hiko
APPLICANT: NAGAIKE, Kazuhito
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
FILE REFERENCE: 177/527361KH
CURRENT FILING DATE: 1998-02-02
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 357
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-3

Query Match 77.1%; Score 263.6; DB 2; Length 357;
Best Local Similarity 87.7%; Pred. No. 5.4e-75;
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCCAGGACTGTGTGAACCTTACAGACCCTGTCTTCACTGCTGTCT 63
DB 16 GAGTCGGGCCCAAGAGACTGTGAACCTTACAGACCCTGTCTTCACTGCTGTCT 75
QY 64 GGTGGCTTCATCCGCACTGGTGGTTTATTACTGAGTTGATCCGCCAGCGTCCAGGAAG 123
DB 76 GTGGCTTCATCCAGCACTGGTGGTTTATTACTGAGTTGATCCGCCAGCGTCCAGGAAG 135
QY 124 GGCCTGAGTGGATCGGGTACATCTATCAACAGTGGCAACCTTCAACAAACCGTCCCTC 183
DB 136 GGCCTGAGTGGATCGGGTACATCTATCAACAGTGGCAACCTTCAACAAACCGTCCCTC 195
QY 184 AAGAGTCAGTTTACATGTCAGTAGACAGTCTAAGAACCTTCTCCCTGAGGCTGAGC 243
DB 196 AAGAGTCAGTTTACATGTCAGTAGACAGTCTAAGAACCTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACCGCGTGTATTACTGTGCGAGGTCAAGTGGTACACTTTG 303

Db 256 TCTCTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGGTCTTACCCGACTACGGGGG 315
Qy 304 ---GACAACTGGGGCCAGGGAACCGTGTCTACCGTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGGAACATGTGTACCGTCTCTTCA 357

RESULT 5

US-09-014-880-3
Sequence 3, Application US/09014880
Patent No. 5990297
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Menderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: May 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
US-09-014-880-3

Query Match 77.1%; Score 263.6; DB 2; Length 357;
Best local similarity 87.7%; Pred.No. 5.4e-75;
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

Qy 4 GAGTCTGCGCCAGAGACTGTGAAGCTTCACAGACCTGTCTCTACTGCACTGTCTCT 63
Db 16 GAGTCGGGCCAGAGACTGTGTGAAGCTTCACAGACCTGTCTCTCACTGCACTGTCTCT 75
Qy 64 GGTGGCTTCATCCGAGAGGTGTATTACTGAGAGTGTGATCCGACAGGTCGAGGGAG 123
Db 76 GGTGGCTTCATCAGCAGTGTGTGTTTCTACTGGAAGCTGATCCGACAGCCAGGGAG 135

Qy 124 GCGCTGAGTGTGATCGGCTACATCTATCAAGTGGCAACCTTACAAACCCGTCCTC 183
Db 136 GCGCTGAGTGTGATCGGCTACATCTATCAAGTGGGAGCACTTACAAACCCGTCCTC 195
Qy 184 AAGAGTGAAGTTACCATGTAGTAGACAGCTTAAGAACACTTCTCCCTGAGGCTAGC 243
Db 196 AAGAGTGAAGTTACCATGTAGTAGACAGCTTAAGAACAGTTCTCTGAAAGCTAGC 255
Qy 244 TCTGTGACTGCGCGGACAGCGCGGTATTACTGTGCGAGTTCAGATGGGTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACAGCGCGGTATTACTGTGCGAGTTCAGATGGGTACACTTTG 315
Qy 304 ---GACAACTGGGGCCAGGGAACCGTGTCTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGGAACATGTGTACCGTCTCTTCA 357

RESULT 6

US-08-450-363-3
Sequence 3, Application US/08450363
Patent No. 6436434
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 6436434Ihiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Menderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,363
FILING DATE: May 25, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:

ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-3

Query Match 77.1%; Score 263.6; DB 3; Length 357;
Best Local Similarity 87.7%; Pred. No. 5.4e-75;
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGAGAGCTGTGTAAGCCTTCACAGACCTGTCTCCTGACCTGCTCTCT 63
DB 16 GAGTCGGGCCCCAGAGAGCTGTGTAAGCCTTCACAGACCTGTCTCCTGACCTGCTCTCT 75
QY 64 GGTGGCTCCATCCGAGAGGTGTATATACAGAGTTGGATCCGACAGCTCCAGGGAG 123
DB 76 GGTGGCTCCATCCGAGAGGTGTATATACAGAGTTGGATCCGACAGCTCCAGGGAG 135
QY 124 GGCCTGGAGTGGATCGGGTACATCTATCAGAGTGGCAACCTTACAAACCCGTCCTC 183
DB 136 GGCCTGGAGTGGATCGGGTACATCTATCAGAGTGGCAACCTTACAAACCCGTCCTC 195
QY 184 AAGAGTCGATTACCATGTCTAGTACACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 196 AAGAGTCGATTACCATGTCTAGTACACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCCCGGAGACACCGCGGTATTAATCTGTGAGAGTCAAGATGGTACACTTTG 303
DB 256 TCTGTGACTGCCCGGAGACACCGCGGTATTAATCTGTGAGAGTCAAGATGGTACACTTTG 315
QY 304 ---GACAACTGGGGCCAGGAAACCTGTGTCAACCGTCTCTCA 342
DB 316 GCTGACTTACTGGGGCCAGGAAACATGATGATCAACCGTCTCTCA 357

RESULT 7
US-09-467-903-3
Sequence 3, Application US/09467903
Patent No. 6787153
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
Toshiaki TAGAWA
Yoko HIRAKAWA

No. 6787153hiko ITO
Kazuhiko NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
Specifically Binding to Surface Antigen of Cancer
Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,903
FILING DATE: 21-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,363
FILING DATE: May 25, 1995
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER: JP158859/1991
FILING DATE: June 28, 1991
APPLICATION NUMBER: JP158860/1991
FILING DATE: June 28, 1991
APPLICATION NUMBER: JP158861/1991
FILING DATE: June 28, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: <Unknown>
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: Hybridoma producing human
antibody GAH
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:

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/ IDENTIFICATION METHOD:
/ OTHER INFORMATION:
/ PUBLICATION INFORMATION:
/ AUTHORS:
/ TITLE:
/ JOURNAL:
/ VOLUME:
/ ISSUE:
/ PAGES:
/ DATE:
/ DOCUMENT NUMBER:
/ FILING DATE:
/ PUBLICATION DATE:
/ RELEVANT RESIDUES IN SEQ ID NO:
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-467-903-3

Query Match      77.1%; Score 263.6; DB 4; Length 357;
Best Local Similarity 87.7%; Pred. No. 5,4e-75;
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1

QY 4 GAGTGTGCGCCAGAGACTGTGTGAAGCCTTACACAGACCTTCTCCCTCACTGACTGTCTT 63
DB 16 GAGTGGGGGCCAGAGACTGTGTGAAGCCTTACACAGACCTTCTCCCTCACTGACTGTCTT 75
QY 64 GGTGGCTCATCGCAGAGTGGTGTATTATCTGAGGTGGATCGGACGGTCCAGGGAAG 123
DB 76 GGTGGCTCATCAGCAGGTGTGTGTCTTCTGAACTGGATCGGACGACCCAGGAAG 135
QY 124 GGCCTGAGTGTGATCGGTATACATCTATCAAGTGGCAACACTACAAACCCGTCCCTC 183
DB 136 GGCCTGAGTGTGATTTGGTATCATTTATCAAGTGGAGACCTACTACAAACCCGTCCCTC 195
QY 184 AAGAGTCGATTACCATGTGAGTACAGACAGCTGTAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 196 AAGAGTCGATTACCATGTGAGTACAGACAGCTGTAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGAGACAGCGCCGTATTTACTGTGGAGGTCAAGATGGTACACTTGG 303
DB 256 TCTGTGACTGCGCGGAGACAGCGCCGTATTTACTGTGGAGGTCTAACCCGACTACGGGGG 315
QY 304 ---GACAACTGGGGCCAGAGGAACCTTGTCACCGTCTCTCA 342
DB 316 GCTGACTACTGGGGCCAGGGGAACATGTCACCGTCTCTTCA 357

RESULT 8
US-08-545-809A-31
; Sequence 31, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603

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1      FILING DATE: 10-MAY-1993
2      ATTORNEY/AGENT INFORMATION:
3      NAME: Freeman, John W.
4      REGISTRATION NUMBER: 29,066
5      REFERENCE/DOCKET NUMBER: 06501/004001
6      TELECOMMUNICATION INFORMATION:
7      TELEPHONE: 617-542-5070
8      TELEFAX: 617-542-8906
9      TELEX: 200154
10     INFORMATION FOR SEQ ID NO: 31:
11     SEQUENCE CHARACTERISTICS:
12     LENGTH: 631 base pairs
13     TYPE: nucleic acid
14     STRANDEDNESS: double
15     TOPOLOGY: linear
16     MOLECULE TYPE: Genomic DNA
17     ORIGINAL SOURCE:
18     ORGANISM: Homo sapiens
19     CELL TYPE: human lymphoblast
20     CELL LINE: GM1
21     US-08-545-809A-31
22
23     Query Match 75.1%; Score 257; DB 3; Length 631;
24     Best Local Similarity 94.7%; Pred. No. 9.4e-73;
25     Matches 266; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
26
27     QY 4 GAGCTTGCCCGAGACCTGCTGGAAGCCCTTCACAGACCCCTGCTCCTGACCTGACTGTCTCT 63
28     DB 305 GAGCTTGCCCGAGACCTGCTGGAAGCCCTTCACAGACCCCTGCTCCTGACCTGACTGTCTCT 364
29
30     QY 64 GGTGGCTCCATCCGACAGTGGGTTATTACTGAGAGTGAATCCGCGCAGCGTCCAGGGAG 123
31     DB 365 GGTGGCTCCATCCGACAGTGGGTTATTACTGAGAGTGAATCCGCGCAGCGTCCAGGGAG 424
32
33     QY 124 GGCCTGGAGTGAATCGGGTATCATCTATCAGAGTGGCAACCTAACAACCCGCTCCCTC 183
34     DB 425 GGCCTGGAGTGAATCGGGTATCATCTATCAGAGTGGCAACCTAACAACCCGCTCCCTC 484
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36     QY 184 AAGAGTGAATTCATGTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
37     DB 485 AAGAGTGAATTCATGTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 544
38
39     QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAG 284
40     DB 545 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAG 585
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42     RESULT 9
43     US-09-582-337-13
44     Sequence 13, Application US/09582337
45     Patent No. 6562618
46     GENERAL INFORMATION:
47     APPLICANT: Japan Tobacco, Inc.
48     TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
49     TITLE OF INVENTION: and Medicinal Uses Thereof
50     FILE REFERENCE: JI-009PCT
51     CURRENT APPLICATION NUMBER: US/09/582,337
52     CURRENT FILING DATE: 2000-06-23
53     PRIOR APPLICATION NUMBER: JP P1997-367699
54     PRIOR FILING DATE: 1997-12-25
55     PRIOR APPLICATION NUMBER: JP P1998-356183
56     PRIOR FILING DATE: 1998-12-15
57     NUMBER OF SEQ ID NOS: 27
58     SOFTWARE: PatentIn Ver. 2.0
59     SEQ ID NO 13
60     LENGTH: 450
61     TYPE: DNA
62     ORGANISM: Homo sapiens
63     FEATURE:
64     NAME/KEY: CDS
65     LOCATION: (1)..(450)
66     NAME/KEY: sig_peptide
67     LOCATION: (1)..(58)

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NAME/KEY: V-region
LOCATION: (59) ..(353)
US-09-582-337-13

Query Match 74.8%; Score 255.8; DB 4; Length 450;
Best Local Similarity 87.1%; Pred. No. 2e-72; Indels 19; Gaps 2;
Matches 311; Conservative 0; Mismatches 27;

QY 4 GAGTGTGCCCCAGAGCTGTGAAGCTTCAAGACCTGTCCCTCACTGTGCTCTCT 63
DB 74 GAGTGTGCCCCAGAGCTGTGAAGCTTCAAGACCTGTCCCTCACTGTGCTCTCT 132
QY 64 GGTGCTTCATCCGAGTGTGTATTACTGTGAAGTGGATCCGCAAGCTTCAAGGAAG 123
DB 133 GGTGCTTCATCCGAGTGTGTATTACTGTGAAGTGGATCCGCAAGCTTCAAGGAAG 192
QY 124 GGCCTGAGTGTGAGTGTGATCATCTATCAAGTGGCAACCTTACAAACCCGCTCTC 183
DB 193 GGCCTGAGTGTGAGTGTGATCATCTATCAAGTGGCAACCTTACAAACCCGCTCTC 252
QY 184 AAGAGTGAAGTATCATGTGATGACAGCTTGAAGCACTTCTCCCTGAGGCTGAGC 243
DB 253 AAGAGTGAAGTATCATGTGATGACAGCTTGAAGCACTTCTCCCTGAGGCTGAGC 312
QY 244 TCTGTGACTGCGCGGACACGCGGTGTATTACTGTGAGGT----- 286
DB 313 TCTGTGACTGCGCGGACACGCGGTGTATTACTGTGAGGTATTACTGATGATGAGT 372
QY 287 -CAGATGGGTACCTTGTGACAACTGGGGCCAGGAAACCTGTGACCTGCTCTCA 342
DB 373 GGTATTATACGACTTGTGACAACTGGGGCCAGGAAACCTGTGACCTGCTCTCA 429

RESULT 10
US-09-049-672A-17
Sequence 17, Application US/09049672A
Patent No. 6135941

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Carrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANTU01
CLONE: 1513264
US-09-049-672A-17

Query Match 73.6%; Score 251.8; DB 3; Length 1567;
Best Local Similarity 84.6%; Pred. No. 6.7e-71;
Matches 302; Conservative 0; Mismatches 37; Indels 18; Gaps 1;

QY 4 GAGTGTGCCCCAGAGCTGTGAAGCTTCAAGACCTGTCCCTCACTGTGCTCTCT 63
DB 150 GAGTGTGCCCCAGAGCTGTGAAGCTTCAAGACCTGTCCCTCACTGTGCTCTCT 209
QY 64 GGTGCTTCATCCGAGTGTGTATTACTGTGAAGTGGATCCGCAAGCTTCAAGGAAG 123
DB 210 GGTGCTTCATCCGAGTGTGTATTACTGTGAAGTGGATCCGCAAGCTTCAAGGAAG 269
QY 124 GGCCTGAGTGTGAGTGTGATCATCTATCAAGTGGCAACCTTACAAACCCGCTCTC 183
DB 270 GGCCTGAGTGTGAGTGTGATCATCTATCAAGTGGCAACCTTACAAACCCGCTCTC 329
QY 184 AAGAGTGAAGTATCATGTGATGACAGCTTGAAGCACTTCTCCCTGAGGCTGAGC 243
DB 330 AAGAGTGAAGTATCATGTGATGACAGCTTGAAGCACTTCTCCCTGAGGCTGAGC 389
QY 244 TCTGTGACTGCGCGGACACGCGGTGTATTACTGTGAGGT----- 292
DB 390 TCTGTGACTGCGCGGACACGCGGTGTATTACTGTGAGGTATTACTGATGATGAGT 449
QY 293 -----GGTACACTTGTGACAACTGGGGCCAGGAAACCTGTGACCTGCTCTCA 342
DB 450 GGGGGAACTACGATGTGACCTGTGGGGCCAGGAAACCTGTGACCTGCTCTCA 506

RESULT 11
US-09-720-493-1
Sequence 1, Application US/09720493
Patent No. 6827925

GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Williams, Andrew J
APPLICANT: Tempest, Philip R
APPLICANT: Holter, Thor L
APPLICANT: Main, Sarah H
APPLICANT: Jackson, Helen
APPLICANT: Daromola, Olaekan
TITLE OF INVENTION: Improvements relating to antibodies
FILE REFERENCE: AHB/CP575333
CURRENT APPLICATION NUMBER: US/09/720,493
CURRENT FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: GB 9814383.7
PRIOR FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 351
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: CDS
LOCATION: (1) ..(351)
US-09-720-493-1

Query Match 72.0%; Score 246.2; DB 4; Length 351;
Best Local Similarity 85.0%; Pred. No. 2.2e-69;

	Query Match	72.0%;	Score 246.2;	DB 4;	Length 351;
	Blast Local Similarity	85.0%;	Pred. No.2.e-69;		
	Matches 288;	Conservative	0;	Mismatches 48;	Indels 3; Gaps 1.
OY	4	GAGTCTGGCCCAAGAAGCTTCACAGACCCTGTCCTC	ACTGTCTCT	63	
Db	336	GAGTCCGCCCAAGAAGCTTCGAGACCTCGTCTCCT	CACCTGGCTGTCT	277	
OY	64	GGTGGCTTCATCCGACAGTGTTGTATTACTGGA	TGGATCCGCACGGCTCACAGAAAG	123	
Db	276	GATTACTCATCAGCA--GTGGTTACTA	CTGGGGCTGGATTCGGCAGCCCCAACAGAAAG	220	
OY	124	GGCCTGAGTGGATGGGGTACATCTATACA	CAAGTGGCAACACTTAACAACAACCCGTCCTC	183	
Db	219	GGCGTGGAGTGGATTGGAGTATCTATCA	TATGGGAGGACCTACTACAAACCCGTCCTC	160	
OY	184	AAGAGTCAGATTACCATGTCAAGTAGACA	CGTCTTAAGAACCACTTCTCCCTGGAGCTGAGC	243	
Db	159	AAGAGTCAGATCAACCATATCAAGTACAC	CGTCCAGAAACCAAGTCTCCCTGAAAGCTGAGC	100	

Query Match	71.9%	Score 245.8	DB 4	Length 1543
Best Local Similarity	83.1%	Pred. No.5.7e-69		
Matches	280	Conservative	0	Mismatches 57
				Indels 0
				Gaps 0
QY	4	GAGTGTGGCCCGAGACTGGTGAAGCCTTACACAGACCCTTCCCTCACTGACTGTCTCT	63	
Db	90	GAGTGGGGCCCAAGACTGGTGAAGCCTTACAGAGACCCTTCCCTCACTGACTGTCTCT	149	
QY	64	GGTGGCTCCATCCGACAGTGGTGTATTACTGAGTTGGATCCGACGCGTCCAGGGAAG	123	
Db	150	GGTGGCTCCATCAGCAGTGGTGTGTCACTACTGGAGTTGGATCCGACGACCCAGGGAAG	209	
QY	124	GCCCTGGAAGTGGATGGGGTACATCTATACAGTGGCAACACTTACAACAACCCTGCTTC	183	
Db	210	GCCCTGGAAGTGGATGGGGTACATCTTTCATATGGGGGTCACTTACTACATCCGTCCCTC	269	
QY	184	AAGAGTCGAGTACCATGTCAGTATGACAGTCAAGAACCACTTCCCTCCGAGAGCTGAGC	243	
Db	270	AAGAGTCGAGTACCATATCTGTATGACAGGCTTCAGAACCAAGTCTTCCCTGAGAGCTGAGC	329	
QY	244	TCTGTGACTGCGCGGACACGCGCCGTGTATTACTGTGCGAGGTCAAGTGGGTACACTTTTG	303	
Db	330	TCTGTGACTGCGCGGACACGCGCCGTGTATTACTGTGCGAAGTAAGATCATGAGGACCAAGA	389	
QY	304	GACAACTGGGGCCAGGGAAACCTTGTCAACGCTCTCT	340	
Db	390	GACGGGTACCAAGTGGAAATACCGAGGCTTTGACTCT	426	

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RESULT 14
US-09-471-276-100
; Sequence 100, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
; Patent No. 6822072
; FILE REFERENCE: GENSET.025C11
; CURRENT APPLICATION NUMBER: US/09/471.276
; CURRENT FILING DATE: 1999-12-21

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; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 100
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 39..503
; NAME/KEY: sig_peptide
; LOCATION: 39..95
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 9.30000019073486
; OTHER INFORMATION: seq FULLVAGPRWLS/QV
US-09-471-276-100
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Query Match 71.6%; Score 244.8; DB 4; Length 504;
Best Local Similarity 83.4%; Pred. No. 7.2e-69;
Matches 287; Conservative 3; Mismatches 51; Indels 3; Gaps 1;
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QY 1 CTGAGTCTGGCCAGAGCTGGTGAAGCTTCACAGACCCCTGCTCAGCTGAGCTGC 60
DB 108 SDRAGTCGGGCCCAAGACTGTGAAGCTTCACAGACCCCTGCTCAGCTGTA 167
QY 61 TCTGTGGCTCCATCCGAGTGTGTATTACTGAGATTGGATCCGCGACGTCAGGG 120
DB 168 TCTGGGCTCCGTCAGAGTCGTGGTACTATTGAGACTGGATCCGCGACGTCAGGG 227
QY 121 AAGGCTGAGTGTGATCGGATCACTATCAAGTGGCAACCTTACAAACCCGTC 180
DB 228 AAGGCTGAGTGTGATCGGATCACTATCAAGTGGCAACCTTACAAACCCGTC 287
QY 181 CTCAAGTGTGAGTGTGATCGGATCACTATCAAGTGGCAACCTTACAAACCCGTC 240
DB 288 CTCAAGTGTGAGTGTGATCGGATCACTATCAAGTGGCAACCTTACAAACCCGTC 347
QY 241 AGCTGTGAGTGTGATCGGATCGGATCACTATCAAGTGGCAACCTTACAAACCCGTC 300
DB 348 AGCTGTGAGTGTGATCGGATCGGATCACTATCAAGTGGCAACCTTACAAACCCGTC 407
QY 301 --TTGACAACTGGGGCCAGGAAACCTGTGTCACCGTCTCTCTC 341
DB 408 CTATTGACCCCTGGGGCCAGGAAACCTGTGTCACCGTCTCTCTC 451
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RESULT 15
US-09-471-276-51
; Sequence 51, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET 025CPI
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 51
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; ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: 38..466
; NAME/KEY: sig_peptide
; LOCATION: 38..94
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 10.899996185303
; OTHER INFORMATION: seq FULLVAAPRWLS/QV
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 423
; OTHER INFORMATION: n=a, y, c or t
; OTHER INFORMATION: Oligonucleotide
US-09-471-276-51
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Query Match 71.4%; Score 244.2; DB 4; Length 466;
Best Local Similarity 82.4%; Pred. No. 1.1e-68;
Matches 285; Conservative 7; Mismatches 47; Indels 7; Gaps 1;
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QY 64 GGTGGCTCCATCCGAGTGTGTTTACTGAGATTGGATCCGCGACGTCAGGGAG 123
DB 170 GGTGGCTCCATCCGAGTGTGTTTACTGAGATTGGATCCGCGACGTCAGGGAG 229
QY 124 GGCCTGAGTGTGATCGGATCACTATCAAGTGGCAACCTTACAAACCCGTCCTC 183
DB 230 GGCCTGAGTGTGATCGGATCACTATCAAGTGGCAACCTTACAAACCCGTCCTC 289
QY 184 AAGAGTGAATTACATGTCACTATCAAGTGGCAACCTTACAAACCCGTCCTC 243
DB 290 AAGAGTGAATTACATGTCACTATCAAGTGGCAACCTTACAAACCCGTCCTC 349
QY 244 TCTGTGACTGGCGGACAGCGCGGTATTAATCTGTGCGAG-----GTGAGTGGGTA 296
DB 350 TCTGTGACTGGCGGACAGCGCGGTATTAATCTGTGCGAG-----GTGAGTGGGTA 409
QY 297 CACTTGGACAACTGGGGCCAGGAAACCTGTGTCACCGTCTCTCTCA 342
DB 410 TGGTTCAAHMCTTGGGGCMAGGAAACCTGTGTCACCGTCTCTCTCA 455
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Perfect score: 318
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Gapop 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	289.2	90.9	796	9	AB064138
5	287.6	90.4	321	6	AR161027
6	286.6	90.1	324	9	AB063929
7	286.6	90.1	828	9	AB064098
8	286	89.9	321	9	HSIGVK16F
9	286	89.9	328	9	HUMIGHHC
10	284.4	89.4	324	9	AB095286
11	284	89.3	369	12	AF453186
12	282.8	88.9	324	9	AB063932
13	282	88.7	321	9	AY240163
14	281.8	88.6	324	9	AB095281
15	281.2	88.4	321	6	AR160973
16	281.2	88.4	321	6	AR160980
17	281.2	88.4	321	6	AR161046
18	281.2	88.4	321	9	HSIGVK110
19	281.2	88.4	711	12	HSIGKLG31

20	280.4	88.2	321	6	E12913
21	280.2	88.1	316	9	HUMIGHHS
22	280.2	88.1	387	12	AF453148
23	279.6	87.9	321	6	AR160978
24	279.6	87.9	321	6	AR160984
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28	278.6	87.6	324	9	HS439875
29	278.6	87.6	324	9	HS439875
30	278.6	87.6	324	9	HS439875
31	278.6	87.6	735	6	CO849413
32	278.6	87.6	735	6	CO849425
33	278.6	87.6	735	6	CO849427
34	278.6	87.6	736	6	CO758827
35	278.6	87.6	736	6	CO849415
36	278.6	87.6	750	6	CO849417
37	278.6	87.6	750	6	CO849421
38	278.2	87.5	761	9	AB064051
39	278.2	87.5	318	9	AF103519
40	278.2	87.5	318	12	AF044451
41	278	87.4	809	9	AB064079
42	277.6	87.3	324	6	BD187174
43	277.6	87.3	324	6	BD187175
44	277.6	87.3	333	6	BD097236
45	277.6	87.3	346	9	HSIGIB61CK

ALIGNMENTS

RESULT 1
HSA458379
LOCUS
DEFINITION
HSA458379 318 bp mRNA linear PRI 30-APR-2002
Variable region (IGKV gene), clone 94.
ACCESSION
HSA458379
VERSION
HSA458379.1 GI:20387057
KEYWORDS
IGKV gene; immunoglobulin kappa; light chain; variable region.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
Flicker, S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y.,
Valent, P., Kraft, D. and Valenta, R.
Conversion of grass allergen-specific human IGB into a protective
IgG1 antibody
Unpublished
JOURNAL
2 (bases 1 to 318)
REFERENCE
Flicker, S.
Direct Submission
Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090
Vienna, AUSTRIA
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EIKR"


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Matches 301; Conservative	0;	Mismatches 17;	Indels 0;	Gaps 0;

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Db	1	GAGCTCACTCAAGTCTCCATCTCCCTGATGGATCTGTGGAGACAGAGTCACTCAAGT	60
QY	61	TGCCGGGCAAGTCAGAGAATTAAACCTATTTTAAATTTGGTATCAGCATAAACGAGGAAA	120
Db	61	TGCCGGGCAAGTCAGAGCATTTAGCAGCTATTTTAAATTTGGTATCAGAGAACGAGGAAA	120
QY	121	GCCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAATGGGGGTCCCATCAAGGTTT	180
Db	121	GCCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAATGGGGGTCCCATCAAGGTTT	180
QY	181	AGTGGCAGTGGATATANGGACAGACATTCACCTTCACCATCAGCAGTGTGCAGCTTGAAGAT	240
Db	181	AGTGGCAGTGGATCTGGGACAGATTTTCACTTCACCATCAGCAGTGTGCAGACTTGAAGAT	240
QY	241	TTTGGCAATTTACTACTGTCAAGAGAGTCTCAATGGCCTCGTAACCTTTTGGCCAGGGGACC	300
Db	241	TTTGGCAATTTACTACTGTCAAGAGATTACAGTACCCTCCGTACACTTTTGGCCAGGGGACC	300
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Db	301	AAGCTGAGATCAAAACGA 318	

RESULT 4	
AB064138	
LOCUS	796 bp mRNA linear PRI 02-JUL-2002
DEFINITION	Homo sapiens IGHK mRNA for immunoglobulin kappa light chain VJ region, partial cds, clone:K97.

ACCESSION	AB064138
VERSION	AB064138.1
	GI:21669482

SOURCE	Homo sapiens (human)
...	...

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
1
Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.

Suzuki, K., Torii, H., Ueki, Y., Honda, T., Katsunji, H., Okada, J.,
Miyata, K. and Kurosawa, Y.

TITLE Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional

genomics
Unpublished
JOURNAL
REFERENCE

REFERENCE	2 (pages 1 to 196)
AUTHORS	Kurosawa, Y.
TITLE	Direct Submission

JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University;

Kutsukake-cho, Toyosake 470-1192, Japan
(E-mail: kurosawa@fujiita-hu.ac.jp, Tel: 81-562-93-9387)

COMMENT Please visit our web site
URL:<http://www.fujita-hu.ac.jp/immunity/>.

FEATURES	Location/Qualifiers
source	1. .796

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/organism="Homo sapiens"
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Oy	1	GAGGTCACTAGTGTCCATCCTCCTGTCGATCTGTGGAGACAGAGTCAACATCAGT	60
Db	73	GTGTCACTAGTGTCCATCCTCCTGTCGATCTGTGGAGACAGAGTCAACATCAGT	132
Oy	61	TGCCGGCAAGTCAGAAATTTAACCTATTAAATTTGTTATCAGCATTAACCAAGGAAA	120
Db	133	TGCCGGCAAGTCAGAGCATTTAGAGAGCTATTAAATTTGTTATCAGCAAAACCAAGGAAA	192
Oy	121	GCCTTAAGCTCCTGATCTATCTGTCGATCCAGTTTGCAAAAGTGGGTTCCATCAAGTTT	180
Db	193	GCCTTAAGCTCCTGATCTATCTGTCGATCCAGTTTGCAAAAGTGGGTTCCATCAAGTTT	252
Oy	181	AGTGGCAGTGGATTTGGGACAGACTTCACTTCACCATCAGCAGTCTGACGCTGGAAGAT	240
Db	253	AGTGGCAGTGGATTTGGGACAGATTTTCACTTCACCATCAGCAGTCTGCAACCTGGAAGAT	312
Oy	241	TTTTCAGATTACTACTGTCAAGAGAGTCTCAGTCCCTCGTACACTTTTGGCAGGGGACC	300
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Oy	301	AAAGTGAAGATCAAAACGA 318	
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RESULT 5	
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ARIS	
INSTRUMENT	201-1-
DATE	1-1-80
TIME	17 00M 0001

LOCUS	ARI61027	321 bp
DEFINITION	Sequence 199 from patent US 6255455.	
ACCESSION	AB161027	

ACCESSION	AR161027
VERSION	AR161027.1
KEYWORDS	GI:16226382

NE WORDS	.
SOURCE	Unknown.
ORGANISM	Unknown

REFERENCE	1 (pages 1 to 321)
UNCLASSIFIED	unclassified.
DECLASSIFICATION	unclassified.

AUTHORS Siegel, D.L.
TITLE Rh(D)-binding proteins and magnetically activated cell sorting

method for production thereof
Patent: US 6255455-A 199 03-JUL-2001;
JOURNAL

FEATURES

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Query Match	90.4%;	Score 287.6;	DB 6;	Length 321;
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Db	64	TGCCGGCAAGTCAGAGATTAGCAGCTATTAAATGGTATCAGAGAAACAGGGAAA	123
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Db	124	GCCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGTTC	183
Qy	181	AGTGCAGTGATGTATGGGACAGACTTCACTCTCCATCAGCAGTCTGACGCTGAAGAT	240
Db	184	AGTGCAGTGATGTATGGGACAGATTTCATCTCCATCAGCAGTCTGCAACTGAAGAT	243
Qy	241	TTTGGAAGTACTACTGTCTAAGAGAGTCTCAGTGCTCGTAACATTTTGGCCAGGGGAAC	300
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Qy	301	AAGGTGGAGATCAAAAGA 318	
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RESULT 6	AB063929	324 bp	mRNA	linear	PRI 02-JUL-2002
LOCUS	AB063929				
DEFINITION	Homo sapiens IGK mRNA for immunoglobulin kappa light chain VJ2 region, partial cds, clone:K102.				

ACCESSION	AB063929
VERSION	AB063929.1
	GI:21669064

SOURCE ORGANISM	Homo sapiens (human)
Homo sapiens	
Homo sapiens	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE	AUTHORS	TITLE
1	Maehori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukat, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.	Construction and Characterization of antibody libraries: isolation

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 324)

TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for

Kutsukake-cho, Toyoake 470-1192, Japan
(E-mail: kurosawa@fujita-hu.ac.jp, Tel: 81-562-93-9387)

COMMENT Please visit our web site
URL: <http://www.fujita-hu.ac.jp/immunity/>

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QY	GCCGGGACAGTCAGAGATTAAACCTATTAAATTGGTATCAGCATPAAACAGGGAAAG	121
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QY	CCCCTAAGCTCCGTATCTATGTCGCATCCAGATTCAGATTGGCAAGGGGGTCCCATCAAGTTCA	181
Db	CCCCTAAGCTCTATCTATGTCGCATCCAGATTCAGATTGGCAAGGGGGTCCCATCAAGTTCA	187
QY	GTGGCAGTGAATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGAGGCTTGAAGTT	241
Db	GTGGCAGTGAATCTGGGACAGATTCTCACTCTCACCATCAGCAGTCTGCAACTGAAGATT	247
QY	TTTGCAGTTACTACTGTTCAGAGAGTCTCAGTGGCTGTATCACTTTTGGCCAGGGAGACA	301
Db	TTTGCAGTTACTACTGTTCAGAGAGTCTCAGTGGCTGTATCACTTTTGGCCAGGGAGACA	307

QY	302	AGTGAGATCAACGA	318
Db	308	AGCTGAGATCAACGA	324

Db 308 AGCTGGAGATCAACGA 324

RESULT 7
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LOCUS	828 bp	mRNA	linear	EX1 02-JUL-2002	
DEFINITION	Homo sapiens IGHK mRNA for immunoglobulin kappa light chain V _{LJ}				

AB064098 CT:31669403
region, partial cds, contig

VERSION
KEYWORDS
SOURCE

ORGANISM Homo sapiens (Mammalia)
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:

REFERENCE

AUTHORS
Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,
Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,

TITLE

of therapeutic human antibodies and application to functional genomics

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 828)

AUTHOR
TITLE

Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; y.kurosawa@fujita-u.ac.jp

Kutsukake-cho, Toyake 4/0-1192, Japan
(E-mail: kurosawa@fujiita-hu.ac.jp, Tel: 81-562-93-9387)

COMMENT	URL	LOCATION/Qualifiers
Please visit our web site	http://www.fujita-hu.ac.jp/immunity/	

FEATURES

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CDS

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Qy 182 GTGGCAGTGATATGGAGACAGACTTCCTCCTGATCAGATTAACCCAGGGAAGTT 241
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Qy 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTCTGATCAAGTGGGGTCCCATCAAGTT 301
Db 314 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTCTGATCAAGTGGGGTCCCATCAAGTT 373
Qy 302 AGGTGAGATCAACGA 318
Db 374 AGGTGAGATCAACGA 390

RESULT 8
HSIGVK16F

LOCUS
DEFINITION H.sapiens mRNA for Ig kappa light chain variable region (V-J), subgroup I.
X73855
ACCESSION X73855.1 GI:516316
VERSION
KEYWORDS autoantibody; Ig J-segment; Ig kappa light chain; Ig subgroup I; Ig variable region; Immunoglobulin.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 321)
AUTHORS Hexham,J.M., Furmaniak,J., Pegg,C., Burton,D.R. and Smith,B.R.
TITLE Cloning of a human autoimmune response: preparation and sequencing of a human anti-thyroglobulin autoantibody using a combinatorial approach
JOURNAL Autoimmunity 12 (2), 135-141 (1992)
MEDLINE 92314301
PUBMED 1617110
REFERENCE 2 (bases 1 to 321)
AUTHORS Hexham,J.M., Partidge,L.J., Furmaniak,J., Petersen,V.B.,

TITLE
JOURNAL
MEDLINE
PUBMED
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Qy 1 GAGTCACTCACTGCTCCATCCCTGCTGATCTGATGGAGACAGATCAATCAGT 60
Db 1 GAGTCACTCACTGCTCCATCCCTGCTGATCTGATGGAGACAGATCAATCAGT 60
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RESULT 9
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LOCUS
DEFINITION Homo sapiens cell-type T-cell immunoglobulin gamma-chain, V region (IGHV) mRNA, partial cds.
L03164
ACCESSION L03164.1 GI:185399
VERSION
KEYWORDS

Colls,J.C., Pegg,C., Rees Smith,B. and Burton,D.R.
Cloning and characterisation of TPO autoantibodies using
combinatorial phage display libraries
Autoimmunity 17 (3), 167-179 (1994)
95035699
7524700
3
Hexham,J.M., Partidge,L.J., Furmaniak,J., Petersen,V.B.,
Colls,J.C., Pegg,C.A.S., Rees-Smith,B. and Burton,D.R.
Probing the human anti-thyroid peroxidase repertoire of a
Hashimoto's thyroiditis patient using combinatorial phage display
libraries
Eur. J. Immunol.
4 (bases 1 to 321)
Hexham,J.
Direct Submission
Submitted (25-JUN-1993) J. Hexham, Univ. of Sheffield, Dept. of
Mol. Biology and Biotechnology, P. O. Box 594, Firth Court, Western
Bank, Sheffield S10 2UH, UK
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ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Collier,T.A., Roben,P., O'Kennedy,R., Barbac,C.F. III, Burton,D.R. and Lerner,R.A.
TITLE A binary plasmid system for shuffling combinatorial antibody libraries
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
MEDLINE 93066172
PUBMED 1438192
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Matches 298; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 GAGCTCACTGATCTCCATCTCCCTGTCTGCATCTGTGGAGACAGATCAATCACT 60
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QY 301 AAGGTGAGATCAACAACA 318
Db 301 AAGGTGAGATCAACAACA 318
RESULT 10
AB095286 324 bp mRNA linear PRI 25-JUL-2003
LOCUS Homo sapiens VL mRNA for immunoglobulin kappa light chain, partial
DEFINITION cds, V region, clone:L-LA10.

ACCESSION AB095286
VERSION AB095286.1 GI:33235623
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Tachibana,H., Matanabe,K., Cheng,X.J., Tsukamoto,H., Kaneda,Y., Takeuchi,T., Ihara,S. and Petri Jr.W.A. Jr.
TITLE Vh3 Gene Usage in Neutralizing Human Antibodies Specific for the Entamoeba histolytica Gal/GalNAc Lectin Heavy Subunit
JOURNAL Infect. Immun. 71 (8), 4313-4319 (2003)
PUBMED 12874307
REFERENCE 2 (bases 1 to 324)
AUTHORS Tachibana,H.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-2002) Hiroshi Tachibana, Tokai University School of Medicine, Department of Infectious Diseases, Bohseidai, Isehara, Kanagawa 259-1193, Japan (E-mail:htachib@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121(ex.2603), Fax:81-463-95-5450)
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Db 307 AAGGTGAGATCAACAACA 324

KEYWORDS	
SOURCE	
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ueki, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y. Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 324)
AUTHORS	Kurosawa, Y.
TITLE	Direct Submision
JOURNAL	Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsudake-cho, Toyosake 4-70-1192, Japan (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387) Please visit our web site URL:http://www.fujita-hu.ac.jp/immunity/.
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QY	301 AAGGTGAGATCAACGCA 318
DB	307 AAGCTGAGATCAACGCA 324

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RESULT 13
LOCUS      AY240163                      321 bp  mRNA  linear  PRI 04-MAR-2004
DEFINITION Homo sapiens clone HAI anti-HAV capsid immunoglobulin G light chain
ACCESSION  AY240163
VERSION     AY240163.1 GI:29650328
KEYWORDS    '
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 321)
AUTHORS     Kim,S.-J., Jang,M.H., Stapleton,J.T., Yoon,S.O., Kim,K.S.,
            Jeon,E.-S., and Hong,H.-J.
TITLE        Neutralizing human monoclonal antibodies to hepatitis A virus
            recovered by phase display
JOURNAL      Virology 318 (2), 598-607 (2004)
PUBMED      14972527
REFERENCE   2 (bases 1 to 321)
AUTHORS     Kim,S.-J., Jang,M.H., Stapleton,J.T., Yoon,S.O., Jeon,E.-S. and
            Hong,H.-J.
TITLE        Direct Submission
JOURNAL      Submitted (20-FEB-2003) Antibody Engineering RU, Korea Research
            Institute of Bioscience and Biotechnology, Yuseung, Daejeon 305-333,
            Korea

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Best Local Similarity 93.6%; Pred. No. 1.9e-81;
Matches 294; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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DB      128 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGTTCA 187
QY      182 GTGGCAGTGATATGGGACAGACACTTCACTTCACCATCAGAGCTGTGAGGCTGAAGATT 241
DB      188 GTGGCAGTGATCTGGGACAGATTTCCTCTCCATCAGAGCTGTGAACTGAAGATT 247
QY      242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCTCGTACACTTTTGGCCAGGGAGCA 301
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QY      302 AGGTGAGATCAAA 315
DB      308 AGGTGAGATCAAA 321

RESULT 14
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DEFINITION Homo sapiens VL mRNA for immunoglobulin kappa light chain, partial
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ACCESSION  AB095281
VERSION     AB095281.1 GI:33235613
KEYWORDS    '
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Tachibana,H., Metanabe,K., Cheng,X.-J., Tsukamoto,H., Kaneda,Y.,
            Takeuchi,T., Ihara,S. and Pectri Jr,W.A. Jr.
TITLE        Vh3 Gene Usage in Neutralizing Human Antibodies Specific for the
            Entamoeba histolytica Gal/GalNAc Lectin Heavy Subunit
JOURNAL      Infect. Immun. 71 (8), 4313-4319 (2003)
PUBMED      12874307
REFERENCE   2 (bases 1 to 324)
AUTHORS     Tachibana,H.
TITLE        Direct Submission
JOURNAL      Submitted (02-NOV-2002) Hiroshi Tachibana, Tokai University School
            of Medicine, Department of Infectious Diseases, Bohseidai, Isehara,
            Kanagawa 259-1193, Japan (E-mail:htachiba@is.icc.u-tokai.ac.jp,
            Tel:81-463-93-1121 (ex.2603), Fax:81-463-95-5450)

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Query Match      88.6%; Score 281.8; DB 9; Length 324;
Best Local Similarity 93.1%; Pred. No. 2.2e-81;
Matches 295; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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QY      122 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGTTCA 181
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QY      182 GTGGCAGTGATATGGGACAGACTTCACTTCACCATCAGAGCTGTGAGGCTGAAGATT 241
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QY      242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCTCGTACACTTTTGGCCAGGGAGCA 301
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RESULT 15

ARI60973

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

321 bp DNA linear PAT 17-OCT-2001

Sequence 102 from patent US 6255455.

ARI60973

ARI60973.1

GI:16226189

Unknown.

Unknown.

Unclassified.

1 (bases 1 to 321)

Siegel, D. L.

Rh(D)-binding proteins and magnetically activated cell sorting

method for production thereof

Patent: US 6255455-A 102 03-JUL-2001;

location/Qualifiers

1..321

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/mol_type="unassigned DNA"

ORIGIN

Query Match

88.4%; Score 281.2; DB 6; Length 321;

Best Local Similarity 92.8%; Pred. No. 3.5e-81;

Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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OY 61 TGCCGGGCAAGTCAAGATTAACCTTTAATTGGTATCAGCATTAACAGGAAA 120

DB 64 TGCCGGGCAAGTCAAGATTAACCTTTAATTGGTATCAGCATTAACAGGAAA 123

OY 121 GCCCTAAGTCTCTGATCTATGCTGATCCAGTTTGAAGTGGGTCCTCATCAAGTTTC 180

DB 124 GCCCTAAGTCTCTGATCTATGCTGATCCAGTTTGAAGTGGGTCCTCATCAAGTTTC 183

OY 181 AGTGGCAGTGTATGAGACAGACTTCACTTCACCATCAGCAGTCTGAGGCTGAAGAT 240

DB 184 AGTGGCAGTGTATGAGACAGACTTCACTTCACCATCAGCAGTCTGAGGCTGAAGAT 243

OY 241 TTGCAAGTCTACTGTCACAGAGTCTCAGTCTGTCACATTGTTGGCCAGGGGACC 300

DB 244 TTGCAAGTCTACTGTCACAGAGTCTCAGTCTGTCACATTGTTGGCCAGGGGACC 303

OY 301 AAGGTGAGATCAACGA 318

DB 304 AAGGTGAGATCAACGA 321

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Job time : 1821.51 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:15:56 ; Search time 1958.75 Seconds

(without alignment)
6179.670 Million cell updates/sec

Title: US-10-027-725a-4

Perfect score: 318
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_est1: *
2: gb_est2: *
3: gb_hc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_g881: *
9: gb_g882: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	280.2	88.1	447	2	AM405752 UI-HF-BL0
2	278.6	87.6	422	2	AM407904 UI-HF-BL0
3	278.6	87.6	525	6	CD705928 EST22455
4	278.6	87.6	624	6	CD690145 EST2668 h
5	277	87.1	487	2	AM405301 UI-HF-BL0
6	275.4	86.6	493	2	AM405753 UI-HF-BL0
7	275.4	86.6	748	6	CB956867 AGENCOURT
8	275.4	86.6	799	6	CB984750 AGENCOURT
9	275.4	86.6	807	6	CB958380 AGENCOURT
10	274.6	86.4	921	4	BC341239 602463904
11	274	86.2	484	5	BC397739 BX397739
12	273.8	86.1	498	6	CD684450 EST970 hu
13	273.8	86.1	499	6	CD685478 EST1998 h
14	273.8	86.1	608	2	AM404714 UI-HF-BL0
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16	273.8	86.1	745	6	CB958128 AGENCOURT
17	273.8	86.1	797	6	CB987347 AGENCOURT
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19	272.2	85.6	598	6	CD692150 EST9689 h
20	272.2	85.6	671	4	BM830877 K-EST0104
21	272.2	85.6	684	4	BM769909 K-EST0053
22	272.2	85.6	750	6	CB985395 AGENCOURT
23	272.2	85.6	819	6	CB985931 AGENCOURT
24	270.8	85.2	471	2	AM406294 UI-HF-BL0

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28	270.6	85.1	693	6	CD684441 EST961 hu
29	269	84.6	391	2	AM404992 UI-HF-BL0
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31	269	84.6	708	6	CB956923 AGENCOURT
32	269	84.6	738	6	CB987788 AGENCOURT
33	269	84.6	742	6	CB984723 AGENCOURT
34	269	84.6	750	6	CB956930 AGENCOURT
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42	267.4	84.1	431	2	AM406886 UI-HF-BL0
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44	267.4	84.1	743	6	CB957909 AGENCOURT
45	267.4	84.1	837	6	CB984807 AGENCOURT

ALIGNMENTS

RESULT 1
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DEFINITION
UI-HF-BL0-abp-a-01-0-UI.r1 NIH MGC_37 Homo sapiens cDNA clone
IMAGE:3057288 5', mRNA sequence.
AM405752
ACCESSION
AM405752.1 GI:6924809
VERSION
AM405752.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 447)
NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
Contact: Robert Strausberg, Ph.D.
COMMENT
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E.B. Consortium/IMG at:
www-bio.lnl.gov/bdbp/image/image.html
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Location/Qualifiers
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constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonafide, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
Query Match 88.1%; Score 280.2; DB 2; Length 447;
Best Local Similarity 92.7%; Pred. No. 2.2e-78;

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 VERSION CD690145.1 GI:32210615
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 624)
 AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
 Zeng, Y.-X.
 TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
 JOURNAL Unpublished (2003)
 COMMENT Contact: Yixin Zeng
 Cancer Center
 Sun Yat-sen University
 651 Dongfeng Road East, Guangzhou 510060, China
 Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506
 Email: yxzeng@gzsunm.edu.cn.
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 IMAGE:3059259 5', mRNA sequence.
 ACCESSION AM405301
 VERSION AM405301.1 GI:6924358
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 487)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.lnl.gov/bdrr/image/image.html
 Seq primer: M13 forward.
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 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
 ORIGIN
 Query Match 87.1%; Score 277; DB 2; Length 487;
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 Matches 292; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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QY	302	AGGTGAGATCAACGA	318
Db	349	AGTAAAGATCAACGA	365
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DEFINITION	UI-HF-BL0-abp-a-02-0-UI.r1 NIH_MGC_37	Homo sapiens cDNA clone	
ACCESSION	AW405753		
VERSION	AW405753.1	GI:6924810	
KEYWORDS	EST.		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 493)		
TITLE	NIH-MGC http://mgs.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strusberg, Ph.D.		
	Email: cga@bbs-rcmail.nih.gov		
	Eco RI site shown at the beginning of the sequence.		
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.		
	cDNA Library Preparation: M.B. Soares Lab		
	cDNA Library Arrayed by: M.B. Soares Lab		
	DNA Sequencing by: M.B. Soares Lab		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLNI at: www-bio.lnl.gov/bbrp/image/image.html		
	Seq primer: M13 Forward.		
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	/note="Vector: pRTT3-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5Kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."		
ORIGIN			
Query Match	86.6%;	Score 275.4;	DB 2; Length 493;
Best Local Similarity	91.8%;	Pred. No. 7.8e-77;	
Matches 291;	Conservative	0;	Mismatches 26; Indels 0; Gaps 0;
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Db	139	GCCGGGCAAGTCAGAGCAATTAGACACTTAATTTGATGATGACAGAAACAGGAAAG	198
QY	122	CCCTCACTCTCTATCTATGTGTCATCCAGTTTGGAAAGTGGGATCCCATTAAGTTCA	181
Db	199	CCCTCACTCTCTATCTATGTGTCATCCAGTTTGGAAAGTGGGATCCCATTAAGTTCA	258
QY	182	GTGGCAGTGGATATAGGAGACAGCTTCACTTCACATCAGACAGTGTGACGCTGAAGATT	241
Db	259	GTGGCAGTGGATCTGGAGACAGATTTCACTTCACATCAGACAGTGTGCACTGAAGATT	318

QY	242	TTGCAACTACTACTCTGCAGAGAGTCTCAGTGTCTGTACACTTTTGGCCAGGGACCA	301
Db	319	TTGGAACTTCTACTCTGTCCACAGAGTTACAGTACCTCTGGACCTTGCCAAAGGACCA	378
QY	302	AGGTGAGATCAACACGA	318
Db	379	AGGTGGAATCAACACGA	395
RESULT 7			
LOCUS	CB956867	748 bp	mRNA linear EST 29-APR-2003
DEFINITION	AGENCOURT 13778741 NIH_MGC_184 Homo sapiens cDNA clone		
ACCESSION	CB956867		
VERSION	CB956867.1	GI:30212984	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 748)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: NDCM149 row: n column: 03 High quality sequence stop: 528. Location/Qualifiers		
FEATURES	1..748		
SOURCE	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:30351770" /lab_host="DH10B (T1 phage-resistant)" /clone_lib="NIH MGC 184" /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc); Site_2: SfiI (ggccgctcgcc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCATTAATGACC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGCGGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."		
ORIGIN			
Query Match	86.6%; Score 275.4; DB 6; Length 748;		
Best Local Similarity	91.8%; Pred. No. 8.9e-77;		
Matches 291; Conservative	0; Mismatches 26; Indels 0; Gaps 0;		
QY	2	AGTCACTCACTTCATCCCTCCCTGCTGATCTGTGGGAGAGAGTCCATTCAGTT	61
Db	102	AGATGACCCAGTCTTCACCTCCCTGCTGATCTGTAGGAGAGAGTCACTT	161
QY	62	GCCGGGCAAGTCAGAGATTAACACTTAATTAATGGTATCAGCATTAACAGGGAAG	121
Db	162	GCCGGGCAAGTCAGAGATTAATTAATTAATGGTATCAGAGAAAGCAGGGAAG	221
QY	122	CCCTTACGCTCTGATCTATGCTGATTCAGTTTGCAAGTGGGGTCCCATCAAGTTCA	181

Db	222	CCCTTACCTCTCTATCTATCTATGTCATCCAGTTTCCAAAGTGGGATCCCATCAAGTTCA	281
Qy	182	GTGGCAGTGATATGAGGACAGACTTCTACTCTCCACCATCAGACAGTCTGACAGCCTGAAGATT	241
Db	282	GTGGCAGTGATATCTGGGACAGATTTCACCTCACCATCAGCAGTCTGGCACTGAAGATT	341
Qy	242	TTGCAGTTTACTACTGTCTAGAGAGATCTCAGTGCTCGTACACTTTTGGCCAGGGACCA	301
Db	342	CTGCACACTTACTACTGTCTCAGCAGATCTCAGTACCCCTTGACCTTTTGGCCAGGGACCA	401
Qy	302	AGGTGAGATCAACCA 318	
Db	402	AGCTGAGATCAACCA 418	
RESULT 8			
CB984750			
LOCUS	CB984750	799 bp	mRNA linear EST 01-MAY-2003
DEFINITION	AGENCOURT.13574990 NIH_MGC.184 Homo sapiens cDNA clone		
ACCESSION	IMAGE:30326373 5', mRNA sequence.		
VERSION	CB984750		
KEYWORDS	CB984750.1 GI:30279274		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	1 (bases 1 to 799)		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cga@b-riemail.nih.gov		
	Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits		
	cDNA Library Preparation: CLONTECH Laboratories, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNLN at:		
	http://image.llnl.gov		
	Plate: NDCM133 row: k column: 22		
	High quality sequence stop: 412.		
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	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:30326373"		
	/lab_host="DH10B (T1 phage-resistant)"		
	/note="Organ: Pooled-Glandular. Vector: pDNR-LIB; Site 1: SfiI (ggcccatagccc); Site 2: SfiI (ggccgcctggccc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCCATTTATGCCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCCGAGGCGCGCCAGCATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contain inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."		
ORIGIN			
Query Match	86.6%;	Score 275.4;	DB 6; Length 799;
Best Local Similarity	91.8%;	Pred. No. 9.1e-77;	
Matches 291;	Conservative 0;	Mismatches 26;	Indels 0; Gaps 0;
Qy	2	AGCTCAGTCAAGTCTTCATCTCTCCCTGTCTGCATCTGTGGGACAGAGTCAACCATCAGTT	61
Db	101	AGATGACCCAGGCTTCATCTCTCCCTGTCTGCATCTGTGGGACAGAGTCAACCATCAGTT	160

Query Match	86.6%	Score 275.4	DB 6	Length 807
Db	161	GCCTGGGCAAGTGCAGAGAAATTAACACCTAATTTAAATGGTATCAGCATTAACACAGGAAAG	122	
Qy	62	GCCTGGGCAAGTGCAGAGAAATTAACACCTAATTTAAATGGTATCAGCATTAACACAGGAAAG	122	
Db	161	GCCTGGGCAAGTGCAGAGCAATTAGTACTCTATTAAATTTGGTATCAGCATTAACACAGGAAAG	220	
Qy	122	CCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGTTCA	181	
Db	221	CCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGTTCA	280	
Qy	182	GTGGCACTGATATATGGGACACACTTCACTCTCAACATCAGCAGCTGTGACCTTGAAGTT	241	
Db	281	GTGGCACTGATATATGGGACACACTTCACTCTCAACATCAGCAGCTGTGACCTTGAAGTT	340	
Qy	242	TTGCAAGTACTACTGCTCAAGAGAGTCTCAGTGGCTGTCACTTTTGGCCAGGAGCA	301	
Db	341	TTGCAAGTACTACTGCTCAAGAGAGTCTCAGTGGCTGTCACTTTTGGCCAGGAGCA	400	
Qy	302	AGGTGAGATCAACGCA 318		
Db	401	AGGTGAGATCAACGCA 417		
RESULT 9				
CB958380		807 bp	mRNA	linear
LOCUS		AGENCOURT 13666601 NIH MGC 184	Homo sapiens	CDNA clone
DEFINITION		IMAGE:30753194 5', mRNA sequence.		
ACCESSION		CB958380		
VERSION		CB958380.1	GI:30214496	
KEYWORDS		EST.		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryotes: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Euteleostomi; Primates; Carnivora; Catarrhini; Hominiidae; Homo.		
TITLE		1 (bases 1 to 807)		
JOURNAL		NIH-MGC http://mgs.nci.nih.gov/.		
COMMENT		National Institutes of Health, Mammalian Gene Collection (MGC)		
		Unpublished (1999)		
		Contact: Robert Strausberg, Ph.D.		
		Email: cgabs-remail.nih.gov		
		Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits		
		CDNA Library Preparation: CLONTECH Laboratories, Inc.		
		CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
		DNA Sequencing by: Agencourt Bioscience Corporation		
		DNA distribution: MGC clone distribution information can be		
		found through the I.M.A.G.E. Consortium/LNLN at:		
		http://image.lnl.gov		
		Plate: NDCM153 row: 1 column: 11		
		High quality sequence stop: 532.		
FEATURES		location/Qualifiers		
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		/mol_type="mRNA"		
		/db_xref="taxon:9606"		
		/clone="IMAGE:30753194"		
		/lab_host="DH10B (T1 phage-resistant)"		
		/clone_id="NIH_MGC_184"		
		/note="Organ: pooled-Glandular; Vector: pDNR-LIB; Site_1:		
		Site1 (ggccatcatggcc); Site_2: Site1 (ggccgctggcc);		
		Library is oligo-dT primed and directionally cloned. CDNA		
		was prepared from a glandular pool of tissues from thyroid,		
		parathyroid, adrenal, cortex and pineal gland. 5' and 3'		
		adaptors were used in cloning as follows: 5' adaptor		
		sequence: 5'-CACGCGCATATGAGCC-3' and 3' adaptor sequence:		
		5'-ATTCTAAGAGCGCGAGCGCGCGACATG-dT(30)BN-3' (where B = A,		
		C, or G and N = A, C, G, or T). Average insert size 1.38		
		kb (range 0.60-3.5 kb). 15/15 colonies contained inserts		
		by PCR. This library was enriched for full-length clones		
		and was constructed by Clontech Laboratories (Palo Alto,		
		CA). Note: this is a NIH_MGC Library."		

Best Local Similarity 91.8%; Pred. No. 9.1e-77;
Matches 291; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 2 AGCTACTGAGTCTTCATCTCTCCCTGCTGCTGAGAGACAGAGTCCATCAGTT 61
DB 101 AGATGACCCAGTCTCCATCTCTCCCTGCTGCTGAGAGACAGAGTCCATCAGTT 160
QY 62 GCCGGGCAAGTCAAGATTAACACCTATTTAAATGGTATCAGCATTAACAGGAAG 121
DB 161 GCCGGGCAAGTCAAGATTAACACCTATTTAAATGGTATCAGCATTAACAGGAAG 220
QY 122 CCCCTAAGCTCTGATCTATGCTGATCAGTTCAGAAAGTGGGGTCCCATCAAGTTCA 181
DB 221 CCCCTAAGCTCTGATCTATGCTGATCAGTTCAGAAAGTGGGGTCCCATCAAGTTCA 280
QY 182 GTGGCAGTGATATGAGACAGACTTCACTCTCACATCAGAGTCTGCAAGCTTAAGATT 241
DB 281 GTGGCAGTGATTTGGGACAGACTTCACTCTCACATCAGAGTCTGCAAGCTTAAGATT 340
QY 242 TTGCAAGTACTACTGTCAAGAGAGTCTCAGTGGCTGCTGTAACATTTTGGCCAGGAGCA 301
DB 341 TTGCAAGTACTACTGTCAAGAGAGTCAAGTACCCCTGTCATTTTGGCCAGGAGCA 400
QY 302 AGTGAGATCAACGA 318
DB 401 AGCTGAGATCAACGA 417

RESULT 10
BG341239 921 bp mRNA linear EST 27-FEB-2001
LOCUS 602463904.F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576560 5',
DEFINITION mRNA sequence.
ACCESSION BG341239
VERSION BG341239.1 GI:13147677
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 921)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
Plate: LNCMI289 row: h column: 01
High quality sequence stop: 732.
Location/Qualifiers
1. .921

FEATURES
source
1. .921
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4576560"
/tissue_type="Primary B-cells from consils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 86.4%; Score 274.6; DB 4; Length 921;
Best Local Similarity 93.7%; Pred. No. 1.7e-76;
Matches 297; Conservative 0; Mismatches 19; Indels 1; Gaps 1;
QY 2 AGCTACTGAGTCTTCATCTCTCCCTGCTGCTGAGAGACAGAGTCCATCAGTT 61
DB 88 AGATGACCCAGTCTCCATCTCTCCCTGCTGCTGAGAGACAGAGTCCATCAGTT 147
QY 62 GCCGGGCAAGTCAAGATTAACACCTATTTAAATGGTATCAGCATTAACAGGAAG 121
DB 148 GCCGGGCAAGTCAAGATTAACACCTATTTAAATGGTATCAGCATTAACAGGAAG 206
QY 122 CCCCTAAGCTCTGATCTATGCTGATCAGTTCAGAAAGTGGGGTCCCATCAAGTTCA 181
DB 207 CCCCTAAGCTCTGATCTATGCTGATCAGTTCAGAAAGTGGGGTCCCATCAAGTTCA 266
QY 182 GTGGCAGTGATATGAGACAGACTTCACTCTCACATCAGAGTCTGCAAGCTTAAGATT 241
DB 267 GTGGCAGTGATTTGGGACAGACTTCACTCTCACATCAGAGTCTGCAAGCTTAAGATT 326
QY 242 TTGCAAGTACTACTGTCAAGAGAGTCTCAGTGGCTGCTGTAACATTTTGGCCAGGAGCA 301
DB 327 TTGCAAGTACTACTGTCAAGAGAGTCAAGTACCCCTGTCATTTTGGCCAGGAGCA 386
QY 302 AGTGAGATCAACGA 318
DB 387 AGCTGAGATCAACGA 403

RESULT 11
BX397739 854 bp mRNA linear EST 28-APR-2004
LOCUS BX397739 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1041YP06 5-PRIME, mRNA sequence.
ACCESSION BX397739
VERSION BX397739.2 GI:46847409
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 854)
Li, W.B., Gruber, C.J., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1696.i
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?cs=CS0D1041DH03QP1&c=1696.r>.

FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1041YP06"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match	86.2%;	Score 274;	DB 5;	Length 854;
Best Local Similarity	93.4%;	Pred. No. 2,6e-76;		
Matches 297;	Conservative	0;	Mismatches 20;	Indels 1;
				Gaps 14;
Qy	2	AGCTCACTCACTTCATCTCTCCCTGTGTGCATCTGTGGAGACAGATCAACCATGTT	61	
Db	21	AGATGACCCCATGCTTCATCTCTCCCTGTGTGCATCTGTAGGAGACAGATCAACCATGTT	80	
Qy	62	GCCGGGCAAGTCAGAGCAATTTAACCCCTTTTAAATGGTATACAGATTAACAGGGAAG	121	
Db	81	GCCGGGCAAGTCAGAGCAATTTAACCCCTTTTAAATGGTATACAGAGAAACAGGGAAG	140	
Qy	122	CCCCTAAGCTCTGTATCTATGCTGCATGCAGTTTGCAAGTGGGGTCCCATCAAGTTCA	181	
Db	141	CCCCTAAGCTCTGTATCTATGCTGCATGCAGTTTGCAAGTGGGGTCCCATCAAGTTCA	200	
Qy	182	GTGGCAGTGATATATGGACAGACATTCACCTTCACCATCAGCAGTGTGAGCTGAAGAT	241	
Db	201	GTGGCAGTGATATATGGACAGATTCACCTTCACCATCAGCAGTGTGAGCTGAAGAT	260	
Qy	242	-TTGCAAGTATCTATCTGTCAAGAGTCTCAAGTGGCTGTACACTTTTGGCCAGGGGACC	300	
Db	261	ATTGCAAGTATCTATCTGTCAAGAGTATACAGTACCCGCTACACTTTTGGCCAGGGGACC	320	
Qy	301	AAGGTGAGATCAAAACA 318		
Db	321	AAGGTGAGATCAAAACA 338		
RESULT 12				
CD684450		498 bp	mRNA	linear EST 25-JUN-2005
LOCUS				
DEFINITION	EST970 human nasopharynx Homo sapiens cDNA, mRNA sequence.			
ACCESSION	CD684450			
VERSION	CD684450.1 GI:32199455			
KEYWORDS	EST.			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens (human)			
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
AUTHORS	Li,X.-Q., Zhou,Y., Zhang,L.-D., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.			
TITLE	Transcriptional Gene Expression Profile of Human Nasopharynx			
JOURNAL	Unpublished (2003)			
COMMENT	Contact: Yixin Zeng Cancer Center Sun Yat-sen University 651 Dongfeng Road East, Guangzhou 510060, China Tel: 86-1380-9770-743 Fax: 86-20-8775-4506 Email: yxzeng@gszsums.edu.cn.			
FEATURES				
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	/clone_lib="human nasopharynx"			
	/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"			
ORIGIN				
Query Match	86.1%;	Score 273.8;	DB 6;	Length 498;
Best Local Similarity	91.5%;	Pred. No. 2.6e-76;		
Matches 290;	Conservative	0;	Mismatches 27;	Indels 0;
				Gaps 0;
Qy	2	AGCTCACTCAAGCTCCATCTCCCTGTGTGCATCTGTGGAGACAGATCAACCATGTT	61	
Db	134	AGATACCCCATGCTTCATCTCTCCCTGTGTGCATCTGTGGAGACAGATCAACCATGTT	193	
Qy	62	GCCGGGCAAGTCAGAGATTAACCCCTTTTAAATGGTATACAGATTAACAGGGAAG	121	

Db	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	ORIGIN
Db	194	CCCGGGGCAAGTCAGGCGCATATGACACCTATTAAATTGATATCAGCAAAACCGAGGAAAG	253										
Qy	122	CCCTTAAGCTCTGATCTATGCTGCATCCAGATTTCGAAAGTGGGGTCCATCAAGTTCA	181										
Db	254	CCCTTAAGCTCTGATCTCTGCTGCATCCAGTTTGGCAAGTGGGGTCCCATCAAGTTCA	313										
Qy	182	GTGGCAGTGGATATGGGACAGATTCCTCACTCTCACCATCAGCAGTCTGACGCTGAAATTT	241										
Db	314	GTGGCAGTGGATATCGGACAGATTCCTCACTCTCACCATCAGCAGTCTGCAACTGAAATTT	373										
Qy	242	TTGCAATTTACTCTGTCGACAGAGAGTCCAGTGCCTGTACACTTTTGGCAGGGGACCA	301										
Db	374	TTGCAACTTTACTCTGTGCAACAGAGTTTCAGTACCTCTGATGCTTGGCCAGGAGACCA	433										
Qy	302	AGGTGGAGATCAAAACGA 318											
Db	434	AGGTGGAAATCAAAACGA 450											
RESULT 13	CD685478	499 bp	mRNA	linear	EST 25-JUN-2003								
LOCUS	CD685478												
DEFINITION	EST1998	human nasopharynx Homo sapiens cDNA, mRNA sequence.											
ACCESSION	CD685478.1	GI:32201469											
VERSION	EST.												
KEYWORDS	Homo sapiens												
SOURCE	Homo sapiens												
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;												
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.												
AUTHORS	1 (bases 1 to 499)												
	Liu,X.-Q., Zhou,Y., Zhang,J.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and												
	Zeng,Y.-X.												
TITLE	Transcriptional Gene Expression Profile of Human Nasopharynx												
JOURNAL	Unpublished (2003)												
COMMENT	Contact: Yixin Zeng												
	Cancer Center												
	Sun Yat-sen University												
	651 Dongfeng Road East, Guangzhou 510660, China												
	Tel: 86-1380-9770-743												
	Fax: 86-20-8775-4506												
	Email: yxzeng@gzsums.edu.cn.												
FEATURES	Location/Qualifiers												
source	1..499												
	/organism="Homo sapiens"												
	/mol_type="mRNA"												
	/db_xref="taxon:9606"												
	/tissue_type="normal nasopharynx"												
	/clone_id="human nasopharynx"												
	/note="ESTs generated from a normal nasopharynx cDNA												
	library from southern Chinese"												
ORIGIN													
Query Match	86.1%;	Score 273.8;	DB 6;	Length 499;									
Best Local Similarity	91.5%;	Pred. No. 2.6e-76;											
Matches 290;	Conservative 0;	Mismatches 27;	Indels 0;	Gaps 0;									
Qy	2	AGCTCACTCAATCTCCATCTCTCTCTGTCATCTGTGGGAGACAGATCCATCACTT	61										
Db	137	AGATGACCCATCTCCATCTCTCTCTCTGTCATCTGTGGGAGACAGATCCATCACTT	196										
Qy	62	GCGGGGCAAGTCAGAGATTTAAACCTATTAAATTGGTATCAGCATTTAAACGAGGAAG	121										
Db	197	GCGGGGCAAGTCAGAGATTTAAACCTATTAAATTGGTATCAGCATTTAAACGAGGAAG	256										
Qy	122	CCCTTAAGCTCTGATCTATGCTGCATCCAGATTTCGAAAGTGGGGTCCCATCAAGTTCA	181										

QY	242	TTGCAAGTTACTACGTGTAAGAAGATCAGGCGCTCGTAACACTTTGGCAGGGGACCA	301
Db	377	TTGCACACTTACTACTGTCAACAGAGTTACAGTACCCTCCTACTTCCGCGAGGACCA	436
QY	302	AGGTGAGATCAACGCA	318
Db	437	CGGTGAGATCAGACGA	453
RESULT 14			
LOCUS	AW404714		
DEFINITION	UI-HF-BL0-acc-c-11-0-UI.r1 NIH MGC_37 Homo sapiens cDNA clone		
ACCESSION	IMAGE:3058580 5', mRNA sequence.		
VERSION	AW404714		
KEYWORDS	AW404714.1 GI:6923771		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 608)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: rgs@bbs-riemail.nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA sequencing by: M.B. Soares Lab clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at: www-bio.liml.gov/bbtp/image/image.html Seq primer: M13 Forward. Location/Qualifiers 1..608 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3058580" /tissue_type="lymph" /cell_type="germinal center B cells" /cell_line="MGC85" /lab_host="DH10B (LT)" /clone_lib="NIH MGC_37" /note="Vector: pRTT3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."		
FEATURES			
SOURCE			
Query Match	86.1%	Score 273.8;	DB 2; Length 608;
Best Local Similarity	91.5%;	Pred. No. 2.7e-76;	
Matches	290;	Conservative 0;	Mismatches 27; Indels 0; Gaps 0;
QY	2	AGCTCACTCACTTCACATCCTCCTCTGTGCACTCTGTGGAGACAGATCAACATCACTT	61
Db	49	AGATGACCCCACTTCATCCTCCCTCTGTGCACTCTGTAGGAGACAGATCAACATCACTT	108
QY	62	GCCGGGCAAGTCAGAGATTAACACTTAAATTTAAATTTGGATCAGATTAACAGGGAAG	121
Db	109	GCCGGGCAAGTCAGAGATTAACACTTAAATTTAAATTTGGATCAGATTAACAGGGAAG	168
QY	122	CCCTTAAGCTCTGTATCTATGCTGCATCACTTTTGAAGAGTGGGCTCCCATCAAGTTCA	181
Db	169	CCCTTAAGCTCTGTATCTATGCTGCATCAAGTTTGAAGAGTGGGCTCCCATCAAGTTCA	228
QY	182	GTGGCAGTGTATTTGGACAGACTTCACTTCAATCAATGACAGTGTGACGCTGAAGTT	241

Db	229	GTGGCACTGATCTGGGAGACGATTTTACTCTCTCACACCATCAGACGACGCTCGCAACTGAATTT	288
Qy	242	TTTGCAACTTACTACTGTCCAGAGAGAGTCTGCTGCTGTGACATTTTGGCCAGGGGACCA	301
Db	289	TTTGCAACTTACTCTCTGTCACAGAGTTTCACTACCCCGTACAGTTTGGCCAGGGGACCA	348
Qy	302	AGGTGGAGATCAACGCA	318
Db	349	GACTGGAGATCAACGCA	365
RESULT 15			
LOCUS	CB959008		
DEFINITION	CB959008	724 bp	mRNA linear EST 29-Apr-2003
ACCESSION	AGNCOURT_13664954	NIH_MGC_184	Homo sapiens cDNA clone
VERSION	IMAGE:30354121	5'	mRNA sequence.
KEYWORDS	CB959008		
SOURCE	CB959008.1	GI:30215124	EST.
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
JOURNAL	Mammalia; Euteheria; Primates; Catarrhini; Homindae; Homo.		
COMMENT	1 (bases 1 to 724)		
	NIH-MGC http://mgc.nci.nih.gov/		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabs-remail.nih.gov		
	Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palokovits		
	CDNA Library Preparation: CLONTECH Laboratories, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.lnl.gov		
	Plate: NDCM55 row: p column: 02		
	High quality sequence stop: 549.		
FEATURES			
source	Location/Qualifiers		
	1..724		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:30354121"		
	/lab_host="DH10B (TI phage-resistant)"		
	/clone_id="NIH_MGC_184"		
	/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:		
	SfiI (ggccatcaggcc); Site_2: SfiI (ggccggcctggcc);		
	Library is oligo-dT primed and directionally cloned. cDNA		
	was prepared from a glandular pool of tissues from thymoid,		
	parathyroid, adrenal, cortex and pineal gland. 5' and 3'		
	adaptors were used in cloning as follows: 5' adaptor		
	sequence: 5'-CACGGCATTAATGCG-3' and 3' adaptor sequence:		
	5'-ATTCTAGAGCCGACGGGGCGGACATG-3' (where B = A,		
	C, or G and N = A, C, G, or T). Average insert size 1.38		
	kb (range 0.60-3.5 kb). 15/15 colonies contained inserts		
	by PCR. This library was enriched for full-length clones		
	and was constructed by Clontech Laboratories (Palo Alto,		
	CA). Note: this is a NIH_MGC Library."		
ORIGIN			
Query Match	86.1%;	Score 273.8;	DB 6; Length 724;
Best Local Similarity	91.5%;	Pred. No. 2.9e-76;	
Matches 290; Conservative	0;	Mismatches 27; Indels	0; Gaps 0;
Qy	2	AGTCTACTCAGTCTCCATCTCTCTGCTGATCTGGGAGAGAGTACCATCACTT	61
Db	97	AGATGACCCAGTCTCCATCTCTCTGCTGATCTGGGAGAGAGTCACTATCACTT	156
Qy	62	GCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATTAACACGAGAA	121
Db	157	GCCGGGCAAGTCAGAGATTAACACGATTAATTTAAATTGTATCAGCAGAAACGAGAA	216

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QY 122 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTGGCAAAGTGGGGTCCCATCAAGGTTCA 181
    |||||
Db 217 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTGGCAAAGTGGGGTCCCATCAAGGTTCA 276
    |||||
QY 182 GTGGCAGTGGATATGGGACAGACTTCACTCAACCATCAGCAGTGTGAGGCTGAAGATT 241
    |||||
Db 277 GTGGCAGTGGATCTGGGACAGATTTCACCTCAACCATCAGCAGTGTGAGGCTGAAGATT 336
    |||||
QY 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTGGCCAGGGACCA 301
    |||||
Db 337 TTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGACGTTGGCCAGGGACCA 396
    |||||
QY 302 AGGTGGAGATCAACGA 318
    |||||
Db 397 AGGTGGAATCAACGA 413
    |||||
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Search completed: July 27, 2005, 12:32:11
Job time : 1961.75 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 03:58:31 ; Search time 299.048 Seconds
(without alignments)
6294.891 Million cell updates/sec

Title: US-10-027-725A-4

Perfect score: 318
Sequence: 1 gagctcactcagtcctcctc.....ccaagtcgagatcaacga 318

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	318	100.0	318	6	ABK89640 DNA encod
2	287.6	90.4	321	5	AAH68701 Human ant
3	287.6	90.4	321	9	ACD45365 Anti-Rh(D
4	281.2	88.4	321	5	AAH68720 Human ant
5	281.2	88.4	321	5	AAH68654 Human ant
6	281.2	88.4	321	5	AAH68647 Human ant
7	281.2	88.4	321	9	ACD45311 Anti-Rh(D
8	281.2	88.4	321	9	ACD45318 Anti-Rh(D
9	281.2	88.4	321	2	AAH68781 Anti-Rh(D
10	280.4	88.2	321	2	AAH68781 Anti-Rh(D
11	279.6	87.9	321	5	AAH68723 Human ant
12	279.6	87.9	321	5	AAH68658 Human ant
13	279.6	87.9	321	5	AAH68724 Human ant
14	279.6	87.9	321	5	AAH68652 Human ant
15	279.6	87.9	321	9	ACD45388 Anti-Rh(D
16	279.6	87.9	321	9	ACD45387 Anti-Rh(D
17	279.6	87.9	321	9	ACD45316 Anti-Rh(D
18	279.6	87.9	321	9	ACD45322 Anti-Rh(D
19	278.6	87.6	735	13	ADR23329 Human CD7
20	278.6	87.6	735	13	ADR23331 Human CD7

21	278.6	87.6	735	13	ADR23317
22	278.6	87.6	736	12	ADH34564
23	278.6	87.6	738	13	ADR23319 Human CD7
24	278.6	87.6	750	13	ADR23321 Human CD7
25	278.6	87.6	750	13	ADR23325 Human CD7
26	277.6	87.3	324	10	AAH52120 Human ant
27	277.6	87.3	333	5	AAH74684 Nucleotid
28	277.6	87.3	333	10	ABT34320 Hepatit
29	277.6	87.3	720	5	ABT34315 Hepatit
30	277.6	87.3	900	5	AAH74688 Nucleotid
31	277.6	87.3	900	10	ABT34324 Hepatit
32	277	87.1	396	2	AAH75423 Human ant
33	276.4	86.9	321	5	AAH68713 Human ant
34	276.4	86.9	321	5	AAH68703 Human ant
35	276.4	86.9	321	9	ACD45377 Anti-Rh(D
36	276.4	86.9	321	9	ACD45367 Anti-Rh(D
37	276.2	86.9	324	5	AAH68657 Human ant
38	276.2	86.9	324	5	AAH68712 Human ant
39	276.2	86.9	324	5	AAH68646 Human ant
40	276.2	86.9	324	9	ACD45321 Anti-Rh(D
41	276.2	86.9	324	9	ACD45376 Anti-Rh(D
42	276.2	86.9	324	9	ACD45310 Anti-Rh(D
43	276	86.8	720	2	AAH36070 DNA encod
44	276	86.8	720	10	ABH76706 Human ser
45	276	86.8	720	12	ADL92368 Human pha

ALIGNMENTS

```
RESULT 1
ID ABK89640 standard; DNA; 318 BP.
XX
AC ABK89640;
XX
DT 21-OCT-2002 (first entry)
XX
DE DNA encoding human IGE Fab clone 94 light chain.
XX
KW Human; fab; ds; gene; antiallergic; vaccine; grass pollen; phi p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..318
XX /tag= a
XX /product= "Fab clone 94 light chain"
XX /tag= b
XX /note= "FR1 region"
XX /tag= c
XX /note= "CDR1 region"
XX /tag= d
XX /note= "FR2 region"
XX /tag= e
XX /note= "CDR2 region"
XX /tag= f
XX /note= "CDR3 region"
XX /tag= g
XX /note= "FR3 region"
XX /tag= h
XX /note= "CDR3 region"
XX
XX WO200253595-A1.
XX 11-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-SE002908.
```

XX	29-DEC-2000; 2000SE-00004892.
XX	(PRAA) PHARMACIA DIAGNOSTICS AB.
XX	Flicker S, Steinberger P, Kraft D, Valenta R;
XX	WPI; 2002-583604/62.
XX	P-PSDB; ABG30448.
XX	Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
XX	variable region of group 2 allergen specific-human IgE Fabs, useful for
XX	diagnosing or passive immunotherapy of type I allergy, for environmental
XX	allergen detection.
XX	Disclosure; Page 34; 45pp; English.
XX	This invention relates to the DNA and protein sequences of group 2
XX	allergen-specific human IgE Fabs and methods for their use. The proteins
XX	of the invention may have antiallergic activities and may be used as a
XX	vaccine or an inhibitor of binding of grass pollen allergen patient's IgE
XX	antibodies to Phl p 2 (a major Timothy grass pollen allergen). The group
XX	2 allergen-specific fabs of the invention may be useful for environmental
XX	allergen detection and for standardisation of allergen extracts. The fabs
XX	- or a vaccine against a type I allergy is useful for passive
XX	immunotherapy of type I allergy, it is also useful for diagnosing a type
XX	I allergy. The allergen-specific fabs of the invention are useful for
XX	inter alia, diagnosis, therapy and prevention of type I allergy. They are
XX	also useful for identification of group 2 allergen-containing pollen and
XX	may be used for blocking the binding of grass pollen allergic patients
XX	IgE antibodies to Phl p 2. The present sequence represents the DNA
XX	encoding the human IgG fab, clone 94 light chain protein of the invention
XX	Sequence 318 BP; 84 A; 81 C; 77 G; 76 T; 0 U; 0 Other.
XX	Query Match 100.0%; Score 318; DB 6; Length 318;
XX	Best Local Similarity 100.0%; Pred. No. 1e-90;
XX	Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 GAGCTCACTCACTCACTCACTCCCTGCTGTCATCTGTGGAGACAGACTCACTCACT 60
DB	1 GAGCTCACTCACTCACTCACTCCCTGCTGTCATCTGTGGAGACAGACTCACTCACT 60
QY	61 TCGCGGGCAAGTCAAGAAATTAAACCTTAAATTTGTTATACAGATTAACCAAGGAAA 120
DB	61 TCGCGGGCAAGTCAAGAAATTAAACCTTAAATTTGTTATACAGATTAACCAAGGAAA 120
QY	121 GCCCTTAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 180
DB	121 GCCCTTAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 180
QY	181 AGTGCAGTGTATATGAGACAGACTTCACTTCAACATCAGACAGTCTGACAGCTGAAGAT 240
DB	181 AGTGCAGTGTATATGAGACAGACTTCACTTCAACATCAGACAGTCTGACAGCTGAAGAT 240
QY	241 TTTCGAAGTACTACTGTCTCAGAGAGTCTCAGTCCCTGTAACCTTTTGGCCAGGGAGCC 300
DB	241 TTTCGAAGTACTACTGTCTCAGAGAGTCTCAGTCCCTGTAACCTTTTGGCCAGGGAGCC 300
QY	301 AAGGTGAGATCAAAACA 318
DB	301 AAGGTGAGATCAAAACA 318
RESULT 2	
AAH68701	AAH68701 standard; DNA, 321 BP.
AAH68701;	
14-SEP-2001	(first entry)
Human anti-Rh(D) antibody clone SH13 nucleotide sequence.	

Query Match	90.4%	Score 287.6	DB 5	Length 321
Best Local Similarity	94.0%	Pred. No. 4.8e-81		
Matches 299	Conservative 0	Mismatches 19	Indels 0	Gaps 0
Sequence 321 BP	84 A	89 C	74 G	74 T
	0 U	0 Other		
1	GAGCTCACGTCGTCATCCCTCCGTCGTCATGTCGGGAGACAGATCCATCAGT	60		
4	GAGCTCACGTCGTCATCCCTCCGTCGTCATGTCGGGAGACAGATCCATCAGT	63		
61	TGCCGGGCAAGTCAGAGATTAAACCTATTAAATTTGGTATCAGCATTAACGAGGAAA	120		
64	TGCCGGGCAAGTCAGAGATTAAACCTATTAAATTTGGTATCAGCATTAACGAGGAAA	123		
121	GCCCTTAAGCTCTGATCTATGCTGCATTCAGTTGGCAAGTGGGGTCCCATCAAGTTC	180		
124	GCCCTTAAGCTCTGATCTATGCTGCATTCAGTTGGCAAGTGGGGTCCCATCAAGTTC	183		
181	AGTGGCAGTGAATATGGGACAGACCTTCACTCTCACCATTATAGCAGTCTGAGCTGAAGT	240		
184	AGTGGCAGTGAATATGGGACAGACCTTCACTCTCACCATTATAGCAGTCTGAGCTGAAGT	243		
241	TTTGAAGTTATTAATCTGTCGAAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC	300		
244	TTTGAAGTTATTAATCTGTCGAAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC	303		
301	AAGGTGAGATCAAAAGA	318		
304	AAGGTGAGATCAAAAGA	321		

ACD45365
ID ACD45365 standard; DNA; 321 BP.
XX
AC ACD45365;
XX
DT 12-SEP-2003 (first entry)
XX
DE Anti-Rh(D) light chain SH13 DNA.
XX
KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;
XX magnetically activated cell sorting.
XX
OS Homo sapiens.
XX
PN US2003040605-A1.
XX
PD 27-FEB-2003.
XX
PF 04-MAY-2001; 2001US-00848798.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-0088404S.
PR 10-APR-1998; 98US-0081380P.
PR 29-JAN-1999; 99US-00240274.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2003-512273/48.
DR P-PSDB; ABO27451.
XX
PT New human Rh(D) -binding protein useful for various diagnostic and
XX therapeutic applications, including typing of blood or blood products.
XX
PS Claim 12; Page 57; 187pp; English.
XX
CC The invention relates to an isolated Rh(D) binding protein. The protein
XX can be used for magnetically activated cell sorting. The protein is
XX useful in various diagnostic and therapeutic applications in humans,
XX including typing of blood or blood products. The present sequence
XX represents DNA encoding a human anti-Rh(D) chain
XX
SQ Sequence 321 BP; 84 A; 89 C; 74 G; 74 T; 0 U; 0 Other;
Query Match 90.4%; Score 287.6; DB 9; Length 321;
Best Local Similarity 94.0%; Pred. No. 4.8e-81;
Matches 299; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1 GAGCTCACTCACTGCTCCCTGCTGATCTGAGGAGACAGATCACTCACT 60
DB 4 GAGCTCACTCACTGCTCCCTGCTGATCTGAGGAGACAGATCACTCACT 63
QY 61 TCCCGGCAAGTCAGAGATTACACTATTAAATGGATACAGATTAACAGGAAA 120
DB 64 TCCCGGCAAGTCAGAGATTACACTATTAAATGGATACAGATTAACAGGAAA 123
QY 121 GCCCTAAGCTCTGATCTATGCTGATCCAGTTTGCAAGTGGGTCCTCAAGGTTT 180
DB 124 GCCCTAAGCTCTGATCTATGCTGATCCAGTTTGCAAGTGGGTCCTCAAGGTTT 183
QY 181 AGTGGCACTGATATGAGACAGACTTCACTCAGATCAGAGATCTGAGCTGAAGT 240
DB 184 AGTGGCACTGATATGAGACAGATTCTCACTCAGATCAGAGATCTGAGCTGAAGT 243
QY 241 TTGCAAGTACTACTGTCAAGAGAGCTCAGTGGCTGTGATCACTTTGGCCAGGGACC 300
DB 244 TTGCAAGTACTACTGTCAAGAGAGCTCAGTGGCTGTGATCACTTTGGCCAGGGACC 303
QY 301 AAGGTGAGATCAAAAGA 318
DB 304 AAGGTGAGATCAAAAGA 321

RESULT 4
AAH68720
ID AAH68720 standard; DNA; 321 BP.
XX
AC AAH68720;
XX
DT 14-SEP-2001 (first entry)
XX
DE Human anti-Rh(D) antibody clone SH49 nucleotide sequence.
XX
XX
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
XX red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
OS Homo sapiens.
XX
PN US6255455-B1.
XX
PD 03-JUL-2001.
XX
PF 29-JAN-1999; 99US-00240274.
XX
PR 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-0088404S.
PR 10-APR-1998; 98US-0081380P.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2001-388931/41.
DR P-PSDB; AAG93663.
XX
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
XX diagnostics requiring a human instead of an animal antibody and in
XX therapeutic medicine.
XX
PS Example 3; Col 79; 162pp; English.
XX
CC The present invention describes an isolated Rh(D) binding protein,
XX preferably a human antibody, (I) having an amino acid sequence comprising
XX one of the sequences (S) given in AAG93558 to AAG93669. (I) has
XX immunostimulant activity, and can be used as an immune system stimulant.
XX (I) can be used in diagnostic and therapeutic medicine. The antibodies
XX are used in diagnostics that require human antibodies instead of animal
XX antibodies, such as determine the Rh phenotype of human red blood cells.
XX AAH68615 to AAH68726 represent the nucleotide sequence which encode
XX AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
XX chain CDR3 amino acid sequences which are given in the exemplification of
XX the present invention
XX
SQ Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;
Query Match 88.4%; Score 281.2; DB 5; Length 321;
Best Local Similarity 92.8%; Pred. No. 5.2e-79;
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 1 GAGTCACTCACTGCTCCCTGCTGATCTGAGGAGACAGATCACTCACT 60
DB 4 GAGTCACTCACTGCTCCCTGCTGATCTGAGGAGACAGATCACTCACT 63
QY 61 TCCCGGCAAGTCAGAGATTACACTATTAAATGGATACAGATTAACAGGAAA 120
DB 64 TCCCGGCAAGTCAGAGATTACACTATTAAATGGATACAGATTAACAGGAAA 123
QY 121 GCCCTAAGCTCTGATCTATGCTGATCCAGTTTGCAAGTGGGTCCTCAAGGTTT 180
DB 124 GCCCTAAGCTCTGATCTATGCTGATCCAGTTTGCAAGTGGGTCCTCAAGGTTT 183
QY 181 AGTGGCACTGATATGAGACAGACTTCACTCAGATCAGAGATCTGAGCTGAAGT 240
DB 184 AGTGGCACTGATATGAGACAGATTCTCACTCAGATCAGAGATCTGAGCTGAAGT 243

```
Oy 241 TTTCAGATTACTACTGTCAGAGAGCTCTCAGTCCCTGTAACATTTTGGCCAGGGGACC 300
Db 244 TTTCACACTTACTACTGTCAGAGAGCTCTCAGTCCCTGTAACATTTTGGCCAGGGGACC 303
Oy 301 AAGGTGAGATCAACGCA 318
Db 304 AAGGTGAGATCAACGCA 321

RESULT 5
AAH68654
ID AAH68654 standard; DNA; 321 BP.
AC AAH68654;
XX
XX 14-SEP-2001 (first entry)
DT
XX
XX Human anti-Rh(D) chain I09 nucleotide sequence.
DE
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KM red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
XX Homo sapiens.
OS
XX US6255455-B1.
PN
XX 03-JUL-2001.
PD
XX 29-JAN-1999; 99US-00240274.
PF
XX 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
XX 10-APR-1998; 98US-0081380P.
XX
XX (TYPE-) UNIV PENNSYLVANIA.
PA
XX
XX Siegel DL;
PI
XX
XX WPI; 2001-388931/41.
DR P-PSDB; AAG93597.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX Example 2; Col 56; 162pp; English.
XX
XX The present invention describes an isolated Rh(D) binding protein,
XX preferably a human antibody, (I) having an amino acid sequence comprising
XX one of the sequences (S) given in AAG93558 to AAG93669. (I) has
XX immunostimulant activity, and can be used as an immune system stimulant.
XX (I) can be used in diagnostic and therapeutic medicine. The antibodies
XX are used in diagnostics that require human antibodies instead of animal
XX antibodies, such as determine the Rh phenotype of human red blood cells.
XX AAH68615 to AAH68726 represent the nucleotide sequence which encode
XX AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
XX chain CDR3 amino acid sequences which are given in the exemplification of
XX the present invention
XX
XX Sequence 321 BP; 85 A; 87 C; 73 G; 76 T; 0 U; 0 Other;
SQ
Query Match 88.4%; Score 281.2; DB 5; Length 321;
Best Local Similarity 92.8%; Pred. No. 5.2e-79;
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
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Oy 121 GCCCTTAAGCTCTGATCTATGCTGATTCACATTTCAGAAAGTGGGTCCTCAAGTTTC 180
Db 124 GCCCTTAAGCTCTGATCTATGCTGATTCACATTTCAGAAAGTGGGTCCTCAAGTTTC 183
Oy 181 AGTGGCAGTGGATATGAGACAGACTTCATCTCAGTCATCGACATCTGACCTGAAGAT 240
Db 184 AGTGGCAGTGGATCTGGACAGATTCCATCTTCACATCGACATCTGCAACTGAAAT 243
Oy 241 TTTCAGATTACTACTGTCAGAGAGCTCTCAGTCCCTGTAACATTTTGGCCAGGGGACC 300
Db 244 TTTCACACTTACTACTGTCAGAGAGCTCTCAGTCCCTGTAACATTTTGGCCAGGGGACC 303
Oy 301 AAGGTGAGATCAACGCA 318
Db 304 AAGGTGAGATCAACGCA 321

RESULT 6
AAH68647
ID AAH68647 standard; DNA; 321 BP.
AC AAH68647;
XX
XX 14-SEP-2001 (first entry)
DT
XX
XX Human anti-Rh(D) chain I02 nucleotide sequence.
DE
XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KM red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
XX Homo sapiens.
OS
XX US6255455-B1.
PN
XX 03-JUL-2001.
PD
XX 29-JAN-1999; 99US-00240274.
PF
XX 11-OCT-1996; 96US-0028550P.
PR 27-JUN-1997; 97US-00884045.
XX 10-APR-1998; 98US-0081380P.
XX
XX (TYPE-) UNIV PENNSYLVANIA.
PA
XX
XX Siegel DL;
PI
XX
XX WPI; 2001-388931/41.
DR P-PSDB; AAG93590.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX Example 2; Col 54; 162pp; English.
XX
XX The present invention describes an isolated Rh(D) binding protein,
XX preferably a human antibody, (I) having an amino acid sequence comprising
XX one of the sequences (S) given in AAG93558 to AAG93669. (I) has
XX immunostimulant activity, and can be used as an immune system stimulant.
XX (I) can be used in diagnostic and therapeutic medicine. The antibodies
XX are used in diagnostics that require human antibodies instead of animal
XX antibodies, such as determine the Rh phenotype of human red blood cells.
XX AAH68615 to AAH68726 represent the nucleotide sequence which encode
XX AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
XX chain CDR3 amino acid sequences which are given in the exemplification of
XX the present invention
XX
XX Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;
SQ
Query Match 88.4%; Score 281.2; DB 5; Length 321;
Best Local Similarity 92.8%; Pred. No. 5.2e-79;
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
```

QY	1	GAGCTCACTCAATCTCCATCTCCCTCGTCTGCATCTGTGGGACACAGAGTCACTCACT	60
Db	4	GAGCTCACTCAATCTCCATCTCCCTCGTCTGCATCTGTGGGACACAGAGTCACTCACT	63
QY	61	TCGCCGGGCAAGTCAGAGAAATTAACACTTATTTAAATTTGGATCAGCATAAACCAAGGAAA	120
Db	64	TCCGGGGCAAGTCAGAGCAATTAAGCACTATTTAAATTTGGATATAGCAGAAACCAAGGAAA	123
QY	121	GCCCCTAAGCTCTGTATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGTTTC	180
Db	124	GCCCCTAAGCTCTGTATCTATGCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGTTTC	183
QY	181	AGTGCAGTGTATATGGGACAGACTTCACTCTCAATCAGACAGTCTGCACCTGAAAGAT	240
Db	184	AGTGCAGTGTATATGGGACAGACTTCACTCTCAATCAGACAGTCTGCACCTGAAAGAT	243
QY	241	TTTGGCAATTAATCTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACC	300
Db	244	TTTGGCAATTAATCTGTCAAGAGAGTTCACGTACCTGTGGACGTTTGGCCAGGGGACC	303
QY	301	AAGGTGAGATCAAAAGCA 318	
Db	304	AAGGTGAAATCAAAAGCA 321	

RESULT 7
ACD45311
ID ACD45311 standard; DNA; 321 BP

DT	12-SEP-2003	(first entry)
XX		
DE	Anti-Rh(D)	chain I02 DNA.

KW Human; ds; gene; RH(D) binding protein; blood typing; blood product
KW magnetically activated cell sorting.

OS Homo sapiens.

PN US2003040605-A1.

PF 04-MAY-2001; 2001US-00848798.

PR 11-OCT-1996; 96US-0028550P.

PR 10-APR-1998; 98US-0081380P.

XX

PA (TYPE-) UNIV PENNSYLVANIA

PI Siegel DL

DR WPI; 2003-512273/48.

DR P-PSDB; ABQ27397.

PT New human Rh(D)-binding protein useful for various diagnostic and therapeutic applications, including typing of blood or blood products

PS Claim 12; Page 39; 187pp; English

CC The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents DNA encoding a human anti-Rh(D) chain

Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;

Query Match	Score	DB	Length
Best Local Similarity	88.4%;	281.2;	321;
	92.8%;	Pred. No. 5.2e-79;	

	Matches	295;	Conservative	0;	Mismatches	22;	Indels	0;	Gaps	0
QY	1	GAGCTCACTCA	GTCTCCATCCTCCTGTCTGTGCATCTGTGGGAGACAGAGTCA	CACCATCA	GT	60				
Db	4	GAGCTCA	CCCGAGTCTCCATCTCCCTCTGTCTGCATCTGTGGAGACAGAGTCA	CCCATCT	CT	63				
QY	61	TGCGGGGCA	ATCGAGAGATTAAACCATTTAAATGTGTATTCAGATTA	ACCAGAGAA	120					
Db	64	TGCGGGGCA	ATCGAGATTAAGCAGCTATTAAATTGTATTCAGAGAAACAGAGAA	123						
QY	121	GCCCCTA	AGCTCTGATCTATCTGCATCCAGTTTGCAAGTGGGTC	CCATCAAGTTT	180					
Db	124	GCCCCTA	AGCTCTGATCTATCTGCATCCAGTTTGCAAGTGGGTC	CCATCAAGTTT	183					
QY	181	AGTGGCAGT	GAATATGSGACAGACTTCACTCTCACCATACAGAGTCTTGACGCTGA	AGAT	240					
Db	184	AGTGGCAGT	GAATCTGGAGCAGATTTCACTCTCACCATCAGCAGCTCCAACTTGA	AGAT	243					
QY	241	TTTGGAA	ATTACTACTGTCAAGAGAGTCTCAGTGTCTGTACACTTTTGGCCAGGGG	AGCC	300					
Db	244	TTTGGAA	ATTACTACTGTCAACAGAGTATACAGTACCTGTGGACCTTGGCCAA	GGAGCC	303					
QY	301	AAGGTGAGAT	CAAAACGA	318						
Db	304	AAAGTGA	AAATCAAAACGA	321						

RESULT 8
ACD45318
ID ACD45318 standard; DNA; 321 BP

AC ACD45318;

DT 12-SEP-2003 (first entry)

DE Anti-Rh(D) chain I09 DNA.

KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;

xx KW magnetically activated cell sorting.

OS Homo sapiens.

PN US2003040605-A1

PD 27-FEB-2003.

PF 04-MAY-2001; 2001US-00848798.

PR 11-OCT-1996; 96US-0028550P

PR 10-APR-1998; 98US-0081380P

XX

PI Siegel DL;

DR WPI; 2003-512273/48

2000

PT therapeutic applications, including typing of blood or blood products.

PS Claim 12; Page 41; 187pp; English

CC The invention relates to an isolated Rh(D) binding protein. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents DNA encoding a human anti-Rh(D) chain

Sequence 321 BP; 85 A; 87 C; 73 G; 76 T; 0 U; 0 Other;

Query Match 88.4%; Score 281.2; DB 9; Length 321;
 Best Local Similarity 92.8%; Pred. No. 5.2e-79;
 Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGCTCACTAGTCCATCTCCCTGCTGTCATCTGTGGAGACAGATCACCATCAGT 60
 |||||
 DB 4 GAGTCACTCCAGTCTCCATCTCCCTGCTGTCATCTGTGGAGACAGATCACCATCAGT 63
 |||||

QY 61 TGGCGGCAAGTCAAGAAATTAAACCTATTAAATTGGTATCAGCATAAACAGAGGAAA 120
 |||||
 DB 64 TGGCGGCAAGTCAAGAAATTAAACCTATTAAATTGGTATCAGCATAAACAGAGGAAA 123
 |||||

QY 121 GCCCCTAAGCTCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTTC 180
 |||||
 DB 124 GCCCCTAAGCTCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTTC 183
 |||||

QY 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCAACAGAGTCTGACAGCTGAAGAT 240
 |||||
 DB 184 AGTGGCAGTGGATATGGGACAGACTTCACTCTCAACAGAGTCTGACAGCTGAAGAT 243
 |||||

QY 241 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 300
 |||||
 DB 244 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 303
 |||||

QY 301 AAGGTGAGATCAAAACGA 318
 |||||
 DB 304 AAGGTGAGATCAAAACGA 321
 |||||

RESULT 9
 ACD45384
 ID ACD45384 standard; DNA; 321 BP.
 XX ACD45384;
 XX
 XX 12-SEP-2003 (first entry)
 XX
 DE Anti-Rh(D) light chain SH49 DNA.
 XX
 KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;
 KW magnetically activated cell sorting.
 XX
 OS Homo sapiens.
 XX
 PN US2003040605-A1.
 XX
 PD 27-FEB-2003.
 XX
 PF 04-MAY-2001; 2001US-00848798.
 XX
 PR 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 PR 29-JAN-1999; 99US-00240274.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Siegel DL;
 XX
 DR WPI; 2003-512273/48.
 DR P-PSDB; ABO27470.
 XX
 PT New human Rh(D)-binding protein useful for various diagnostic and
 PT therapeutic applications, including typing of blood or blood products.
 XX
 PS Claim 12; Page 61; 187pp; English.
 XX
 CC The invention relates to an isolated Rh(D) binding protein. The protein
 CC can be used for magnetically activated cell sorting. The protein is
 CC useful in various diagnostic and therapeutic applications in humans,
 CC including typing of blood or blood products. The present sequence
 CC represents DNA encoding a human anti-Rh(D) chain
 XX

SQ Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;
 Query Match 88.4%; Score 281.2; DB 9; Length 321;
 Best Local Similarity 92.8%; Pred. No. 5.2e-79;
 Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGCTCACTAGTCCATCTCCCTGCTGTCATCTGTGGAGACAGATCACCATCAGT 60
 |||||
 DB 4 GAGTCACTCCAGTCTCCATCTCCCTGCTGTCATCTGTGGAGACAGATCACCATCAGT 63
 |||||

QY 61 TGGCGGCAAGTCAAGAAATTAAACCTATTAAATTGGTATCAGCATAAACAGAGGAAA 120
 |||||
 DB 64 TGGCGGCAAGTCAAGAAATTAAACCTATTAAATTGGTATCAGCATAAACAGAGGAAA 123
 |||||

QY 121 GCCCCTAAGCTCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTTC 180
 |||||
 DB 124 GCCCCTAAGCTCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTTC 183
 |||||

QY 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCAACAGAGTCTGACAGCTGAAGAT 240
 |||||
 DB 184 AGTGGCAGTGGATATGGGACAGACTTCACTCTCAACAGAGTCTGACAGCTGAAGAT 243
 |||||

QY 241 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 300
 |||||
 DB 244 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 303
 |||||

QY 301 AAGGTGAGATCAAAACGA 318
 |||||
 DB 304 AAGGTGAGATCAAAACGA 321
 |||||

RESULT 10
 AAT6781
 ID AAT6781 standard; cDNA; 321 BP.
 XX AAT6781;
 XX
 XX 29-JAN-1998 (first entry)
 XX
 DE Anti-cancer specific antigen MAb light chain variable region cDNA.
 XX
 KW Light chain; variable region; cancer specific antigen; human;
 KW monoclonal antibody; hMab; diagnosis; cancer; immunotherapy;
 KW purification; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP09098786-A.
 XX
 PD 15-APR-1997.
 XX
 PF 06-OCT-1995; 95JP-00284400.
 XX
 PR 06-OCT-1995; 95JP-00284400.
 XX
 PA (MOMI) MORINAGA & CO LTD.
 PA (SHKO) SHINGIJUTSU JIGYODAN.
 XX
 DR WPI; 1997-275445/25.
 DR P-PSDB; AAM16649.
 XX
 PT cDNA encoding human monoclonal antibody - useful in medicine, or to
 PT purify cancer specific antigen.
 XX
 PS Claim 2; Fig 2; 7pp; Japanese.
 XX
 CC The present sequence encodes the light chain variable region of an anti-
 CC cancer specific antigen human monoclonal antibody (hMab). The hMab can be
 CC used in medicine, e.g. clinical diagnosis of cancer or immunotherapy, or

CC to purify cancer specific antigen. The industrial scale production of
CC large amounts of the hMab is made feasible by genetic engineering using
CC the hMab cDNA

XX Sequence 321 BP; 86 A; 89 C; 72 G; 74 T; 0 U; 0 Other;

Query Match 88.2%; Score 280.4; DB 2; Length 321;

Best Local Similarity 93.3%; Pred. No. 9.3e-79;
Matches 293; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

CC AGCTCATCTGCTCTCCATCCCTCTGCTGATCTGTGGAGACAGAGTCACCATGTT 61

DB AGATGACCCAGTCTCCATCCCTCCCTGCTGATCTGTGGAGACAGAGTCACCATGTT 67

QY GCCGGGCAAGTCAGAGATTAAACCTATTAAATGGTATCAGCATTAACAGGAAAG 121

DB GCCGGGCAAGTCAGAGATTAAACCTATTAAATGGTATCAGCATTAACAGGAAAG 127

QY CCCCTAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 181

DB CCCCTAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 187

QY GTGGCAGTGTATGAGACAGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 241

DB GTGGCAGTGTATGAGACAGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 247

QY TTGCAAGTCTACTGTCAGAGAGTCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 301

DB TTGCAAGTCTACTGTCAGAGAGTCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 307

QY 302 AGGTGAGATCAAA 315

DB 308 AGCTGAGATCAAA 321

RESULT 11

AAH68723 standard; DNA; 321 BP.

XX AAH68723;

DT 14-SEP-2001 (first entry)

DE Human anti-Rh(D) antibody clone SHS2 nucleotide sequence.

XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;

KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.

XX Homo sapiens.

XX US6255455-B1.

PD 03-JUL-2001.

PE 29-JAN-1999; 99US-00240274.

XX 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

XX (UYPE-) UNIV. PENNSYLVANIA.

PI Siegel DL;

XX WPI; 2001-388931/41.

DR P-PSDB; AAG93666.

XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX Example 3; Col 79; 162p; English.

CC The present invention describes an isolated Rh(D) binding protein.

CC preferably a human antibody, (I) having an amino acid sequence comprising

CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has

CC immunostimulant activity, and can be used as an immune system stimulant.

CC (I) can be used in diagnostic and therapeutic medicine. The antibodies

CC are used in diagnostics that require human antibodies instead of animal

CC antibodies, such as determine the Rh phenotype of human red blood cells.

CC AAH6815 to AAH68726 represent the nucleotide sequence which encode

CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy

CC chain CDR3 amino acid sequences which are given in the exemplification of

CC the present invention

XX Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;

Query Match 87.9%; Score 279.6; DB 5; Length 321;

Best Local Similarity 92.5%; Pred. No. 1.7e-78;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGCTCACTGATCTCCATCTCTCTGCTGATCTGTGGAGACAGAGTCACCATGACT 60

DB 4 GAGCTCACTGATCTCCATCTCTCTGCTGATCTGTGGAGACAGAGTCACCATGACT 63

QY TGCCGGGCAAGTCAGAGATTAAACCTATTAAATGGTATCAGCATTAACAGGAA 120

DB TGCCGGGCAAGTCAGAGATTAAACCTATTAAATGGTATCAGCATTAACAGGAA 123

QY GCCCTAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 180

DB GCCCTAAGCTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 183

QY AGTGGCAGTGTATGAGACAGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 240

DB AGTGGCAGTGTATGAGACAGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 243

QY TTTGCAAGTCTACTGTCAGAGAGTCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 300

DB TTTGCAAGTCTACTGTCAGAGAGTCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 303

QY 301 AAGGTGAGATCAAA 318

DB 304 AAGGTGAGATCAAA 321

RESULT 12

AAH68658 standard; DNA; 321 BP.

XX AAH68658;

DT 14-SEP-2001 (first entry)

DE Human anti-Rh(D) chain I13 nucleotide sequence.

XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;

KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.

XX Homo sapiens.

XX US6255455-B1.

PD 03-JUL-2001.

PE 29-JAN-1999; 99US-00240274.

XX 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.

PR 10-APR-1998; 98US-0081380P.

XX (UYPE-) UNIV. PENNSYLVANIA.

PI Siegel DL;

XX WPI; 2001-388931/41.

DR P-PSDB; AAG93601.
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX Example 2; Col 57; 162pp; English.
XX
CC The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93659. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH6815 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93659. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 321 BP; 82 A; 88 C; 77 G; 74 T; 0 U; 0 Other;
Query Match 87.9%; Score 279.6; DB 5; Length 321;
Best Local Similarity 92.5%; Pred. No. 1.7e-78;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1 GAGCTCACTAGTCCATCTCTCCCTGTCTGTCATCTGTGGAGACAGATCACCATCACT 60
DB 4 GAGCTCACCAGTCTCCATCTCTCCCTGTCTGTCATCTGTGGAGACAGATCACCATCACT 63
QY 61 TGGCGGCAAGTCAAGATTAACACCTATTAAATGGTATCGATCAAAACCGGGGAAA 120
DB 64 TGGCGGCAAGTCAAGATTAACACCTATTAAATGGTATCGATCAAAACCGGGGAAA 123
QY 121 GCCCCTAAGCTCCGATCTATGTCATCCAGTTTGGAGGAGTCCCATCAAGTTTC 180
DB 124 GCCCCTAAGCTCCGATCTATGTCATCCAGTTTGGAGGAGTCCCATCAAGTTTC 183
QY 181 AGTGGCAGTGGATGGGACAGATTTCACTCTCAACATCAGACGTGCAACTGAAGAT 240
DB 184 AGTGGCAGTGGATGGGACAGATTTCACTCTCAACATCAGACGTGCAACTGAAGAT 243
QY 241 TTGSCAAGTTACTACTGTCAGAGAGTCTGAGTCCCTGTAACATTTGGCCAGGGAGCC 300
DB 244 TTGSCAAGTTACTACTGTCAGAGAGTCTGAGTCCCTGTAACATTTGGCCAGGGAGCC 303
QY 301 AAGGTGAGATCAACGA 318
DB 304 AAGGTGAGATCAACGA 321
RESULT 13
AAH68724
ID AAH68724 standard; DNA; 321 BP.
XX
AC AAH68724;
XX
DT 14-SEP-2001 (first entry)
XX
DE Human anti-Rh(D) antibody clone SH54 nucleotide sequence.
XX
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
OS Homo sapiens.
XX
PN US6255455-B1.
XX
PD 03-JUL-2001.
XX
PF 29-JAN-1999; 99US-00240274.
XX
PR 11-OCT-1996; 96US-0028550P.

PR 27-JUN-1997; 97US-00884045.
PR 10-APR-1998; 98US-0081380P.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Siegel DL;
XX
DR WPI; 2001-388931/41.
DR P-PSDB; AAG93667.
XX
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX Example 3; Col 80; 162pp; English.
XX
CC The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93659. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH6815 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93659. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
SQ Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;
Query Match 87.9%; Score 279.6; DB 5; Length 321;
Best Local Similarity 92.5%; Pred. No. 1.7e-78;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1 GAGCTCACTAGTCCATCTCTCCCTGTCTGTCATCTGTGGAGACAGATCACCATCACT 60
DB 4 GAGCTCACCAGTCTCCATCTCTCCCTGTCTGTCATCTGTGGAGACAGATCACCATCACT 63
QY 61 TGGCGGCAAGTCAAGATTAACACCTATTAAATGGTATCGATCAAAACCGGGGAAA 120
DB 64 TGGCGGCAAGTCAAGATTAACACCTATTAAATGGTATCGATCAAAACCGGGGAAA 123
QY 121 GCCCCTAAGCTCCGATCTATGTCATCCAGTTTGGAGGAGTCCCATCAAGTTTC 180
DB 124 GCCCCTAAGCTCCGATCTATGTCATCCAGTTTGGAGGAGTCCCATCAAGTTTC 183
QY 181 AGTGGCAGTGGATGGGACAGATTTCACTCTCAACATCAGACGTGCAACTGAAGAT 240
DB 184 AGTGGCAGTGGATGGGACAGATTTCACTCTCAACATCAGACGTGCAACTGAAGAT 243
QY 241 TTGSCAAGTTACTACTGTCAGAGAGTCTGAGTCCCTGTAACATTTGGCCAGGGAGCC 300
DB 244 TTGSCAAGTTACTACTGTCAGAGAGTCTGAGTCCCTGTAACATTTGGCCAGGGAGCC 303
QY 301 AAGGTGAGATCAACGA 318
DB 304 AAGGTGAGATCAACGA 321
RESULT 14
AAH68652
ID AAH68652 standard; DNA; 321 BP.
XX
AC AAH68652;
XX
DT 14-SEP-2001 (first entry)
XX
DE Human anti-Rh(D) chain I07 nucleotide sequence.
XX
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
OS Homo sapiens.

XX US6255455-B1.
XX 03-JUL-2001.
XX 29-JAN-1999; 99US-00240274.
XX 11-OCT-1996; 96US-0028550P.
XX 27-JUN-1997; 97US-00884045.
XX 10-APR-1998; 98US-0081380P.
XX (TYPE-) UNIV PENNSYLVANIA.
XX Siegel DL;
XX WPI; 2001-388931/41.
XX P-PSDB; AAG93595.
XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
XX PT diagnostics requiring a human instead of an animal antibody and in
XX PT therapeutic medicine.
XX Example 2; Col 55; 162pp; English.
XX The present invention describes an isolated Rh(D) binding protein,
XX CC preferably a human antibody, (I) having an amino acid sequence comprising
XX CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
XX CC immunostimulant activity, and can be used as an immune system stimulant.
XX CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
XX CC are used in diagnostics that require human antibodies instead of animal
XX CC antibodies, such as determine the Rh phenotype of human red blood cells.
XX CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
XX CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
XX CC chain CDR3 amino acid sequences which are given in the exemplification of
XX CC the present invention
XX SQ Sequence 321 BP; 85 A; 87 C; 76 G; 73 T; 0 U; 0 Other;
Query Match 87.9%; Score 279.6; DB 5; Length 321;
Best Local Similarity 92.5%; Pred. No. 1.7e-78;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1 GAGCTCACTGATCCATCCCTCCCTGTCGATCTGGGAGACAGATCACCATCAGT 60
DB 4 GAGCTCACTGATCCATCCCTCCCTGTCGATCTGGGAGACAGATCACCATCAGT 63
QY 61 TGCCGGGCAAGTCAGAGATTAAACCTATTAAATTGGTATCAGCATPAAACAGGGAAA 120
DB 64 TGCCGGGCAAGTCAGAGATTAAACCTATTAAATTGGTATCAGCATPAAACAGGGAAA 123
QY 121 GCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGCAAAAGTGGGTCCTCCATCAAGTTTC 180
DB 124 GCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGCAAAAGTGGGTCCTCCATCAAGTTTC 183
QY 181 AGTGCAGTGAATATGGAGACAGATTCATCTCAACATCAGAGCTGTGAGGCTGAAGAT 240
DB 184 AGTGCAGTGAATATGGAGACAGATTCATCTCAACATCAGAGCTGTGAGGCTGAAGAT 243
QY 241 TTGGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCTGTATCACTTTTGGCCAGGGGACC 300
DB 244 TTGGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCTGTATCACTTTTGGCCAGGGGACC 303
QY 301 AAGGTGAGATCAAAACGA 318
DB 304 AAGGTGAGATCAAAACGA 321

RESULT 15
ACD45388
ID ACD45388 standard; DNA; 321 BP.
XX
AC ACD45388;
XX

DT 12-SEP-2003 (first entry)
XX Anti-Rh(D) light chain SH54 DNA.
XX Human; de; Gene; RH(D) binding protein; blood typing; blood product;
XX KW magnetically activated cell sorting.
XX OS Homo sapiens.
XX US2003040605-A1.
XX 27-FEB-2003.
XX 04-MAY-2001; 2001US-00848798.
XX 11-OCT-1996; 96US-0028550P.
XX 27-JUN-1997; 97US-00884045.
XX 10-APR-1998; 98US-0081380P.
XX 29-JAN-1999; 99US-00240274.
XX (TYPE-) UNIV PENNSYLVANIA.
XX Siegel DL;
XX WPI; 2003-512273/48.
XX P-PSDB; ABO27474.
XX New human Rh(D)-binding protein useful for various diagnostic and
XX PT therapeutic applications, including typing of blood or blood products.
XX Claim 12; Page 61; 187pp; English.
XX The invention relates to an isolated Rh(D) binding protein. The protein
XX CC can be used for magnetically activated cell sorting. The protein is
XX CC useful in various diagnostic and therapeutic applications in humans,
XX CC including typing of blood or blood products. The present sequence
XX CC represents DNA encoding a human anti-Rh(D) chain
XX SQ Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;
Query Match 87.9%; Score 279.6; DB 9; Length 321;
Best Local Similarity 92.5%; Pred. No. 1.7e-78;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1 GAGCTCACTGATCCATCCCTCCCTGTCGATCTGGGAGACAGATCACCATCAGT 60
DB 4 GAGCTCACTGATCCATCCCTCCCTGTCGATCTGGGAGACAGATCACCATCAGT 63
QY 61 TGCCGGGCAAGTCAGAGATTAAACCTATTAAATTGGTATCAGCATPAAACAGGGAAA 120
DB 64 TGCCGGGCAAGTCAGAGATTAAACCTATTAAATTGGTATCAGCATPAAACAGGGAAA 123
QY 121 GCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGCAAAAGTGGGTCCTCCATCAAGTTTC 180
DB 124 GCCCTTAAGCTCTGATCTATGCTGATCCAGTTTGCAAAAGTGGGTCCTCCATCAAGTTTC 183
QY 181 AGTGCAGTGAATATGGAGACAGATTCATCTCAACATCAGAGCTGTGAGGCTGAAGAT 240
DB 184 AGTGCAGTGAATATGGAGACAGATTCATCTCAACATCAGAGCTGTGAGGCTGAAGAT 243
QY 241 TTGGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCTGTATCACTTTTGGCCAGGGGACC 300
DB 244 TTGGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCTGTATCACTTTTGGCCAGGGGACC 303
QY 301 AAGGTGAGATCAAAACGA 318
DB 304 AAGGTGAGATCAAAACGA 321

Search completed: July 27, 2005, 05:59:48
Job time : 302.048 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 09:08:49 ; Search time 476.839 Seconds
(without alignments)
4312.305 Million cell updates/sec

Title: US-10-027-725A-4

Perfect score: 318
Sequence: 1 gagctcactcagctcctcctc.....ccaaagtcgagatcaacga 318

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 7277826 seqs, 323339505 residues

Total number of hits satisfying chosen parameters: 14555652

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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24: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
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26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	318	100.0	318	14	US-10-027-725A-4
2	287.6	90.4	321	10	US-09-848-798-199
3	281.2	88.4	321	10	US-09-848-798-102
4	281.2	88.4	321	10	US-09-848-798-109
5	281.2	88.4	321	10	US-09-848-798-218
6	279.6	87.9	321	10	US-09-848-798-107
7	279.6	87.9	321	10	US-09-848-798-113

8	279.6	87.9	321	10	US-09-848-798-221	Sequence 221, App
9	279.6	87.9	321	10	US-09-848-798-222	Sequence 222, App
10	277.6	87.3	324	19	US-10-344-514-3	Sequence 3, Appl1
11	277.6	87.3	324	19	US-10-344-514-4	Sequence 4, Appl1
12	277.6	87.3	333	16	US-10-203-754A-64	Sequence 60, Appl1
13	277.6	87.3	900	16	US-10-203-754A-60	Sequence 64, Appl1
14	277.6	87.3	900	16	US-10-203-754A-64	Sequence 15, Appl1
15	277.6	87.1	405	21	US-10-783-511-15	Sequence 15, Appl1
16	276.4	86.9	321	10	US-09-848-798-201	Sequence 201, App
17	276.4	86.9	321	10	US-09-848-798-211	Sequence 211, App
18	276.2	86.9	324	10	US-09-848-798-101	Sequence 101, App
19	276.2	86.9	324	10	US-09-848-798-112	Sequence 112, App
20	276.2	86.9	324	10	US-09-848-798-210	Sequence 210, App
21	276	86.8	720	9	US-09-192-854-1	Sequence 1, Appl1
22	276	86.8	720	9	US-09-968-561A-1	Sequence 1, Appl1
23	276	86.8	720	10	US-09-968-561A-1	Sequence 1, Appl1
24	276	86.8	720	10	US-09-968-561A-1	Sequence 1, Appl1
25	276	86.8	720	10	US-10-744-774-2	Sequence 2, Appl1
26	275.4	86.6	729	15	US-10-216-484-125	Sequence 15, App
27	275.4	86.6	729	16	US-10-384-933-125	Sequence 15, App
28	274.8	86.4	321	10	US-09-848-798-105	Sequence 105, App
29	274.8	86.4	321	10	US-09-848-798-216	Sequence 216, App
30	274.2	86.2	322	18	US-10-038-591-54	Sequence 54, Appl1
31	274.2	86.2	322	20	US-10-775-444A-54	Sequence 54, Appl1
32	273.8	86.1	333	16	US-10-203-754A-61	Sequence 61, Appl1
33	273.8	86.1	900	16	US-10-203-754A-65	Sequence 65, Appl1
34	273.2	85.9	321	10	US-09-848-798-104	Sequence 104, App
35	273.2	85.9	321	10	US-09-848-798-106	Sequence 106, App
36	273.2	85.9	321	10	US-09-848-798-215	Sequence 215, App
37	273.2	85.9	321	10	US-09-848-798-217	Sequence 217, App
38	273	85.8	324	10	US-09-848-798-206	Sequence 206, App
39	272.2	85.6	472	21	US-10-805-177-19	Sequence 19, Appl1
40	271.8	85.5	322	17	US-10-309-762-225	Sequence 225, App
41	271.8	85.5	322	17	US-10-309-762-227	Sequence 227, App
42	271.4	85.3	324	10	US-09-848-798-110	Sequence 110, App
43	270.6	85.1	714	14	US-10-153-382-18	Sequence 18, Appl1
44	270.6	85.1	714	20	US-10-612-697-62	Sequence 62, Appl1
45	270.6	85.1	714	20	US-10-776-649-62	Sequence 62, Appl1

ALIGNMENTS

RESULT 1
US-10-027-725A-4
; Sequence 4, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259, 436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-4

Query Match	Score 318;	DB 14;	Length 318;
Best Local Similarity	100.0%;	Pred. No. 1.9e-95;	
Matches 318;	Conservative 0;	Mismatches 0;	Gaps 0;

QY 1 GAGCTCACTCAGTCTCCATCTCTCCCTGTCATCTGTGGAGACAGATCAGTCACTAGT 60
DB 1 GAGCTCACTCAGTCTCCATCTCTCCCTGTCATCTGTGGAGACAGATCAGTCACTAGT 60
QY 61 TGGCGGGCACTCAGAGATTAACTATTAAATGGTATCAGCATTAACAGGAGAA 120


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; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
; FEATURE:
;
; OTHER INFORMATION: anti-Rh(D) chain I09
US-03-848-798-109

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Query Match	88.4%;	Score 281.2;	DB 10;	Length 321;
Best Local Similarity	92.8%;	Pred. No. 3.6e-83;		
Matches 295;	Conservative 0;	Mismatches 23;	Indels 0;	Gaps 0;

Qy	1	GAGCTCACTAGTCTCCATCTCCCTGTCGATCTGTGGGAGACAGAGTCACTCAGT	60	
Db	4	GAGCTCACCCAGTCTCCATCTCCCTGTCGATCTGTGGGAGACAGAGTCACTCAGT	63	
Qy		61	TGCCGGGCAAGTCACAGAAATTAAACCACTATTTTAAATTTGGTATATAGATTAACAGGGAAA	120
Db		64	TGCCGGGCAAGTCACAGCAATTAGCAAGCTATTTTAAATTTGGTATATAGAGAAACAGGGAAA	123
Qy		121	GCCCCTAAGTCTCTGATCTATGCTGATCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC	180
Db		124	GCCCCTAAGTCTCTGATCTATGCTGATCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC	183
Qy		181	AGTGCAGTGGATATATGGGACAGACTTCACTTTCACCATCAGCAGTCTGCAAGCTTGAAGAT	240
Db		184	AGTGCAGTGGATATATGGGACAGATTCACCTTCACCATCAGCAGTCTGCAAACTTGAAGAT	243
Qy		241	TTTGCAGTTACTACTGTCTCAGAGAGTCTCAGTGCTCGTACACTTTTGGCCAGGGAGCC	300
Db		244	TTTGCAGTTACTATCTGTCAACAGCTTAADAGTTAACCCGTAACACTTTTGGCCAGGGAGCC	303
Qy		301	AAAGTGGAGATCAAAACA 318	
Db		304	AAAGTGGAGATCAAAACA 321	

RESULT 5
US-09-848-798-218
; Sequence 218, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:

	Query Match	Similarity	88.4%	Score	281.2	DB	10	Length	321
	Best Local	Similarity	92.8%	Pred.	No.3	6e-83			
	Matches	295	Conservative	0	Mismatches	23	Indels	0	Gaps
Qy	1	GAGCTCAGTCAGTCCATCTCCCTGTCGTGATCTGTGGAGACAGAGTCCATTCAGT	60						
Db	4	GAGCTCAGCCAGTCTCCATCTCCTCTGTGATCTGTGGAGACAGAGTCCATCTACT	63						
Qy	61	TGCGGGGCAAGTCAGAGAAATTAACCTATTTAAATTTGGTATCAGCATTAACCAAGGAAA	120						
Db	64	TGCGGGGCAAGTCAGAGCATTAAGCAGCTATTTAAATTTGGTATCAGGAGAAACCAAGGAAA	123						
Qy	121	GCCCCAAGCTCTGATCTATAGCTGATCCAGTTGGCAAGTGGGGTCCCATCAAGTTTC	180						

Db 124 GCCCTTAAGCTCCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGTTTC 183

QY 181 AGTGGCAGTGGATATGGAACAGACTTTCATCTCACCATCAGAGTCTGCAGCCTGAAGAT 240

Db 184 AGTGGCAGTGGATCTGGGACAGATTTCATCTCACCATCAGAGTCTGCAGCCTGAAGAT 243

QY 241 TTTCGAAGTTCATCTGTCGAAGAGTCTCACTGCTCTGTACATCTTTGGCCAGGGGACC 300

Db 244 TTTCGAATTCATCTACTGTCACACAGAGTTACAGTACCCTGGAGCGTTCCGCCAAGGACC 303

QY 301 AAGGTGAGATCAAAAGA 318

Db 304 AAGGTGAAATCAAAAGA 321

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RESULT 6
US-09-848-798-107
, Sequence 107, Application US/09848798
, Publication No. US20030040605A1
, GENERAL INFORMATION:
, APPLICANT: Siegel, Donald L.
, TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL-CELL INTERACTIONS
, TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
, FILE REFERENCE: 09596-4202
, CURRENT APPLICATION NUMBER: US/09/848, 798
, CURRENT FILING DATE: 2001-05-04
, PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
, PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
, PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
, PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
, NUMBER OF SEQ ID NOS: 224
, SOFTWARE: PatentIn Ver. 2.0
, SEQ ID NO 107
, LENGTH: 321
, TYPE: DNA
, ORGANISM: Homo sapiens
, FEATURE:
, OTHER INFORMATION: anti-Rh(D) chain 107
US-09-848-798-107

```

Query Match	Similarity	Score	279.6	DB 10	Length	321
Best Local	Similarity	92.5%	Pred.	1.2e-82		
Matches	294	Conservative	0	Mismatches	24	Indels
						Gaps
						0
QY	1	GAGCTCACTCAAGTCTCCATCTCTCTGCTGTGCATCTGTGGAGACAGAGTCAACATCAAGT	60			
DB	4	GAGCTCAACCCAGTCTCCATCTCTCTCTGCTGTGCATCTGTGAGAGAGAGTCAACATCAAGT	63			
QY	61	TGCCGGGCAATCGACAGAAATTAACAACCTATTTTAAATTGGTATTCAGCATTAACCAAGGAAA	120			
DB	64	TGCCGGGCAATCGACAGATTTAGCAGCATTTAAATTGGTATTCAGCAATAACCAAGGAAA	123			
QY	121	GCCCTTAAGCTTCGTGATCTTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGTTTC	180			
DB	124	GCCCTTAAGCTTCGTGATCTTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGTTTC	183			
QY	181	AGTGCAGTGGATATGGGACAGACTTCACTCTCAACCATCAGCAGCTCTCAGCCTGAAGAT	240			
DB	184	AGTGCAGTGGATCTGGGACAGATTTCACTCTCAACCATCAGCAGCTCTCAACCTGAAGAT	243			
QY	241	TTTGGAAATTACTACTCTGTCAAGAGAGTCTCAGTGGCTCTGTACTCACTTTTGGCCAGGGGACC	300			
DB	244	TTTGGAAATTACTACTCTGTCAAGAGAGTCTCAGTGGCTCTGTACTCACTTTTGGCCAGGGGACC	303			
QY	301	AAGGTGAGATCAAAACGA 318				
DB	304	AAGGTGAGATCAAAACGA 321				

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; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 113
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I13
US-09-848-798-113

Query Match      87.9%; Score 279.6; DB 10; Length 321;
Best Local Similarity 92.5%; Pred. No. 1,2e-82;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGCTCACTGAGTCTCCATCTCCCTGCTGTCATCTGTGGAGACAGATCAGTCACT 60
DB 4 GAGCTCACTGAGTCTCCATCTCCCTGCTGTCATCTGTGGAGACAGATCAGTCACT 63
QY 61 TGGCGGGCAAGTCAAGAGATTAACCTATTAAATTGATACAGATTAACCGAGGAAA 120
DB 64 TGGCGGGCAAGTCAAGAGATTAACCTATTAAATTGATACAGATTAACCGAGGAAA 123
QY 121 GCCCTTAAGCTCTGATCTATGTCATCTGTCATCTGTCAGATTTGCAAGGGGTC 180
DB 124 GCCCTTAAGCTCTGATCTATGTCATCTGTCATCTGTCAGATTTGCAAGGGGTC 183
QY 181 AGTGGCAGTGGATATGGAGACAGATTCATCTCAACCATCAGCAGTCTGACCTGAAGAT 240
DB 184 AGTGGCAGTGGATATGGAGACAGATTCATCTCAACCATCAGCAGTCTGACCTGAAGAT 243
QY 241 TTTGCAAGTACTACTGTCACAGAGATCTCAGTGTGCTGTACCTTTGGCCAGGGAGCC 300
DB 244 TTTGCAAGTACTACTGTCACAGAGATCTCAGTGTGCTGTACCTTTGGCCAGGGAGCC 303
QY 301 AAGGTGAGATCAACGA 318
DB 304 AAGGTGAGATCAACGA 321

RESULT 8
US-09-848-798-221
; Sequence 221, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 221
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-848-798-221

Query Match      87.9%; Score 279.6; DB 10; Length 321;
Best Local Similarity 92.5%; Pred. No. 1,2e-82;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGCTCACTGAGTCTCCATCTCCCTGCTGTCATCTGTGGAGACAGATCAGTCACT 60
DB 4 GAGCTCACTGAGTCTCCATCTCCCTGCTGTCATCTGTGGAGACAGATCAGTCACT 63
QY 61 TGGCGGGCAAGTCAAGAGATTAACCTATTAAATTGATACAGATTAACCGAGGAAA 120
DB 64 TGGCGGGCAAGTCAAGAGATTAACCTATTAAATTGATACAGATTAACCGAGGAAA 123
QY 121 GCCCTTAAGCTCTGATCTATGTCATCTGTCATCTGTCAGATTTGCAAGGGGTC 180
DB 124 GCCCTTAAGCTCTGATCTATGTCATCTGTCATCTGTCAGATTTGCAAGGGGTC 183
QY 181 AGTGGCAGTGGATATGGAGACAGATTCATCTCAACCATCAGCAGTCTGACCTGAAGAT 240
DB 184 AGTGGCAGTGGATATGGAGACAGATTCATCTCAACCATCAGCAGTCTGACCTGAAGAT 243
QY 241 TTTGCAAGTACTACTGTCACAGAGATCTCAGTGTGCTGTACCTTTGGCCAGGGAGCC 300
DB 244 TTTGCAAGTACTACTGTCACAGAGATCTCAGTGTGCTGTACCTTTGGCCAGGGAGCC 303
QY 301 AAGGTGAGATCAACGA 318
DB 304 AAGGTGAGATCAACGA 321

RESULT 9
US-09-848-798-222
; Sequence 222, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 222
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-222

Query Match      87.9%; Score 279.6; DB 10; Length 321;
Best Local Similarity 92.5%; Pred. No. 1,2e-82;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGCTCACTGAGTCTCCATCTCCCTGCTGTCATCTGTGGAGACAGATCAGTCACT 60
DB 4 GAGCTCACTGAGTCTCCATCTCCCTGCTGTCATCTGTGGAGACAGATCAGTCACT 63
QY 61 TGGCGGGCAAGTCAAGAGATTAACCTATTAAATTGATACAGATTAACCGAGGAAA 120
DB 64 TGGCGGGCAAGTCAAGAGATTAACCTATTAAATTGATACAGATTAACCGAGGAAA 123
QY 121 GCCCTTAAGCTCTGATCTATGTCATCTGTCATCTGTCAGATTTGCAAGGGGTC 180
DB 124 GCCCTTAAGCTCTGATCTATGTCATCTGTCATCTGTCAGATTTGCAAGGGGTC 183
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Db      68 GCCGGGCAAGTCAGAGCATTTAGCAGCTATTAAATTGGTATCAGACGAACCAAGGGAAG 127
Qy      122 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGTTCA 181
Db      128 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGTTCA 187
Qy      182 GTGGCAGTGATATGGGACAGACACTTCTCACCATTAGACAGTCTGACAGCTGAAGATT 241
Db      188 GTGGCAGTGATCTGGGACAGATTTCACTCTCACCATTAGACAGTCTGCAACCTGAAGATT 247
Qy      242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTAACACTTTTGGCCAGGGGACCA 301
Db      248 TTGCAACTTACTACTGTCAAGAGTTACAGAGTTACCCGCTCACTTTGGCCAGGGGACCA 307
Qy      302 AGGTGAGATCAAAAG 317
Db      308 AGGTGAGATCAAAAG 323
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RESULT 13
US-10-203-754A-64
; Sequence 64, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
; APPLICANT: ITAMI, Seima
; APPLICANT: SEKI, Makoto
; APPLICANT: MATSURA, Yoshiharu
; APPLICANT: SHIBUI, Tatsuro
; APPLICANT: YOTSUMOTO, Yoshinisa
; APPLICANT: MIYAMURA, Tatsuo
; TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
; FILE REFERENCE: P22257
; CURRENT APPLICATION NUMBER: US/10/203,754A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/JP01/00967
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent version 3.1
; SEQ ID NO 64
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-203-754A-64
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Query Match      87.3%; Score 277.6; DB 16; Length 900;
Best Local Similarity 92.4%; Pred. No. 8.2e-82;
Matches 292; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy      2 AGCTCACTCATCTTCCTCCTCCTGCTGTCATCTGTGGAGACAGAGTCAACCATGATT 61
Db      503 AGATGACCCAGTCTCCATCCCTGCTGATCTGTGGAGACAGAGTCAACCATGATT 562
Qy      62 GCCGGGCAAGTCAGAGATTTAAACCTATTTAAATGATTCAGATCAAAACAGGGGAAG 121
Db      563 GCCGGGCAAGTCAGAGATTTAAACCTATTTAAATGATTCAGAGATCAAAACAGGGGAAG 622
Qy      122 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGTTCA 181
Db      623 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGTTCA 682
Qy      182 GTGGCAGTGATATGGGACAGACACTTCTCACCATTAGACAGTCTGACAGCTGAAGATT 241
Db      683 GTGGCAGTGATCTGGGACAGATTTCACTCTCACCATTAGACAGTCTGCAACCTGAAGATT 742
Qy      242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTAACACTTTTGGCCAGGGGACCA 301
Db      743 TTGCAACTTACTACTGTCAAGAGTTACAGAGTTACCCGCTCACTTTGGCCAGGGGACCA 802
Qy      302 AGGTGAGATCAAAAG 317
Db      803 AGGTGAGATCAAAAG 818
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RESULT 14
US-10-783-311-15
; Sequence 15, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light Chain nucleic acid sequence
US-10-783-311-15
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Query Match      87.1%; Score 277; DB 21; Length 405;
Best Local Similarity 92.1%; Pred. No. 9.8e-82;
Matches 292; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy      2 AGCTCACTCATCTTCCTCCTCCTGCTGTCATCTGTGGAGACAGAGTCAACCATGATT 61
Db      68 AGATGACCCAGTCTCCATCCCTGCTGATCTGTGGAGACAGAGTCAACCATGATT 127
Qy      62 GCCGGGCAAGTCAGAGATTTAAACCTATTTAAATGATTCAGATCAAAACAGGGGAAG 121
Db      128 GCCGGGCAAGTCAGAGATTTAAACCTATTTAAATGATTCAGATCAAAACAGGGGAAG 187
Qy      122 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGTTCA 181
Db      188 CCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGTTCA 247
Qy      182 GTGGCAGTGATATGGGACAGACACTTCTCACCATTAGACAGTCTGACAGCTGAAGATT 241
Db      248 GTGGCAGTGATCTGGGACAGATTTCACTCTCACCATTAGACAGTCTGCAACCTGAAGATT 307
Qy      242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGTAACACTTTTGGCCAGGGGACCA 301
Db      308 TTGCAACTTACTACTGTCAAGAGTTACAGAGTTACAGTGCAGTTCGGCCAGGGGACCA 367
Qy      302 AGGTGAGATCAAAAG 318
Db      368 AGGTGAAATCAAAAG 384
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RESULT 15
US-10-783-311-16
; Sequence 16, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: Light Chain nucleic acid sequence
US-10-783-311-16

Query Match 87.1%; Score 277; DB 21; Length 405;
Best Local Similarity 92.1%; Pred. No. 9.8e-82;
Matches 292; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY	2	AGCTCACTCACTTCATCTCCCTGTCGATCTGTGGAGACAGAGTCACCATCACTT	61
Db	68	AGATGACCCAGTCTCCATCTCCCTGTCGATCTGTGGAGACAGAGTCACCATCACTT	127
QY	62	GCCGGGCAAGTCAGAGATTAACTTTAAATTGGTATCAGCATTAACCGGAAAG	121
Db	128	GCCGGGCAAGTCAGAGATTAACTTTAAATTGGTATCAGCATTAACCGGAAAG	187
QY	122	CCCCTAAGCTCTGATCTATGTCGATCCAGTTTGCAAGTGGGGTCCCATCAAGTTCA	181
Db	188	CCCCTAAGCTCTGATCTATGTCGATCCAGTTTGCAAGTGGGGTCCCATCAAGTTCA	247
QY	182	GTGGCAGTGAATATGGAGACAGACTTCACCTTCACCATCAGAGTCTGAGCCTGAAATT	241
Db	248	GTGGCAGTGAATATGGAGACAGACTTCACCTTCACCATCAGAGTCTGAGCCTGAAATT	307
QY	242	TTGCAAGTACTACTGTCAAGAGAGTCTCAGTGCTGTACACTTTGGCCAGGGGACCA	301
Db	308	TTGCAAGTACTACTGTCAAGAGAGTCTCAGTGCTGTACACTTTGGCCAGGGGACCA	367
QY	302	AGTGGAGATCAACGA	318
Db	368	AGTGGAAATCAACGA	384

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Job time : 477.839 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:09:06 ; Search time 1956.83 Seconds

(without alignments)
8468.649 Million cell updates/sec

Title: US-10-027-725a-3

Perfect score: 342
Sequence: 1 ctctgagctgcgcacagact.....ccctgctcaccgctcctca 342

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb ba:*
2: gb beg:*
3: gb_in:*
4: gb_on:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
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10: gb_ro:*
11: gb_sbs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	338.8	99.1	342	9	HS458384 Homo sapi
2	332.8	94.4	342	9	HS458383 Homo sapi
3	308.4	90.2	342	9	HS458382 Homo sapi
4	300.6	87.9	355	9	AY640487 Homo sapi
5	299	87.4	355	9	AY640580 Homo sapi
6	297.4	87.0	355	9	AY640579 Homo sapi
7	292.6	85.6	355	9	AY640509 Homo sapi
8	291	85.1	355	9	AY640564 Homo sapi
9	284.6	83.2	414	9	AF062112 Homo sapi
10	284.4	83.2	351	9	HS4244930 Homo sapi
11	284.4	83.2	360	6	AX061463 Sequence
12	283.6	82.9	411	9	HS722X1
13	283	82.7	354	9	HS4245064 Homo sapi
14	283	82.7	360	9	HS480129 Human immun
15	283	82.7	360	9	HS480130 Human immun
16	282.8	82.7	358	9	AF021954 Homo sapi
17	281.8	82.4	403	12	AF452917 Synthetic
18	281.4	82.3	351	9	HS4245020 Homo sapi
19	280.2	81.9	341	9	AY607380 Homo sapi

20	280.2	81.9	414	9	HS458384 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
21	280.2	81.9	414	9	HS458383 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
22	280	81.9	363	9	HS458382 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
23	279.8	81.8	355	9	AY640507 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
24	279.8	81.8	432	9	HS458383 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
25	278.4	81.4	357	9	HS4244949 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
26	278.2	81.3	432	9	HS4244951 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
27	277.2	81.1	354	9	HS4244952 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
28	276.6	80.9	354	9	HS4244953 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
29	276.4	80.8	357	9	HS4244954 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
30	276.2	80.8	362	9	HS4244955 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
31	275.8	80.6	412	12	AF452912 Synthetic	342 bp mRNA linear PRI 30-APR-2002
32	275.6	80.6	417	9	HS4244956 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
33	275.4	80.5	400	12	AF452909 Synthetic	342 bp mRNA linear PRI 30-APR-2002
34	275	80.4	406	12	AF453047 Synthetic	342 bp mRNA linear PRI 30-APR-2002
35	274.8	80.4	357	9	HS4244957 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
36	274.8	80.4	357	9	HS4244958 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
37	274.2	80.2	351	9	AY607364 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
38	273.8	80.1	369	6	AX061433 Sequence	342 bp mRNA linear PRI 30-APR-2002
39	273.6	80.0	363	9	HS480128 Human immun	342 bp mRNA linear PRI 30-APR-2002
40	273.6	80.0	409	12	AF452947 Synthetic	342 bp mRNA linear PRI 30-APR-2002
41	272	79.5	366	9	HS4233698 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
42	271.8	79.5	339	9	AY607360 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
43	271.8	79.5	351	9	HS4244953 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
44	271.8	79.5	351	9	HS4244958 Homo sapi	342 bp mRNA linear PRI 30-APR-2002
45	271.8	79.5	360	9	HS4579300 Homo sapi	342 bp mRNA linear PRI 30-APR-2002

ALIGNMENTS

RESULT 1	HS458384	342 bp mRNA linear PRI 30-APR-2002
DEFINITION	Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 100.	
ACCESSION	AJ458384.1	GI:20387067
VERSION	AJ458384.1	GI:20387067
KEYWORDS	IGHV gene; immunoglobulin heavy chain; variable region.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	1	Flicker S., Steinberger P., Norderhaug L., Sperr W.R., Majlesi Y., Valent P., Kratz D. and Valenta R. Conversion of grass allergen-specific human IgE into a protective IgG1 antibody
AUTHORS	1	Flicker S., Steinberger P., Norderhaug L., Sperr W.R., Majlesi Y., Valent P., Kratz D. and Valenta R.
TITLE	2	(bases 1 to 342)
JOURNAL	2	Unpublished
REFERENCE	2	(bases 1 to 342)
AUTHORS	2	Flicker S., Steinberger P., Norderhaug L., Sperr W.R., Majlesi Y., Valent P., Kratz D. and Valenta R.
TITLE	2	Conversion of grass allergen-specific human IgE into a protective IgG1 antibody
JOURNAL	2	Unpublished
FEATURES	2	(bases 1 to 342)
source	2	Submitted (24-APR-2002) Flicker S., Department of Pathophysiology, General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090 Vienna, AUSTRIA
location/Qualifiers	2	location/Qualifiers
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/clone="100"	2	location/Qualifiers
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ORIGIN

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Best Local Similarity 99.4%; Pred. No. 3.9e-86;
Matches 340; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCAGTCTGGCCAGGACTGTGTAGAGCTTCACAGACCTGTCCCTCAGCTGACTGTC 60
Db 1 CTCAGTCTGGCCAGGACTGTGTAGAGCTTCACAGACCTGTCCCTCAGCTGACTGTC 60

QY 61 TCTGTGGCTTCATCCGAGTGTGTATTACTGAGATTGGATCCGCAAGCTCCAGG 120
Db 61 TCTGTGGCTTCATCCGAGTGTGTATTACTGAGATTGGATCCGCAAGCTCCAGG 120

QY 121 AAGGGCTGGAGTGGATCGGGTACATCTATCAGTGGCAACACCTAACACCCGTCC 180
Db 121 AAGGGCTGGAGTGGATCGGGTACATCTATCAGTGGCAACACCTAACACCCGTCC 180

QY 181 CTCAGAGTGGAGTTACATGTCACTAGACACGCTTAAGAACACTTCTCCCTGAGGCTG 240
Db 181 CTCAGAGTGGAGTTACATGTCACTAGACACGCTTAAGAACACTTCTCCCTGAGGCTG 240

QY 241 AGCTCTGTACTGCGGGAGACAGCGCGGTATTACTGTGCGAGGTGATGGGTACACT 300
Db 241 AGCTCTGTACTGCGGGAGACAGCGCGGTATTACTGTGCGAGGTGATGGGTACACT 300

QY 301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342
Db 301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342

RESULT 2
HSA458383 342 bp mRNA linear PRI 30-APR-2002
LOCUS HSA458383
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 60.
ACCESSION AU458383.1 GI:20387065
VERSION IGHV gene; immunoglobulin heavy chain; variable region.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Flicker S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y., Valent, P., Kraft, D. and Valenta, R.
TITLE Conversion of grass allergen-specific human IGB into a protective IgG1 antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 342)
AUTHORS Flicker S.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2002) Flicker S., Department of Pathophysiology, General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090 Vienna, AUSTRIA

FEATURES
source 1..342
Location/Qualifiers
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gene
CDS

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Query Match 94.4%; Score 322.8; DB 9; Length 342;
Best Local Similarity 96.5%; Pred. No. 1.5e-81;
Matches 330; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 CTCAGTCTGGCCAGGACTGTGTAGAGCTTCACAGACCTGTCCCTCAGCTGACTGTC 60
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QY 61 TCTGTGGCTTCATCCGAGTGTGTATTACTGAGATTGGATCCGCAAGCTCCAGG 120
Db 61 TCTGTGGCTTCATCCGAGTGTGTATTACTGAGATTGGATCCGCAAGCTCCAGG 120

QY 121 AAGGGCTGGAGTGGATCGGGTACATCTATCAGTGGCAACACCTAACACCCGTCC 180
Db 121 AAGGGCTGGAGTGGATCGGGTACATCTATCAGTGGCAACACCTAACACCCGTCC 180

QY 181 CTCAGAGTGGAGTTACATGTCACTAGACACGCTTAAGAACACTTCTCCCTGAGGCTG 240
Db 181 CTCAGAGTGGAGTTACATGTCACTAGACACGCTTAAGAACACTTCTCCCTGAGGCTG 240

QY 241 AGCTCTGTACTGCGGGAGACAGCGCGGTATTACTGTGCGAGGTGATGGGTACACT 300
Db 241 AGCTCTGTACTGCGGGAGACAGCGCGGTATTACTGTGCGAGGTGATGGGTACACT 300

QY 301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342
Db 301 TTGGACAACCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342

RESULT 3
HSA458382 342 bp mRNA linear PRI 30-APR-2002
LOCUS HSA458382
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 94.
ACCESSION AU458382.1 GI:20387063
VERSION IGHV gene; immunoglobulin heavy chain; variable region.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Flicker S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y., Valent, P., Kraft, D. and Valenta, R.
TITLE Conversion of grass allergen-specific human IGB into a protective IgG1 antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 342)
AUTHORS Flicker S.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2002) Flicker S., Department of Pathophysiology, General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090 Vienna, AUSTRIA

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gene
CDS

V_region

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Matches 321; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CTGAGTCTGGCCAGAGACTGTGTAAGCTTCACAGACCCCTGCTCCCTACCTGACATGTC 60
Db 1 CTCGAGTCTGGCCAGAGACTGTGTAAGCTTCACAGACCCCTGCTCCCTACCTGACATGTC 60
Qy 61 TCTGTGGCTTCATCCGACAGTGTGTATTACTGAGTTGATCCGCGACGTCAGAGG 120
Db 61 TCTGTGGCTTCATCCGACAGTGTGTATTACTGAGTTGATCCGCGACGTCAGAGG 120
Qy 121 AAGGCTGAGTGAATCGGATCATCTATACAGTGGCAACACCTACCAACCCGCTCC 180
Db 121 AAGGCTGAGTGAATCGGATCATCTATACAGTGGCAACACCTACCAACCCGCTCC 180
Qy 181 CTCAGAGTGAATTCATCTACATGACACACCTCTAAGAACCACTTCCTCCAGAGTGG 240
Db 181 CTCAGAGTGAATTCATCTACATGACACACCTCTAAGAACCACTTCCTCCAGAGTGG 240
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Db 241 AACTCTGTACTGCGGAGACACGCGCTGTATTACTGTGAGAGTTCAGATGGGTAACCT 300
Qy 301 TTGGACAACCTGGGCGCAGGGAACCCCTGTCTCAACCGTCTCTCTCA 342
Db 301 TTGGACAACCTGGGCGCAGGGAACCCCTGTCTCAACCGTCTCTCTCA 342

RESULT 4
AY640487 355 bp mRNA linear PRI 03-JUL-2004
LOCUS Homo sapiens clone AP immunoglobulin E variable region mRNA,
DEFINITION partial cds.
ACCESSION AY640487
VERSION AY640487.1 GI:49354726
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 355)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Biased use of VHS Ige+ B cells in the nasal mucosa of allergic
rhinitis patients
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 355)
AUTHORS Coker, H.A., Durham, S.R. and Gould, H.J.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St
Thomas Street, London SE1 1UL, UK
FEATURES
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/organism="Homo sapiens"
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Matches 315; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 4 GAGTCTGGCCAGAGACTGTGTAAGCTTCACAGACCCCTGCTCCCTACCTGACATGTC 63
Db 16 GAGTCTGGCCAGAGACTGTGTAAGCTTCACAGACCCCTGCTCCCTACCTGACATGTC 75
Qy 64 GGTGGCTTCATCCGACAGTGTGTATTACTGAGTTGATCCGCGACGTCAGAGGAG 123
Db 76 GGTGGCTTCATCCGACAGTGTGTATTACTGAGTTGATCCGCGACGTCAGAGGAG 135
Qy 124 GGCCTGAGTGAATCGGATCATCTATACAGTGGCAACACCTACCAACCCGCTCC 183
Db 136 GGCCTGAGTGAATCGGATCATCTATACAGTGGCAACACCTACCAACCCGCTCC 195
Qy 184 AAGAGTGAATTCATCTACATGACACGCTTAAGAACCACTTCCTGAGGCTGAGC 243
Db 196 AAGAGTGAATTCATCTACATGACACGCTTAAGAACCACTTCCTGAGGCTGAGC 255
Qy 244 TCTGTACTGCGGAGACACGCGCTGTATTACTGTGAGAGTTCAGATGGTACACTTTG 303
Db 256 TCTGTACTGCGGAGACACGCGCTGTATTACTGTGAGAGTTCAGATGGTACACTTTG 315
Qy 304 GACAACCTGGGCGCAGGGAACCCCTGTCAACCGTCTCTCA 342
Db 316 GACTACTGGGCGCAGGGAACCCCTGTCAACCGTCTCTCA 354

RESULT 5
AY640580 355 bp mRNA linear PRI 03-JUL-2004
LOCUS Homo sapiens clone RU immunoglobulin E variable region mRNA,
DEFINITION partial cds.
ACCESSION AY640580
VERSION AY640580.1 GI:49354901
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 355)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Biased use of VHS Ige+ B cells in the nasal mucosa of allergic
rhinitis patients
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 355)
AUTHORS Coker, H.A., Durham, S.R. and Gould, H.J.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St
Thomas Street, London SE1 1UL, UK
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ORIGIN XPDYWGQGLTVTVSS"

Query Match 87.4%; Score 299; DB 9; Length 355;
Best Local Similarity 92.6%; Pred. No. 1e-74;
Matches 314; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCCAAGAGCTGTGTAAGCCCTTCACAGACCTGTCCCTCAGCTGCTCT 63
DB 16 GAGTCGGGCCCAAGAGCTGTGTAAGCCCTTCACAGACCTGTCCCTCAGCTGCTCT 75
QY 64 GGTGGCTCCATCCGACAGTGGTGTATTATCTAGATTGATCGGCACGCGTCCAGGGAG 123
DB 76 GGTGGCTCCATCCGACAGTGGTGTATTATCTAGATTGATCGGCACGCGTCCAGGGAG 135
QY 124 GGCTGGAGTGAATCGGGGTACATCTATCAGATGGCAACCTTCAACAACCCGCTCC 183
DB 136 GGCTGGAGTGAATGGGTAGTACTATTAAGTGGAAACCTTCAACAACCCGCTCC 195
QY 184 AAGAGTGAATTCACATGTCAGTGAACAGCTCTAAGAACCTTCTCTGAGGCTGAGC 243
DB 196 AAGAGTGAATTCACATGTCAGTGAACAGCTCTAAGAACCTTCTCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCCCGGACACGCGCGTGTATTACTGTGCGAGGTGAGATGGGTACCTTTG 303
DB 256 TCTGTGACTGCCCGGACACGCGCGTGTATTACTGTGCGAGGTGAGTGGCTACGACTTT 315
QY 304 GACAACCTGGGGCCAGGGAACTGTGTCACCGTCTCTCA 342
DB 316 GACTACTGGGGCCAGGGAACTGTGTCACCGTCTCTCA 354

RESULT 6
AY640579 355 bp mRNA linear PRI 03-JUL-2004
LOCUS Homo sapiens clone RT immunoglobulin E variable region mRNA,
DEFINITION partial cds.

ACCESSION AY640579
VERSION AY640579.1 GI:49354899
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Coker,H.A., Durham,S.R. and Gould,H.J.
JOURNAL 1 (bases 1 to 355)
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.
TITLE Biased use of VHS Igb+ B cells in the nasal mucosa of allergic
JOURNAL rhinitis patients
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 355)
TITLE Coker,H.A., Durham,S.R. and Gould,H.J.
JOURNAL Direct Submission
AUTHORS Submitted (28-MAY-2004) Randall Centre, King's College London, St
JOURNAL Thomas Street, London SE1 1UL, UK

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patients"
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/clone="RT"
/codon_start=1
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ORIGIN

Query Match 87.0%; Score 297.4; DB 9; Length 355;

Best Local Similarity 92.3%; Pred. No. 2.9e-74;
Matches 313; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCCAAGAGCTGTGTAAGCCCTTCACAGACCTGTCCCTCAGCTGCTCT 63
DB 16 GAGTCGGGCCCAAGAGCTGTGTAAGCCCTTCACAGACCTGTCCCTCAGCTGCTCT 75
QY 64 GGTGGCTCCATCCGACAGTGGTGTATTATCTAGATTGATCGGCACGCTCCAGGGAG 123
DB 76 GGTGGCTCCATCCGACAGTGGTGTATTATCTAGATTGATCGGCACGCTCCAGGGAG 135
QY 124 GGCTGGAGTGAATCGGGGTACATCTATCAGATGGCAACCTTCAACAACCCGCTCC 183
DB 136 GGCTGGAGTGAATGGGTAGTACTATTAAGTGGAAACCTTCAACAACCCGCTCC 195
QY 184 AAGAGTGAATTCACATGTCAGTGAACAGCTCTAAGAACCTTCTCTGAGGCTGAGC 243
DB 196 AAGAGTGAATTCACATGTCAGTGAACAGCTCTAAGAACAGTCTCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCCCGGACACGCGCGTGTATTACTGTGCGAGGTGAGATGGGTACCTTTG 303
DB 256 TCTGTGACTGCCCGGACACGCGCGTGTATTACTGTGCGAGGTGAGATGGGTACCTTTT 315
QY 304 GACAACCTGGGGCCAGGGAACTGTGTCACCGTCTCTCA 342
DB 316 GACTACTGGGGCCAGGGAACTGTGTCACCGTCTCTCA 354

RESULT 7
AY640509 355 bp mRNA linear PRI 03-JUL-2004
LOCUS Homo sapiens clone BM immunoglobulin E variable region mRNA,
DEFINITION partial cds.

ACCESSION AY640509
VERSION AY640509.1 GI:49354765
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL 1 (bases 1 to 355)
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.
JOURNAL Biased use of VHS Igb+ B cells in the nasal mucosa of allergic
REFERENCE rhinitis patients
AUTHORS Unpublished
JOURNAL 2 (bases 1 to 355)
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.
JOURNAL Direct Submission
AUTHORS Submitted (28-MAY-2004) Randall Centre, King's College London, St
JOURNAL Thomas Street, London SE1 1UL, UK

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ORIGIN

Query Match 85.6%; Score 292.6; DB 9; Length 355;
Best Local Similarity 91.4%; Pred. No. 6.9e-73;
Matches 310; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Db 16 GAGTCGGAGCCAGGACCTGTTGAAAGCCCTTCTCAGACCCCTGCTCACCCTGACCTGACCTGCTCTCT 75
Qy 64 GGTGGCTCCATCCGACAGTGGTGTATTATTAAGATTGGATCGGCGACGCTCCAGGGAG 123
Db 76 GGTGGCTCCATCCGACAGTGGTGTATTATTAAGATTGGATCGGCGACGCTCCAGGGAG 135
Qy 124 GGCCTGGAGTGGATCGGGTACATCTATCAGATGGGCAACCTTCAACCAACCCGCTCC 183
Db 136 GGCCTGGAGTGGATCGGGTACATCTATTAAGATTGGATCGGCGACGCTCCAGGGAG 195
Qy 184 AAGAGTGGAGTTCACATGTCAGTAGACAGCTTAAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTGGAGTTCACATGTCAGTAGACAGCTTAAAGAACCACTTCTCCCTGAGGCTGAGC 255
Qy 244 TCTGTGACTGCGCGGACACGCGCGTGTATTATCTGTGAGAGTCAAGATGGTATACCTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCGTGTATTATCTGTGAGAGTCAAGATGGTATACCTTTG 315
Qy 304 GACAACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342
Db 316 GACTACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 354

RESULT 8
AY640564 355 bp mRNA linear PRI 03-JUL-2004
LOCUS Homo sapiens clone RE immunoglobulin E variable region mRNA.
DEFINITION
ACCESSION AY640564
VERSION AY640564.1 GI:49354872
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 355)
AUTHORS Coker, H.A., Durham, S.R. and Gould, H.J.
TITLE Biased use of VHS IGE+ B cells in the nasal mucosa of allergic rhinitis patients
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 355)
AUTHORS Coker, H.A., Durham, S.R. and Gould, H.J.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St Thomas Street, London SE1 1UU, UK
FEATURES
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ORIGIN
Query Match 85.1%; Score 291; DB 9; Length 355;
Best Local Similarity 91.2%; Pred. No. 2e-72;
Matches 309; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 4 GAGTCTGGCCCAAGAGACTGTGTAAGACCTTCAAGACCTTCAAGACCTTCAAGACCTTCAAG 63
Db 16 GAGTCTGGCCCAAGAGACTGTGTAAGACCTTCAAGACCTTCAAGACCTTCAAGACCTTCAAG 75
Qy 64 GGTGGCTCCATCCGACAGTGGTGTATTATTAAGATTGGATCGGCGACGCTCCAGGGAG 123

Db 76 GGTGGCTCCATCCGACAGTGGTGTATTATTAAGATTGGATCGGCGACGCTCCAGGGAG 135
Qy 124 GGCCTGGAGTGGATCGGGTACATCTATCAGATGGGCAACCTTCAACCAACCCGCTCC 183
Db 136 GGCCTGGAGTGGATCGGGTACATCTATTAAGATTGGATCGGCGACGCTCCAGGGAG 195
Qy 184 AAGAGTGGAGTTCACATGTCAGTAGACAGCTTAAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTGGAGTTCACATGTCAGTAGACAGCTTAAAGAACCACTTCTCCCTGAGGCTGAGC 255
Qy 244 TCTGTGACTGCGCGGACACGCGCGTGTATTATCTGTGAGAGTCAAGATGGTATACCTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCGTGTATTATCTGTGAGAGTCAAGATGGTATACCTTTG 315
Qy 304 GACAACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342
Db 316 GACTACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 354

RESULT 9
AF062112 414 bp mRNA linear PRI 08-MAY-2001
LOCUS Homo sapiens clone 21u-26 immunoglobulin heavy chain variable region (IGH) mRNA, partial cds.
DEFINITION
ACCESSION AF062112
VERSION AF062112.1 GI:3170686
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 414)
AUTHORS Wang, X. and Stoll, B.D.
TITLE Immunoglobulin VH gene expression in human aging
JOURNAL Clin. Immunol. 93 (2), 132-142 (1999)
MEDLINE 99459182
PUBMED 10527689
REFERENCE 2 (bases 1 to 414)
AUTHORS Wang, X. and Stoll, B.D.
TITLE Direct Submission
JOURNAL Submitted (22-APR-1998) Biochemistry Department, Tufts University School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES
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1. .57
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Query Match 83.2%; Score 284.6; DB 9; Length 414;
Best Local Similarity 90.0%; Pred. No. 1.3e-70;

Matches 305; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 4 GAGTCTGCCCCAGAGACTGTGTGAAGCCCTTCACAGACCCTGTCCCTCACCTGCATGTCTCT 63
DB 73 GAGTCGGGGCCAGAGACTGTGTGAAGCCCTTCACAGACCCTGTCCCTCACCTGCATGTCTCT 132

QY 64 GGTGGCTCCATCCGACATGGTGTGTATTACGTGAGATTGAGATCCGCGACCGTCCAGGAG 123
DB 133 GGTGGCTCCATCCGACATGGTGTGTATTACGTGAGATTGAGATCCGCGACCGTCCAGGAG 192

QY 124 GGCTGTGAGTGTGATCGGGTACATCTATCACAGTGGCAACCTTCAACAACCCGTCCTC 183
DB 193 GGCTGTGAGTGTGATGGGTATCTATCTATTCAGTGGAGACCTTACTACACCCGTCCTC 252

QY 184 AAGAGTCGAGTTACCATGTGACATGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 253 AAGAGTCGAGTTACCATGTGACATGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 312

QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGTGAGAGTCAAGATGGTACACTTTG 303
DB 313 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGTGAGAGTCAAGATGGTACACTTTG 372

QY 304 GACAACTGGGGCCAGGGAACCTGTGACCGTCTCTCTCA 342
DB 373 GACAACTGGGGCCAGGGAACCTGTGACCGTCTCTCTCA 411

RESULT 10
HSA244930 351 bp mRNA linear PRI 01-JUN-2000
LOCUS Homo sapiens mRNA for immunoglobulin mu heavy chain variable
DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable
region, partial, clone 1-A34.
AJ244930
VERSION AJ244930.1 GI:4995319
KEYWORDS IGM; IGM heavy chain; immunoglobulin mu heavy chain; variable
region.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A.,
Chiorazzi, N. and Ferrarini, M.
Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalents
J. Immunol. 164 (11), 5596-5604 (2000)

JOURNAL
MEDLINE
PUBMED
20281644
10820234

REFERENCE 2 (bases 1 to 351)
Dono, M.
Direct Submission
Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, I.go Rosanna benzi 10- Genova,
ITALY

FEATURES
source Location/Qualifiers
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Best Local Similarity 91.5%; Pred. No. 1.5e-70;
Matches 313; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

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QY 64 GGTGGCTCCATCCGACATGGTGTGTATTACGTGAGATTGAGATCCGCGACCGTCCAGGAG 123
DB 70 GGTGGCTCCATCCGACATGGTGTGTATTACGTGAGATTGAGATCCGCGACCGTCCAGGAG 129

QY 124 GGCTGTGAGTGTGATCGGGTACATCTATCACAGTGGCAACCTTCAACAACCCGTCCTC 183
DB 130 GGCTGTGAGTGTGATGGGTATCTATCTATTCAGTGGAGACCTTCAACAACCCGTCCTC 189

QY 184 AAGAGTCGAGTTACCATGTGACATGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 190 AAGAGTCGAGTTACCATGTGACATGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 249

QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGTGAGAGTCAAGATGGTACACT 300
DB 250 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGTGAGAGTCAAGATGGTACACT 309

QY 301 TTGGACAACTGGGGCCAGGGAACCTGTGACCGTCTCTCTCA 342
DB 310 TTGGACAACTGGGGCCAGGGAACCTGTGACCGTCTCTCTCA 351

RESULT 11
AX061463 360 bp DNA linear PAT 22-JAN-2001
LOCUS AX061463
DEFINITION Sequence 32 from Patent WO0100678.
ACCESSION AX061463
VERSION AX061463.1 GI:12406598
KEYWORDS Human immunodeficiency virus 1 (HIV-1)
SOURCE Human immunodeficiency virus 1
ORGANISM Human immunodeficiency virus 1
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
lentivirus group.

REFERENCE 1
Watkins, B.A. and Reitz, M.S.
Human monoclonal antibodies to hiv-1 envelope glycoprotein gp120
Patent: WO 0100678-A 32 04-JAN-2001;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)

FEATURES
source Location/Qualifiers
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ORIGIN
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Best Local Similarity 91.5%; Pred. No. 1.5e-70;
Matches 313; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 4 GAGTCGGCCCCAGAGACTGTGTGAAGCCCTTCACAGACCCTGTCCCTCACCTGCATGTCTCT 63
DB 19 GAGTCGGCCCCAGAGACTGTGTGAAGCCCTTCACAGACCCTGTCCCTCACCTGCATGTCTCT 78

QY 64 GGTGGCTCCATCCGACATGGTGTGTATTACGTGAGATTGAGATCCGCGACCGTCCAGGAG 123
DB 79 GGTGGCTCCATCCGACATGGTGTGTATTACGTGAGATTGAGATCCGCGACCGTCCAGGAG 138

QY 124 GGCTGTGAGTGTGATCGGGTACATCTATCACAGTGGCAACCTTCAACAACCCGTCCTC 183


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Db 139 GGCCTGAGTGGATGGGTACATCTATTACAGTGGAGACACTACTACAAACCCGTCCTC 198
Qy 184 AAGAGTGAAGTATACATGATGATGAGACACGCTTAAGAACCACTTCCTGAGGCTGAGC 243
Db 199 AAGAGTGAAGTATACATGATGATGAGACACGCTTAAGAACCACTTCCTGAGGCTGAGC 258
Qy 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGA--GATCAGATGGGTACACT 300
Db 259 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAAGGGGTAGTGTGACTGG 318
Qy 301 TTGACAACTGGGGCCAGGGAAACCTGTGACCGTCTCTCTCA 342
Db 319 TTCAGCCCTGGGGCCAGGGAAACCTGTGACCGTCTCTCTCA 360

RESULT 12
HST22X1 411 bp mRNA linear PRI 09-SEP-2004
LOCUS H.sapiens mRNA for Ig heavy chain variable region (VH4D) (clone T22.1). 275385
ACCESSION Z75385.1 GI:2062048
VERSION 1
KEYWORDS immunoglobulin; immunoglobulin heavy chain; immunoglobulin superfamily; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 411)
AUTHORS Tonnelle,C., D'Excote,C., Depaertere,V., Metrae,D., Boublil,L. and Fougereau,M.
TITLE Human thymic B cells largely overexpress the VH4 Ig gene family. A possible role in the control of tolerance in situ?
JOURNAL Int. Immunol. 9 (3), 407-414 (1997)
MEDLINE 97244170
PUBMED 9088979
REFERENCE 2 (bases 1 to 411)
AUTHORS Tonnelle,C.
TITLE Direct Submission
JOURNAL Submitted (26-JUN-1996) Cecile Tonnelle, Centre d'Immunologie Marseille Luminy, Marseille, 13288, France
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sig_peptide 1..57
V_region 58..354
V_segment /note="Ig VH4-segment"
355..377
D_segment 378..411
J_segment

Query Match 82.9%; Score 283.6; DB 9; Length 411;
Best Local Similarity 89.9%; Pred. No. 2.6e-70;
Matches 304; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 4 GAGTGGCCGAGAGTGGTGAAGCTTCACAGACCCCTGCTCCCTGACCTGACCTGCTCT 63
Db 73 GAGTGGCCGAGAGTGGTGAAGCTTCACAGACCCCTGCTCCCTGACCTGACCTGCTCT 132
Qy 64 GGTGCTCCATCCGAGTGGTGGTATTACTGAGTGGATCCGCCAGCGTCCAGGGAG 123
Db 133 GGTGCTCCATCCGAGTGGTGGTATTACTGAGTGGATCCGCCAGCGTCCAGGGAG 192
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Qy 124 GGCCTGAGTGGATGGGTATCATCTATACAGTGGCAACCTTAACAACCCGTCCTC 183
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Qy 184 AAGAGTGAAGTATACATGATGATGAGACACGCTTAAGAACCACTTCCTGAGGCTGAGC 243
Db 253 AAGAGTGAAGTATACATGATGATGAGACACGCTTAAGAACCACTTCCTGAGGCTGAGC 312
Qy 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGGTGAGATGGGTACACTTGG 303
Db 313 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGAGGGGTATTGTAGTAGT 372
Qy 304 GACAACTGGGGCCAGGGAAACCTGTGACCGTCTCTCTC 341
Db 373 TTCAGCTGGGGCCAGGGAAACCTGTGACCGTCTCTCTC 410

RESULT 13
HSA245064 354 bp mRNA linear PRI 02-JUN-1999
LOCUS HSA245064
DEFINITION Homo sapiens mRNA for immunoglobulin gamma heavy chain variable region, partial, clone 2-D123.
ACCESSION AJ245064.1 GI:4995589
VERSION AJ245064.1
KEYWORDS Ig; IgG heavy chain; immunoglobulin gamma heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Dono,M., Zupo,S., Chiorazzi,N. and Ferrarini,M.
TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 354)
AUTHORS Dono,M.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, I.go Rosanna Benzi 10- Genova, ITALY
FEATURES
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/tissue_type="tonsil"
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/protein_id="CAB44197.1"
/db_xref="GI:4995590"
/translation="QVQLQESGPGLVKPSQTLSTCTVSGSISADPVMWIRPPG KGLRWIGITIVYSGSTYRNPISLKSRTISVDTSKQPSLKLSVTAADTAAYVYCCARGIS YFDYWGQALVTSS"
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Query Match 82.7%; Score 283; DB 9; Length 354;
Best Local Similarity 89.7%; Pred. No. 3.9e-70;
Matches 304; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
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QY      4  GAGTCTGGCCCAAGACCTGTGTAACCTTTCACAGACCCCTGTCTCCACCTGACCTGTCTCT 63
D      16  GAGTCGGGGCCCAAGACCTGTGTAACCTTTCACAGACCCCTGTCTCCACCTGACCTGTCTCT 75
QY      64  GGTGGCTCCATCCGACAGTGGTGTATTACTGAGATTGGATCCGACAGCGTCCAGGGAG 123
D      76  GGTGGCTCCATCCGACAGTGGTGTATTACTGAGATTGGATCCGACAGCGTCCAGGGAG 135
QY      124  GGCCTGAGTGGATCGGGTACATCTATCAGATGGCAACACTTAACAACCCGCTCC 183
D      136  GGCCTGAGTGGATCGGGTACATCTATCAGATGGCAACACTTAACAACCCGCTCC 195
QY      184  AAGAGTGAATTACCATATGTCATGACACGCTTAAAGAACCTTCTCCCTGAGGCTGAGC 243
D      196  AAGAGTGAATTACCATATGTCATGACACGCTTAAAGAACCTTCTCCCTGAGGCTGAGC 255
QY      244  TCTGTGACTGCGCGGACAGCGCGGTATTAAGTGTGAGATGAGATGGGTACACTTTG 303
D      256  TCTGTGACTGCGCGGACAGCGCGGTATTAAGTGTGAGATGAGATGGGTACACTTTG 315
QY      304  GACAACCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCTCA 342
D      316  GACTACTGGGGCCAGGGAGCCCTGTGTCACCGTCTCTCTCA 354

RESULT 14
HSU80129      360 bp  DNA  linear  PRI 19-FEB-1997
LOCUS      Human immunoglobulin heavy chain variable region (V4-31) gene,
DEFINITION  partial cds.
ACCESSION  U80129
VERSION    U80129.1  GI:1791100
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1  (bases 1 to 360)
            Glas,A.M., Nottenburg,C. and Milner,E.C.
            Analysis of rearranged immunoglobulin heavy chain variable region
            genes obtained from a bone marrow transplant (BMT) recipient
            Clin. Exp. Immunol. 107 (2), 372-380 (1997)
JOURNAL    Clin. Exp. Immunol. 107 (2), 372-380 (1997)
MEDLINE    97182739
PUBMED     9030878
REFERENCE  2  (bases 1 to 360)
            Glas,A.M., Nottenburg,C. and Milner,E.C.B.
            Direct Submission
            Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
            1000 Seneca Street, Seattle, WA 98101, USA
            Location/Qualifiers
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gene
CDS
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Query Match      82.7%; Score 283; DB 9; Length 360;
Best Local Similarity 91.0%; Pred. No. 3,9e-70;
Matches 314; Conservative 0; Mismatches 25; Indels 6; Gaps 1;

KGEWIGIYVSGSTYNEBSKSRVITISVDTSKNQPISLKSSVTAADTAVYRCARGVS
GMYTFYWGGLTVVSS"

QY      4  GAGTCTGGCCCAAGACCTGTGTAACCTTTCACAGACCCCTGTCTCCACCTGACCTGTCTCT 63
D      16  GAGTCGGGGCCCAAGACCTGTGTAACCTTTCACAGACCCCTGTCTCCACCTGACCTGTCTCT 75
QY      64  GGTGGCTCCATCCGACAGTGGTGTATTACTGAGATTGGATCCGACAGCGTCCAGGGAG 123
D      76  GGTGGCTCCATCCGACAGTGGTGTATTACTGAGATTGGATCCGACAGCGTCCAGGGAG 135
QY      124  GGCCTGAGTGGATCGGGTACATCTATCAGATGGCAACACTTAACAACCCGCTCC 183
D      136  GGCCTGAGTGGATCGGGTACATCTATCAGATGGCAACACTTAACAACCCGCTCC 195
QY      184  AAGAGTGAATTACCATATGTCATGACACGCTTAAAGAACCTTCTCCCTGAGGCTGAGC 243
D      196  AAGAGTGAATTACCATATGTCATGACACGCTTAAAGAACCTTCTCCCTGAGGCTGAGC 255
QY      244  TCTGTGACTGCGCGGACAGCGCGGTATTAAGTGTGAGATGAGATGGGTACACTTTG 297
D      256  TCTGTGACTGCGCGGACAGCGCGGTATTAAGTGTGAGATGAGATGGGTACACTTTG 315
QY      298  ACTTGGACAACCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCTCA 342
D      316  TATTTGACTGACCTGGGGCCAGGGAGCCCTGTGTCACCGTCTCTCTCA 360

RESULT 15
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LOCUS      Human immunoglobulin heavy chain variable region (V4-31) gene,
DEFINITION  partial cds.
ACCESSION  U80130
VERSION    U80130.1  GI:1791102
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1  (bases 1 to 360)
            Glas,A.M., Nottenburg,C. and Milner,E.C.
            Analysis of rearranged immunoglobulin heavy chain variable region
            genes obtained from a bone marrow transplant (BMT) recipient
            Clin. Exp. Immunol. 107 (2), 372-380 (1997)
JOURNAL    Clin. Exp. Immunol. 107 (2), 372-380 (1997)
MEDLINE    97182739
PUBMED     9030878
REFERENCE  2  (bases 1 to 360)
            Glas,A.M., Nottenburg,C. and Milner,E.C.B.
            Direct Submission
            Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
            1000 Seneca Street, Seattle, WA 98101, USA
            Location/Qualifiers
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                        /tissue_type="peripheral blood"
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                        /gene="V4-31"
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gene
CDS
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ORIGIN

Query Match 82.7%; Score 283; DB 9; Length 360;

Best Local Similarity 91.0%; Pred. No. 3.9e-70;

Matches 314; Conservative 0; Mismatches 25; Indels 6; Gaps 1;

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QY 4 GAGCTGGCCCGAGACTGGTGAAGCCTTCAAGACCCCTGCTCCCTGACCTGACGTCTCT 63  
Db 16 GAGTCGGGCCCGAGACTGGTGAAGCCTTCAAGACCCCTGCTCCCTGACCTGACGTCTCT 75  
QY 64 GGTGGCTCCATCCGCACTGCTGTTATTACTGAGTTGATCCGCCAGCGTCCAGGGAAAG 123  
Db 76 GGTGGCTCCATCCAGCACTGCTGTTATTACTGAGTTGATCCGCCAGCGTCCAGGGAAAG 135  
QY 124 GGCCTGGAAGTGAATGGGTACATCTATCAAGTGGCAACACCTACACACCCGTCCTC 183  
Db 136 GGCCTGGAAGTGAATGGGTACATCTATCAAGTGGCAACACCTACACACCCGTCCTC 195  
QY 184 AAGAGTCGAGTTACATGTCAGTAGACACGCTAAAGACCACTTCCCTGAGGCTGAGC 243  
Db 196 AAGAGTCGAGTTACATGTCAGTAGACACGCTAAAGACCACTTCCCTGAGGCTGAGC 255  
QY 244 TCTGTGACTGCCGCGGACACGCGCTGATTACTGTGCGAG-----GTCAATGGGTAC 297  
Db 256 TCTGTGACTGCCGCGGACACGCGCTGATTACTGTGCGAGAGGGGTCAAGTGGCTGTAC 315  
QY 298 ACTTTGACAACTGGGGCCAGGGAAACCTGTGTCACCGTCTCTCA 342  
Db 316 TATTTTGACTAGGGGCCAGGGAAACCTGTGTCACCGTCTCTCA 360
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Search completed: July 27, 2005, 09:08:39
Job time : 1957.83 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:15:56 ; Search time 2106.58 Seconds
(without alignments)
6179.670 Million cell updates/sec

Title: US-10-027-725A-3

Perfect score: 342

Sequence: 1 ctgcagctgcgcccaggact.....ccctgcacccctctctca 342

Scoring table: IDENTITY NUC

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : EST:

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est1:*
9: gb_est2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	273.4	79.9	832	1	AUI22174 AUI22174
2	264	77.2	607	4	BM783015 K-EST0060
3	261.4	76.4	677	4	BG686767 602650737
4	258.8	75.7	509	2	AM406349 UI-HF-BK0
5	257.8	75.4	490	6	CD689564 EST6087 h
6	256.6	75.0	369	2	AM404242 UI-HF-BK0
7	254	74.3	643	1	AUI34293 AUI34293
8	252.6	73.9	1108	5	BM920469 AGENCOURT
9	249.8	73.0	914	4	BG757054 602710478
10	248	72.5	904	5	BQ710488 AGENCOURT
11	246.4	72.0	447	2	AM402200 UI-HF-BK0
12	246.2	72.0	725	4	BG431274 602499844
13	246.2	72.0	959	5	BUS99307 AGENCOURT
14	246	71.9	813	5	BQ710364 AGENCOURT
15	245.8	71.9	582	5	AM401348 UI-HF-BK0
16	244.6	71.6	363	2	AM403420 UI-HF-BK0
17	244.6	71.5	903	5	BQ706579 AGENCOURT
18	244.2	71.4	814	4	BG685325 602637756
19	244.2	71.4	828	4	BP974568 602243482
20	244	71.3	421	2	AM407630 UI-HF-BK0
21	243.8	71.3	856	5	BQ421299 AGENCOURT
22	241.6	70.6	508	7	CR747031 CR747031
23	241.6	70.6	542	2	AM951834 EST363904
24	241.6	70.6	1019	5	BQ072420 AGENCOURT

25	241.6	70.6	1195	5	BQ707644 AGENCOURT
26	241.4	70.6	474	2	AM408410 UI-HF-BK0
27	241.4	70.6	924	5	BQ708516 AGENCOURT
28	240.6	70.4	368	2	AM403989 UI-HF-BK0
29	240.2	70.2	921	5	BQ710000 AGENCOURT
30	240.2	70.2	939	5	BQ708070 AGENCOURT
31	239.8	70.1	915	5	BQ706358 AGENCOURT
32	239.4	70.0	924	5	BG758027 602715076
33	239.4	70.0	942	5	BQ706244 AGENCOURT
34	239.2	69.9	856	4	BG757400 602711031
35	238.6	69.8	357	5	BP432480 BP432480
36	238.6	69.8	548	2	AM402602 UI-HF-BK0
37	238.6	69.8	661	4	BG686421 602638356
38	238.4	69.7	915	5	BQ711871 AGENCOURT
39	238.4	69.7	923	5	BQ707945 AGENCOURT
40	238.4	69.7	928	5	BQ707875 AGENCOURT
41	238.4	69.7	959	5	BQ709473 AGENCOURT
42	238	69.6	987	5	BQ707970 AGENCOURT
43	237.8	69.5	435	2	BF871158 MRI-ET014
44	237.4	69.4	524	5	BQ429270 UI-HF-BK0
45	237.2	69.4	367	2	AM403544 UI-HF-BK0

ALIGNMENTS

RESULT 1	AUI22174	AUI22174	832 bp	mRNA	linear	EST 01-AUG-2002
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DEFINITION	AUI22174	MAMMA1	Homo sapiens	CDNA	clone	MAMMA1001802 5', mRNA
ACCESSION	AUI22174					
VERSION	AUI22174					
KEYWORDS	EST.					
SOURCE	AUI22174.1	GI:10937409				
ORGANISM	Homo sapiens (human)					
REFERENCE	1 (bases 1 to 832)					
AUTHORS	Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.					
TITLE	HRI human CDNA project					
JOURNAL	Unpublished (2000)					
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human CDNA Project; 5'- & 3'-end one pass sequencing; Helix Research Institute; CDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.					
FEATURES	Location/Qualifiers					
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	/note="Vector: pWE18FL3"					
ORIGIN						
Query Match	79.9%	Score 273.4	DB 1	Length 832		
Best Local Similarity	87.9%	Pred. No. 2.6e-69				
Matches	298	Conservative	0	Mismatches	41	Indels
				Gaps	0	
QY	4	GAGTGTGAGCCAGAGAGCTGTGAAGCTTACAGACCTGTCTCCTGACCTGTCTCT	63			
DB	110	GAGTGTGAGCCAGAGAGCTGTGAAGCTTACAGACCTGTCTCCTGACCTGTCTCT	169			

QY 64 GGTGGCTCCATCCGAGTGTGTTTATTACTGAGTTGGATCCGCGACGCTCCAGGGAG 123
Db 170 GGTGGCTCCATCCAGAGTGTGAGCGCCCTAGATTGGATCCGCGACGCGCGAGGGAG 229
QY 124 GGCCTGAGTGGATCCGGTATCATCTATCAAGTGGCAACACTTACAAACACCCGCTCC 183
Db 230 GGCCTGAGTGGATGGCTATCATCTATTAAGTGAACACCTTACAAACCCGCTCC 289
QY 184 AAGAGTCAGATTACCATGTAGTACAGACGCTTGAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 290 AAGAGTCAGATTACCATGTATCAACAGACATGTCCAAAGAACGATTCTCCCTGAAGCTAAC 349
QY 244 TCTGTGACTGCGCGGACACGCGCGCTGTATTACTGTGCGAGGTGAGTGGTACATTGG 303
Db 350 TCTGTGACTGCGGACACGCGCGGTATTACTGTGCGAGTATATATACACAGAGGG 409
QY 304 GACAACTGGGGCCAGGGAACCCCTGTGACCGCTTCCTCA 342
Db 410 GACTTCTGGGGCCAGGGAACCTGTGACCGCTTCATCA 448

RESULT 2
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LOCUS K-BST0060735 S18N669761 Homo sapiens cDNA clone S18N669761-2-E06
DEFINITION 5', mRNA sequence.
ACCESSION BM783015
VERSION BM783015.1 GI:19131247
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Kim N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boseun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.krrib.re.kr
Plate: 2 row: E column: 06
High quality sequence stop: 607.
Location/Qualifiers
1. 607
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/sex="F"
/lab_host="Top10P"
/clone_lib="S18N669761"
/note="Organ: Stomach; Vector: pcns; Site_1: EcoRI;
Site_2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deacapped
with tabacco acid pyrophosphatase (TAP). The deacapped
intact mRNA was ligated with DNA-RNA linker including EcoRI
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10P by electroporation method.
The cDNA libraries constructed by this method are

ORIGIN full-length enriched cDNA library."

Query Match 77.2%; Score 264; DB 4; Length 607;
Best Local Similarity 87.4%; Pred. No. 1,4e-66;
Matches 304; Conservative 0; Mismatches 35; Indels 9; Gaps 1;

QY 4 GAGTCTGGCCAGAGACTGTTGAAGCCCTTCAACAGCCCTGTCCCTACCTGACATGTCTCT 63
Db 112 GAGTCGGGCCAGAGACTGTTGAAGCCCTTCAACAGCCCTGTCCCTACCTGACATGTCTCT 171
QY 64 GGTGGCTCCATCCGAGTGTGTTTATTACTGAGTTGGATCCGCGACGCTCCAGGGAG 123
Db 172 GGTGGCTCCATGAACAGTGTGTTTACTTACTGTGAGCTGGATCCGCAACCCAGGGAG 231
QY 124 GGCCTGAGTGGATCCGGTATCATCTATCAAGTGGCAACACTTACAAACCCGCTCC 183
Db 232 GGCCTGAGTGGATGGGTATCATCTATCAACAGTGGCAACACTTACAAACCCGCTCC 291
QY 184 AAGAGTCAGATTACCATGTAGTACAGACGCTTGAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 292 AAGAGTCAGATTACCATGTATCAACAGACATGTCCAAAGAACGATTCTCCCTGAAGCTGAGC 351
QY 244 TCTGTGACTGCGCGGACACGCGCGCTGTATTACTGTGCGAGTATATATACATGCGG 294
Db 352 TCTGTGACTGCGGACACGCGCGGTATTACTGTGCGAGTATATATACATGCGG 411
QY 295 TACACTTTGGACAACTGGGGCCAGGGAACCCCTGTGACCGCTTCCTCA 342
Db 412 TACGATATGACATGCTGTGGGCGCAAGGAGCAACGCTTCTCTCA 459

RESULT 3
BG686767 677 bp mRNA linear EST 01-MAY-2001
LOCUS BG686767
DEFINITION 602650737F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763217 5',
mRNA sequence.
ACCESSION BG686767
VERSION BG686767.1 GI:13918164
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
1 (bases 1 to 677)
NHLBI National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-ri@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLB)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLB at:
http://image.llnl.gov
Plate: LNCM1618 row: 1 column: 10
High quality sequence stop: 675.
Location/Qualifiers
1. 677
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/db_xref="taxon:9606"
/clone="IMAGE:4763217"
/tissue="IMAGE:4763217"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling

ORIGIN

Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

Query Match 76.4%; Score 261.4; DB 4; Length 677;
Best Local Similarity 89.0%; Pred. No. 8.5e-66;
Matches 307; Conservative 0; Mismatches 31; Indels 7; Gaps 2;

QY 4 GAGTCTGCCCCAGAGACTGTGAAGCTTTCACAGACCTCTGCTCCTGACCTGCTCTCT 63
DB 99 GAGTCTGCCCCAGAGACTGTGAAGCTTTCACAGACCTCTGCTCCTGACCTGCTCTCT 158
QY 64 GGTGCTCCATCCGAGAGTGTGTTATTAATCACTGAGTTGGATCCGACAGCTCCAGGGAG 123
DB 159 GGTGCTCCATCCGAGAGTGTGTTATTAATCACTGAGTTGGATCCGACAGCTCCAGGGAG 217
QY 124 GGCCTGAGTGGATCGGGTACATCTATCAACAGTGGCAACCTTACAAACCCGTCCTC 183
DB 218 GGCCTGAGTGGATCGGGTACATCTATCAACAGTGGCAACCTTACAAACCCGTCCTC 277
QY 184 AAGAGTCGAGTTACCATCTGCTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 278 AAGAGTCGAGTTACCATCTGCTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 337
QY 244 TCTGTGACTCGCGGAGACAGCGCGGTATTAATCACTGTGCA-----GGTCAGATGGGTAC 297
DB 338 TCTGTGACTCGCGGAGACAGCGCGGTATTAATCACTGTGCAAGATCGGAGAGAGAGAGGC 397
QY 298 ACTTGGACAACCTGGGCGAGGAAACCTGTGCAACCTGCTCTCTCA 342
DB 398 GGGTTCACCCCTGGGCGAGGAAACCTGTGCAACCTGCTCTCTCA 442

RESULT 4
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LOCUS
DEFINITION UH-HF-BLO-acc-h-03-0-U1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3059933 5', mRNA sequence.
ACCESSION
AM406349
VERSION
AM406349.1 GI:5925406
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 509)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
FEATURES
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3059933"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_37"

/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 75.7%; Score 258.8; DB 2; Length 509;
Best Local Similarity 86.8%; Pred. No. 4.7e-65;
Matches 297; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCCAGAGACTGTGAAGCTTTCACAGACCTCTGCTCCTGACCTGCTCTCT 63
DB 54 GAGTCTGCCCCAGAGACTGTGAAGCTTTCACAGACCTCTGCTCCTGACCTGCTCTCT 113
QY 64 GGTGCTCCATCCGAGAGTGTGTTATTAATCACTGAGTTGGATCCGACAGCTCCAGGGAG 123
DB 114 GGTGCTCCATCCGAGAGTGTGTTATTAATCACTGAGTTGGATCCGACAGCTCCAGGGAG 173
QY 124 GGCCTGAGTGGATCGGGTACATCTATCAACAGTGGCAACCTTACAAACCCGTCCTC 183
DB 174 GGCCTGAGTGGATCGGGTACATCTATTAATCACTGAGTTGGATCCGACAGCTCCAGGGAG 233
QY 184 AAGAGTCGAGTTACCATCTGCTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 234 AAGAGTCGAGTTACCATCTGCTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 293
QY 244 TCTGTGACTCGCGGAGACAGCGCGGTATTAATCACTGTGCA-----GTCAAGATGGGTAC 300
DB 294 TCTGTGACTCGCGGAGACAGCGCGGTATTAATCACTGTGCAAGATCGGAGAGAGAGAGGC 353
QY 301 TTGGAACAACCTGGGCGAGGAAACCTGTGCAACCTGCTCTCTCA 342
DB 354 TTGGAACAACCTGGGCGAGGAAACCTGTGCAACCTGCTCTCTCA 395

RESULT 5
CD689564 490 bp mRNA linear EST 25-JUN-2003
LOCUS
DEFINITION EST6087 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION
CD689564
VERSION
CD689564.1 GI:32209443
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 490)
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
Zeng, Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel.: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn
FEATURES
SOURCE
1..490
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN

Query Match 75.4%; Score 257.8; DB 6; Length 490;
Best Local Similarity 86.8%; Pred. No. 9.1e-65;
Matches 296; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

QY	5	AGTGTGGGCCAGGAGCTGGTGAAGCCTTACAGACCCTGTCCTACCTGACCTGTCTTG	64
Db	111	AGTGGGGCCAGGAGCTGGTGAAGCCTTACAGACCCTGTCTCTCACTGTCTCTTG	170
QY	65	GTGGCTCCATCCGAGAGTGTGTTATTACTGAGATTGGATCGCGCAGGCGTCCAGGGAAAG	124
Db	171	GTGACTCCATCAGCAGTGTGTGTTACTGTGAGTTGGATTTCGCCAGACCAGGGAAAG	230
QY	125	GCCGTGAATGGATCGGGTACATCTATCAAGTGGCMAACCTTACAACAACCCGTCTCA	184
Db	231	GCCTCGATGGATTGGGTATCATCTATCAAGTGGGAGTGGCAGTACACACCCTCTCTCA	290
QY	185	AGAGTCGAGTTACCATGTCACTGAGACACGTCCTAAGAACCACTTCTCCCTGAGCTGAGCT	244
Db	291	AGAGTCGAGTTACCATGTCACTGAGACACGTCCTAAGAACCAAGTTCCTCGCAGTTGAGGT	350
QY	245	CTGTGACTGCCCGCGGACACGGCCGTTATTACTGTGCGAGGTCAAGAT--GGGTACACTT	301
Db	351	CTGTGACGGCCGCGGACACGGCCCTATTATTACTGTGCGAGATGGGTCCCGACGATTAA	410
QY	302	TGAGCAACTGGGGCAGGGAAACCTGTGACACGTCCTCMA	342
Db	411	TTGACTACTGGGGCCAGGGAAATCTGTGACACCGTCTCTCA	451

RESULT 6	AM404242	369 bp	mRNA	linear	EST 16-FEB-2000
LOCUS	AM404242				
DEFINITION	UI-HF-BL0-abd-f-09-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone				
ACCESSION	IMAGE:3057545 5', mRNA sequence.				
VERSION	AM404242				
KEYWORDS	AM404242.1	GI:6923299			
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
JOURNAL	1 (bases 1 to 369)				
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at: www-bio.lnl.gov/bbrip/image/image.html Seq primer: M13 Forward. Location/Qualifiers 1..369 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3057545" /tissue_type="lymph" /cell_type="germinal center B cells" /cell_line="MGC85" /lab_host="DH10B (LT1)" /clone_id="NIH MGC_37" /note="Vector: pRT73-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldi, Ph.D. and M. Bento Soares, Ph.D."				
FEATURES					
SOURCE					
ORIGIN					
Query Match	75.0%;	Score 256.6;	DB 2;	Length 369;	
Best Local Similarity	87.8%;	Pred.No. 1.9e-64;			

Matches	280;	Conservative	0;	Mismatches	39;	Indels	0;	Gaps	0;
QY	4	GAGTCCTGCCCCAGAGACTGTGTGAAGACCTTTCACACAGACCTGTGTCCCTCCACCTGTGACACTGTCTCT	63						
Db	34	GAGTCGGGGCCCCAGAGACTGTGTGAAGACCTTTCACACAGACCTGTGTCCCTCCACCTGTGACACTGTCTCT	93						
QY	64	GGTGGCTTCATCCGACAGTGGTGGTTATTATTCAGAGTTGGATCCGCGACAGCTGCCAGGGGAAAG	123						
Db	94	GGTGGCTTCATCCAGACAGTGGATGTTACTCTGGAGCTGGATCCGCGACAGACCTCCAGGGGAAAG	153						
QY	124	GGCCTGGAGTGGATCGGGTACATCTTATCACAGTGGCAACCTTCACACACCCGTCCTC	183						
Db	154	GGCCTGGAGTGGATCTGGGTACATCTTATTAACAGTGGAGACCTTACACACCCGTCCTC	213						
QY	184	AAGAGTCGAGTTACCATGTCTAGTACAGACCGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC	243						
Db	214	AAGAGTCGAGCTTACCATGTCTAATAGACACGCTTAAGAACCACTTCTCCCTGAAACTGAGC	273						
QY	244	TCTGTGACTGCGCGGGGACACGGCCGTGTATTACTGTGTGAGGTACAGATGGGTACACTTTG	303						
Db	274	TCTGTGACTGCGCGGGGACACGGCCGTGTATTACTGTGTGAGATCTTTGGCGGTATTACTTTT	333						
QY	304	GACAACTGGGGCCAGGGAA	322						
Db	334	GATAGTAGTGGTTACGGAA	352						

[illegible]

Db 110 AGTGGGCCCCAGACTGTGTGAAGCTTCCACAGACCCTGTCCCTCACTGTCTCTG 169
 Qy 65 GTGGCTCATCCGAGTGTGTGTTATCTAGTGTGGATCGGCAGCGTCCAGGGAAG 124
 Db 170 GTGGCTCATCAGCAGTGTGTATCTTCTGTGACCTGTGATCCGCAACCCAGGGAAG 229
 Qy 125 GCGTGAAGTGTAGTGGGTATCTATCTACAGTGGCAACACTACAAACCCGTCCTCA 184
 Db 230 GCGTGAAGTGTAGTGGGTATCTATCTACAGTGGCAACACTACAAACCCGTCCTCA 289
 Qy 185 AGAGTCGAGTTACCATGTCTAGTAGACAGCTTAAAGAACCTTCTCTGAGGCT 244
 Db 290 AGAGTCGAGTTACCATGTCTAGTAGACAGCTTAAAGAACCTTCTCTGAGGCT 349
 Qy 245 CTGTGACCTGGCGGACACGGCCGTGTATCTGTGCGAGGTCAAGATGGTAACT 300
 Db 350 CTGTGACCTGGCGGACACGGCCGTGTATCTGTGCGAGGTCAAGATGGTAACT 409
 Qy 301 -----TTGACAACTGGGGCCAGGAACTTGTCTCTCTCA 342
 Db 410 GGAGCTACAGTAACTTGTACCACTGGGSCCAGGAACTTGTCTCTCTCA 465

RESULT 8 1108 bp mRNA linear EST 12-MAR-2002
 BM920469
 LOCUS AGNCCOURT_6709612 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5750444
 DEFINITION 5', mRNA sequence.

ACCESSION BM920469
 VERSION BM920469.1 GI:19370848
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1108)
 NIH-MGC http://mgi.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L16M12781 row: 9 column: 21
 High quality sequence stop: 626.

FEATURES

SOURCE

1. 1108
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5750444"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_122"
 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
 Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
 anonymous pool of 24 week female lung; 16 week female
 spleen, and 20-22 week male spleen. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.4 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 026. Note:
 this is a NIH_MGC Library."

ORIGIN

Query Match. 73.9%; Score 252.6; DB 5; Length 1108;
 Best Local Similarity 85.5%; Pred. No. 3.7e-63;
 Matches 295; Conservative 0; Mismatches 44; Indels 6; Gaps 1;

Qy 4 GAGTGTGCCCCAGAGCTGTGTAAACCTTTCACAGACCCTGTCTCTACCTGTGCTCT 63
 Db 110 GAGTGTGCCCCAGAGCTGTGTAAACCTTTCAGAGACCCTGTCTCTACCTGTGCTCT 169
 Qy 64 GGTGGCTTCATCCGAGTGTGTATTACTGTAGTTGATCCGCCAGCTCCAGGGAAG 123
 Db 170 GGTGGCTCCGTCACAGTGTGTATTACTGTAGTTGATCCGCCAGCTCCAGGGAAG 229
 Qy 124 GCGTGAAGTGTAGTGGGTATCTATCTACAGTGGCAACACTACAAACCCGTCCTC 183
 Db 230 GCGTGAAGTGTAGTGGGTATCTATCTATCTACAGTGGCAACACTACAAACCCGTCCTC 289
 Qy 184 AGAGTCGAGTTACCATGTCTAGTAGACAGCTTAAAGAACCTTCTCTGAGGCTAGC 243
 Db 290 AGAGTCGAGTTACCATGTCTAGTAGACAGCTTAAAGAACCTTCTCTGAGGCTAGC 349
 Qy 244 TCTGTGACTGGCGGACACGGCCGTGTATTACTGTGCGAGGTCAAGATGGG-----TAC 297
 Db 350 TCTGTGACTGGCGGACACGGCCGTGTATTACTGTGCGAGGTCAAGATGGG-----TAC 409
 Qy 298 ACTTTGACAACTGGGGCCAGGGAACCTTGTCTACCGTCTCTCA 342
 Db 410 TACATGACGCTGTGGCGCAAGAGGACACGCTACCGTCTCTCA 454

RESULT 9 914 bp mRNA linear EST 15-MAY-2001
 BG757054
 LOCUS 602710478P1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4850851 5',
 DEFINITION mRNA sequence.

ACCESSION BG757054
 VERSION BG757054.1 GI:14067707
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 914)
 NIH-MGC http://mgi.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L16M1692 row: 1 column: 20
 High quality sequence stop: 854.

FEATURES

SOURCE

1. 914
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4850851"
 /tissue_type="Primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_48"
 /note="Organ: B-cells; Vector: pORF7, Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 73.0%; Score 249.8; DB 4; Length 914;
Best Local Similarity 86.7%; Pred. No. 2.4e-62;
Matches 301; Conservative 0; Mismatches 37; Indels 9; Gaps 2;

QY 4 GAGTCTGGCCAGAGACTGTGTAAGCCTTCACAGACCCCTGTCCTCCTGCTGCTGCTCT 63
DB 93 GAGTCTGGCCAGAGACTGTGTAAGCCTTCACAGACCCCTGTCCTCCTGCTGCTGCTCT 152
QY 64 GGTGGCTCCATCCGACGTGTGTATTATCTGAGATTGGATCCGCGACGTCAGGGAAG 123
DB 153 GGTGGCTCCATCCGACGTGTGTATTATCTGAGATTGGATCCGCGACGTCAGGGAAG 211
QY 124 GGCTTGAGTGGATCCGGTATATCTATACAGTGGCAACCTTACAAACACCCGTCCTC 183
DB 212 GGCTTGAGTGGATCCGGTATATCTATACAGTGGCAACCTTACAAACACCCGTCCTC 271
QY 184 AAGAGTCGAGTTACCATGTACGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 272 AAGAGTCGAGTTACCATGTACGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 331
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGTGCAGATGGGTACACTTTG 303
DB 332 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGGGAAGGAGTACGAGTGGC 391
QY 304 GAGCACT-----GGGCGCAGGGAACCTGTCACCGTCTCTCA 342
DB 392 CACGACTTGTGACTGTGGGCGCAGGAACCTGTGTACCGTCTCTCA 438

RESULT 10
LOCUS B0710488 904 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT 8352970 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278137
5', mRNA sequence.
B0710488
ACCESSION B0710488.1 GI:21849387
VERSION ESR.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 904)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgsapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LICM2465 row: k column: 02
High quality sequence stop: 728.

FEATURES
Source

1..904
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6278137"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 72.5%; Score 248; DB 5; Length 904;
Best Local Similarity 84.5%; Pred. No. 8e-62;
Matches 294; Conservative 0; Mismatches 45; Indels 9; Gaps 1;

QY 4 GAGTCTGGCCAGAGACTGTGTAAGCCTTCACAGACCCCTGTCCTCCTGCTGCTGCTCT 63
DB 86 GAGTCTGGCCAGAGACTGTGTAAGCCTTCACAGACCCCTGTCCTCCTGCTGCTGCTCT 145
QY 64 GGTGGCTCCATCCGACGTGTGTATTATCTGAGATTGGATCCGCGACGTCAGGGAAG 123
DB 146 GGTGGCTCCATCCGACGTGTGTATTATCTGAGATTGGATCCGCGACGTCAGGGAAG 205
QY 124 GGCTTGAGTGGATCCGGTATATCTATACAGTGGCAACCTTACAAACACCCGTCCTC 183
DB 206 GGCTTGAGTGGATCCGGTATATCTATACAGTGGCAACCTTACAAACACCCGTCCTC 265
QY 184 AAGAGTCGAGTTACCATGTACGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 266 AAGAGTCGAGTTACCATGTACGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 325
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGTGCAGATGGGTACACTTTG 294
DB 326 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGGGAAGGAGTACGAGTGGC 385
QY 295 TACACTTGGACAACCTGGGCGCAGGGAACCTTGTACCGTCTCTCA 342
DB 386 CATTACTTCAGACACTGTGGGCGCAGGGAACCTTGTGTACCGTCTCTCA 433

RESULT 11
LOCUS AM402200 447 bp mRNA linear EST 16-FEB-2000
DEFINITION UI-HF-BKO-aat-d-09-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3054785 5', mRNA sequence.
AM402200
ACCESSION AM402200.1 GI:6920886
VERSION ESR.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 447)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgsapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bdrip/image/image.html
Seq primer: M13 Forward.

FEATURES
Source

1..447
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3054785"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_36"
/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonafide, Ph.D. and M. Bento Soares, Ph.D."

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1. .725
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="raxon:9606"
/clone="IMAGE:4613435"
/lab_host="HD10B (T1 phage-resistant)"
/clone_11b="NH1 MGc.75"
/notes="Organ: Kidney; Vector: pDNR-11B (Clontech); Site:1
5'fl (ggcgcctcctccgc); Site 2: 5'fl (ggcctatcgc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCCATTATGCGC-3' and 3' adaptor sequence
5'-ATTCTAGAGCGCCGAGCGCCGCAGCATC-dT(30)BN-3' (where B = A,
C, G or T). Average insert size 1.6
kb (range 0.5-5.4 kb). 15/15 colonies contained inserts

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location/Qualifiers
1. 959
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cdate="IMAGS:6280128"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH MGC 113"
/note="Organ: spleen; Vector: pOH87; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAAGGAG(G). Library constructed by Ling Hong in the

```

ORIGIN

laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

Query Match 72.0%; Score 246.2; DB 5; Length 959;
Best Local Similarity 84.3%; Pred. No. 2.7e-61;
Matches 291; Conservative 0; Mismatches 48; Indels 6; Gaps 1;

QY 4 GAGCTGAGCCAGAGACTGTTGAAGCCTTCACAGACCCGTGCTCCCTGACCTGACGTCTCT 63
DB 86 GAGCTGAGCCAGAGACTGTTGAAGCCTTCACAGACCCGTGCTCCCTGACCTGACGTCTCT 145
QY 64 GGTGCTCCATCCGACAGTGTGTATTACTGAGTTGATCCGCGACGCTCAGGGAG 123
DB 146 GGTGCTCCATCCGACAGTGTGTATTACTGAGTTGATCCGCGACGCTCAGGGAG 205
QY 124 GGCCTGAGTGGATCGGGTACATCTATCAGTGGCAACACTTACAAACCCGTCCTC 183
DB 206 GGCCTGAGTGGATCGGGTACATCTATCAGTGGCAACACTTACAAACCCGTCCTC 265
QY 184 AAGAGTCGAGTTACATGTCAGTACAGACGCTTAAGAACACTTCTCCCTGAGGCTGAGC 243
DB 266 AAGAGTCGAGTTACATGTCAGTACAGACGCTTAAGAACACTTCTCCCTGAGGCTGAGC 325
QY 244 TCTGTGACTGCGCGAGACAGCGCCGTGTATTACTGTGCGAGGTGAG-----ATGGGTAC 297
DB 326 TCTGTGACTGCGCGAGACAGCGCCGTGTATTACTGTGCGAGGTGAGGTGAGGTGAGGT 385
QY 298 ACTTGGACAACTGGGGCGAGGAAACCTGTGTCACCGTCTCTCA 342
DB 386 GCTTTGATATCTGGGCGAAGGACATGTGTCAACCGTCTCTCA 430

RESULT 14

LOCUS BO710364 813 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENTCOURT 8351485 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6282412
5', mRNA sequence.

ACCESSION BO710364
VERSION BO710364.1 GI:21849263
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 813)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LUCM2476 row: m column: 05
High quality sequence stop: 529.

FEATURES

source

1..813
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6282412"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 113"
/note="Organ: spleen; Vector: POTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:

ORIGIN

GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

Query Match 71.9%; Score 246; DB 5; Length 813;
Best Local Similarity 91.3%; Pred. No. 3e-61;
Matches 261; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 4 GAGCTGAGCCAGAGACTGTTGAAGCCTTCACAGACCCGTGCTCCCTGACCTGACGTCTCT 63
DB 82 GAGCTGAGCCAGAGACTGTTGAAGCCTTCACAGACCCGTGCTCCCTGACCTGACGTCTCT 141
QY 64 GGTGCTCCATCCGACAGTGTGTATTACTGAGTTGATCCGCGACGCTCAGGGAG 123
DB 142 GGTGCTCCATCCGACAGTGTGTATTACTGAGTTGATCCGCGACGCTCAGGGAG 201
QY 124 GGCCTGAGTGGATCGGGTACATCTATCAGTGGCAACACTTACAAACCCGTCCTC 183
DB 202 GGCCTGAGTGGATCGGGTACATCTATCAGTGGCAACACTTACAAACCCGTCCTC 261
QY 184 AAGAGTCGAGTTACATGTCAGTACAGACGCTTAAGAACACTTCTCCCTGAGGCTGAGC 243
DB 262 AAGAGTCGAGTTACATGTCAGTACAGACGCTTAAGAACACTTCTCCCTGAGGATGAC 321
QY 244 TCTGTGACTGCGCGAGACAGCGCCGTGTATTACTGTGCGAGGTGAG 289
DB 322 TCTGTGACTGCGCGAGACAGCGCCGTGTATTACTGTGCGAGGCGG 367

RESULT 15

LOCUS AM401348 582 bp mRNA linear EST 16-FEB-2000
DEFINITION UI-HF-BKO-aa-u-d-08-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3055142 5', mRNA sequence.

ACCESSION AM401348
VERSION AM401348.1 GI:6920130
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 582)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Straut, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
www-bio.llnl.gov/bdrrp/image/image.html
Seq primer: M13 Forward.

FEATURES

source

1..582
Location/Qualifiers

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/tissue_type="lymph"
/cell_type="germinal center B cells"
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/lab_host="DH10B (LTI)"
/clone_lib="NIH MGC 36"
/note="Vector: pRT73-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic RNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis

ORIGIN

M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "

Query Match	71.9%;	Score 245.8;	DB 2;	Length 582;
Best Local Similarity	86.1%;	Pred. No. 3.2e-61;		
Matches 297;	Conservative 0;	Mismatches 42;	Indels 6;	Gaps 2;

QY	4	GAGTGTGGGCCCAGGAGCTGGTGAAGCCTTCAAGACCCTGGCCCTCAACCTGCACTGTCTCT	63
Db	34	GAGTGGGGCCCAAGACTGGTGAAGCCTTCAAGACCCTGGCCCTCAACCTGCACTGTCTCT	93
QY	64	GATGGCTCCA---TCGCGAGTGGTGGTTATTACTGGAGTGGATTCGCGCAGCTCCAGGG	120
Db	94	GGTGGCTCCATTTCAACAGTGGTATTAATCTTGTGACCTTGGATTCGCGCAGCACCAAGG	153
QY	121	AAGGCGCTGGAGTGGATCGGGTACATCTATCAACAGTGGCAACAACCTTCAACAAACCCGTCC	180
Db	154	AAGGCGCTGGAGTGGATGGTATTGTTACGCTATTACATACATGGGAGCACTATTACAAACCCGTCC	213
QY	181	CTCAAGAGTCCGAGTTACCATGTCTCAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGGCTG	240
Db	214	CTCAAGAGTCCGAGTTTCCATATCAGTAGGACACGCTCTAAGAACCAAGTTCTCTCCGAACTTG	273
QY	241	AGCTGTGACATGCGCCGCGGACAACGGCCGGTATTAATCTGGCCAGGATCAATGGGTAC---	297
Db	274	AGCTGTGACATGCGCCGCGGACAACGGCCAGTATTAATCTGGCCAGAGAGGGGTGGCTTAAT	333
QY	298	ACTTTGGACAACACTGGGGCCAGGGAACCCGTGTCACCGTCTCCCA	342
Db	334	GCTTTTGATATCTGGGGCCCAAGGACAAATAGTACCGGTCTCTTCA	378

Search completed: July 27, 2005, 12:32:08
Job time : 2107.58 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 03:58:31 ; Search time 321.618 Seconds
(without alignments)
6294.891 Million cell updates/sec

Title: US-10-027-725A-3
Perfect score: 342
Sequence: 1.ctcgagctgcgcacagact.....ccctgctcaccgtctctca 342

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
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4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	338.8	99.1	342	6	ABK89639 DNA encod
2	332.8	94.4	342	6	ABK89638 DNA encod
3	308.4	90.2	342	6	ABK89637 DNA encod
4	284.6	83.2	352	10	ADCC9786 Anti-huma
5	284.6	83.2	352	10	ADDO5390 Anti-MUC1
6	284.6	83.2	352	10	ADFO9828 Human ant
7	284.4	83.2	360	4	AAF29076 Human HIV
8	276.6	80.9	354	13	ADs84403 Human ant
9	276.6	80.9	354	13	ADr68545 Anti-EPO-
10	276.6	80.9	1996	13	ADs84453 Human ant
11	276.6	80.9	1996	13	ADs84453 Human ant
12	276.6	80.9	1996	13	ADr68595 Human ant
13	276.6	80.9	1996	13	ADr68596 Human ant
14	275.8	80.6	663	10	ADJ32125 Human int
15	275	80.4	352	10	ADCC9778 Anti-huma
16	275	80.4	352	10	ADDO5382 Anti-MUC1
17	275	80.4	352	10	ADFO9820 Human ant
18	274.2	80.2	560	12	ADK52387 Human ant
19	273.8	80.1	369	4	AAF29046 Human HIV
20	271.8	79.5	355	13	ADs84415 Human ant

21	271.8	79.5	355	13	ADr68557 Anti-EPO-
22	271.8	79.5	1996	13	ADs84472 Human ant
23	271.8	79.5	1996	13	ADs84471 Human ant
24	271.8	79.5	1996	13	ADr68614 Human ant
25	271.8	79.5	1996	13	ADr68613 Human ant
26	270.2	79.0	1838	10	ADP90705 Human hep
27	270	78.9	1338	12	ADK52355 Human ant
28	268.4	78.5	358	10	ADCC9798 Anti-huma
29	268.4	78.5	358	10	ADDO5402 Anti-MUC1
30	268.4	78.5	358	10	ADFO9840 Human ant
31	267.2	78.1	516	3	AAA46876 DNA encod
32	264	77.2	357	2	AAAF2906 Human HIV
33	263.6	77.1	357	2	AAQ38670 MAB GAH v
34	262.8	76.8	352	10	ADCC9806 Anti-huma
35	262.8	76.8	352	10	ADDO5410 Anti-MUC1
36	262.8	76.8	352	10	ADFO9848 Human ant
37	261.4	76.4	741	3	AAZ28998 Anti-muri
38	258.6	75.6	1644	2	AAZ24434 Human bla
39	257	75.1	324	4	ABS46332 Human liv
40	257	75.1	340	6	ABK84446 Human CDN
41	257	75.1	340	8	ACA64884 Human Ig
42	257	75.1	340	10	ADP90613 Human hep
43	257	75.1	384	12	ADP22095 Human ant
44	257	75.1	384	12	ADP22103 Human ant
45	257	75.1	384	12	ADP22123 Human ant

ALIGNMENTS

RESULT 1	ABK89639	standard; DNA; 342 BP.
ID	ABK89639	
XX	ABK89639;	
AC		
XX		
DT	21-OCT-2002	(first entry)
XX		
DE	DNA encoding human Ige Fab clone 100 heavy chain.	
XX		
KW	Human; fab; ds; gene; antiallergic; vaccine; grass pollen; phi p 2;	
KW	timothy grass pollen allergen; passive immunotherapy.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
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FT	misc_feature	7..78
FT		/tag= b
FT		/note= "FR1 region"
FT	misc_feature	79..99
FT		/tag= c
FT		/note= "CDR1 region"
FT	misc_feature	100..123
FT		/tag= d
FT		/note= "FR2 region"
FT	misc_feature	134..141
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FT	misc_feature	142..189
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XX	WO200253595-A1.
XX	11-JUL-2002.
XX	27-DEC-2001; 2001WO-SE002908.
XX	29-DEC-2000; 2000SE-00004892.
XX	(PHAA) PHARMACIA DIAGNOSTICS AB.
XX	Flicker S, Steinberger P, Kraft D, Valenta R;
XX	WPI; 2002-583604/62.
XX	P-PSDB; ABG30447.
XX	Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
XX	variable region of group 2 allergen specific-human IgE Fabs, useful for
XX	diagnosing or passive immunotherapy of type I allergy, for environmental
XX	allergen detection.
XX	Disclosure; Page 33; 45pp; English.
XX	This invention relates to the DNA and protein sequences of group 2
XX	allergen-specific human IgE Fabs and methods for their use. The proteins
XX	of the invention may have antiallergic activities and may be used as a
XX	vaccine or an inhibitor of binding of grass pollen allergen patient's IgE
XX	antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
XX	2 allergen-specific fabs of the invention may be useful for environmental
XX	allergen detection and for standardization of allergen extracts. The fabs
XX	- or a vaccine against a type I allergy is useful for passive
XX	immunotherapy of type I allergy, it is also useful for diagnosing a type
XX	I allergy. The allergen-specific fabs of the invention are useful for
XX	inter alia, diagnosis, therapy and prevention of type I allergy. They are
XX	also useful for identification of group 2 allergen-containing pollen and
XX	may be used for blocking the binding of grass pollen allergic patients
XX	IgE antibodies to Phi p 2. The present sequence represents the DNA
XX	encoding the human IgG fab, clone 100 heavy chain protein of the
XX	invention
XX	Sequence 342 BP; 69 A; 103 C; 94 G; 76 T; 0 U; 0 Other;
XX	SO
XX	Query Match 99.1%; Score 338.8; DB 6; Length 342;
XX	Best Local Similarity 99.4%; Pred. No. 1.6e-85;
XX	Matches 340; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 CTCGAGTCGCGCCGAGGACTGGTGAAGCCTTACAGACCCCTGCTCCTACCTGCATCTC 60
DB	1 CTCGAGTCGCGCCGAGGACTGGTGAAGCCTTACAGACCCCTGCTCCTACCTGCATCTC 60
QY	61 TCTGCTGGCTCCATCCGACAGTGGTGGTATTATCTAGAGTTGGATCCGACGAGTCCAGAG 120
DB	61 TCTGCTGGCTCCATCCGACAGTGGTGGTATTATCTAGAGTTGGATCCGACGAGTCCAGAG 120
QY	121 AAGGCTCTGAGTGGATGGGCTGATCTTATCAACAGTGGCAACACTTAACAACCCGCTCC 180
DB	121 AAGGCTCTGAGTGGATGGGCTGATCTTATCAACAGTGGCAACACTTAACAACCCGCTCC 180
QY	181 CTCGAGAGTCCGAGTTACCAATGTCAGTAGACACGCTTAAGAACCACTTCTCCTTAGAGCTG 240
DB	181 CTCGAGAGTCCGAGTTACCAATGTCAGTAGACACGCTTAAGAACCACTTCTCCTTAGAGCTG 240
QY	241 AGCTCTGTGACTGCGCGGACACGCGCCGATTTACTGTGGCAGAGGTCAGATGGGTAACT 300
DB	241 AGCTCTGTGACTGCGCGGACACGCGCCGATTTACTGTGGCAGAGGTCAGATGGGTAACT 300
QY	301 TTGACAACTGGGAGGACAGGAAACCTGTGTCACCGTCTCCTCA 342
DB	301 TTGACAACTGGGAGGACAGGAAACCTGTGTCACCGTCTCCTCA 342

1D	ABX89638	standard; DNA; 342 BP.
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AC	ABX89638;	
XX		
DT	21-OCT-2002	(first entry)
XX		
DE	DNA encoding human IGE Fab clone 60 heavy chain.	
XX		
KW	Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;	
KW	timothy grass pollen allergen; passive immunotherapy.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
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FT		/*tag= a
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FT		7..78
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FT		79..99
FT	misc_feature	/*tag= c
FT		/note= "CDR1 region"
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FT	misc_feature	/*tag= d
FT		/note= "FR2 region"
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FT	misc_feature	/*tag= e
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FT	misc_feature	/*tag= f
FT		/note= "CDR2 region"
FT		190..285
FT	misc_feature	/*tag= g
FT		/note= "FR3 region"
FT		286..309
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FT		/note= "PR4 region"
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FN	W0200253595-A1.	
XX		
PD	11-JUL-2002.	
XX		
PE	27-DEC-2001; 2001WO-SR002908.	
XX		
PR	29-DEC-2000; 2000SE-00004892.	
XX		
PA	(PHAA) PHARMACIA DIAGNOSTICS AB.	
XX		
PI	Flicker S, Steinberger P, Kraft D, Valenta R;	
XX		
DR	WPI; 2002-563604/62.	
DR	P-PSDB; ABG30446.	
XX		
PT	Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising	
PT	Variable region of group 2 allergen specific-human IgE Fabs, useful for	
PT	diagnosing or passive immunotherapy of type I allergy, for environmental	
PT	allergen detection.	
XX		
XX		
PS	Disclosure; Page 32; 45pp; English.	
XX		
CC	This invention relates to the DNA and protein sequences of group 2	
CC	allergen-specific human IgE Fabs and methods for their use. The proteins	
CC	of the invention may have antiallergic activities and may be used as a	
CC	vaccine or an inhibitor of binding of grass pollen allergenic patient's IgE	
CC	antibodies to Phi p 2 (a major timothy grass pollen allergen). The group	
CC	2 allergen-specific fabs of the invention may be useful for environmental	
CC	allergen detection and for standardisation of allergen extracts. The fabs	
CC	- or a vaccine against a type I allergy is useful for diagnosing a type	
CC	immunotherapy of type I allergy, it is also useful for diagnosing a type	

CC I allergy. The allergen-specific fabs of the invention are useful for
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
 CC also useful for identification of group 2 allergen-containing pollen and
 CC may be used for blocking the binding of grass pollen allergic patients
 CC IgE antibodies to Phi p 2. The present sequence represents the DNA
 CC encoding the human IgE fab, clone 60 heavy chain protein of the invention
 XX

Sequence 342 BP; 70 A; 105 C; 90 G; 77 T; 0 U; 0 Other;

Query Match 94.4%; Score 322.8; DB 6; Length 342;
 Best Local Similarity 96.5%; Pred. No. 5.1e-81;
 Matches 330; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 CTCGAGTCTGGCCCGAGAGCTGTGTAAGCCTTCAAGACCTTCCTCCATCGACTGTC 60
 Db 1 CTCGAGTCTGGCCCGAGAGCTGTGTAAGCCTTCAAGACCTTCCTCCATCGACTGTC 60
 Qy 61 TCTGAGTCTCCATCCGAGTGTGTATTATCTGAGATTGAGTCCGACGCTCCAGGG 120
 Db 61 TCTGAGTCTCCATCCGAGTGTGTATTATGAGATTGAGTCCGACGCTCCAGGG 120
 Qy 121 AAGGCTCTGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 Db 121 AAGGCTCTGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 Qy 181 CTCGAGTCTGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Db 181 CTCGAGTCTGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Qy 241 AGCTCTGTGACTGCGCGGAGACGCGCGGTATTATGATGATGATGATGATGATGATGAT 300
 Db 241 AGCTCTGTGACTGCGCGGAGACGCGCGGTATTATGATGATGATGATGATGATGATGAT 300
 Qy 301 TTGAGCACTGGGGCCAGGGAACCTTGTGACCGTCTCTCA 342
 Db 301 TTGAGCACTGGGGCCAGGGAACCTTGTGACCGTCTCTCA 342

RESULT 3

ABK89637 ID ABK89637 standard; DNA; 342 BP.

AC ABK89637;

DT 21-OCT-2002 (first entry)

XX DNA encoding human IgE Fab clone 94 heavy chain.

XX Human; fab; ds; gene; anti-allergic; vaccine; grass pollen; Phi p 2;

KM timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..342
 /tag= a
 /product= "Fab clone 94 heavy chain"

FT misc_feature 7..78
 /tag= b
 /note= "FRI region"

FT misc_feature 79..99
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FT misc_feature 100..123
 /tag= d
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FT misc_feature 134..141
 /tag= e
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FT misc_feature 142..189
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FT misc_feature 190..285

FT /tag= g
 FT /note= "FR3 region"
 FT misc_feature 286..309
 FT /tag= h
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 FT misc_feature 310..342
 FT /tag= i
 FT /note= "FR4 region"

XX WO200253595-A1.

XX 11-JUN-2002.

XX 27-DEC-2001; 2001WO-SE002908.

XX 29-DEC-2000; 2000SE-00004892.

XX (PHAA) PHARMACIA DIAGNOSTICS AB.

XX Flicker S, Steinberger P, Kraft D, Valenta R;

XX WPI; 2002-583604/62.

XX P-PSDB; ABG30445.

PT Group 2 allergen-specific immunoglobulins (Ig) E fabs or IgG comprising
 PT variable region of group 2 allergen specific-human IgE fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for environmental
 PT allergen detection.

XX Disclosure; Page 31-32; 45pp; English.

XX This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human IgE fabs and methods for their use. The proteins
 CC of the invention may have anti-allergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
 CC 2 allergen-specific fabs of the invention may be useful for environmental
 CC allergen detection and for standardisation of allergen extracts. The fabs
 CC - or a vaccine against a type I allergy is useful for passive
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type
 CC I allergy. The allergen-specific fabs of the invention are useful for
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
 CC also useful for identification of group 2 allergen-containing pollen and
 CC may be used for blocking the binding of grass pollen allergic patients
 CC IgE antibodies to Phi p 2. The present sequence represents the DNA
 CC encoding the human IgE fab, clone 94 heavy chain protein of the invention
 XX

Sequence 342 BP; 69 A; 100 C; 98 G; 75 T; 0 U; 0 Other;

Query Match 90.2%; Score 308.4; DB 6; Length 342;
 Best Local Similarity 93.9%; Pred. No. 5.9e-77;
 Matches 321; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CTCGAGTCTGGCCCGAGAGCTGTGTAAGCCTTCAAGACCTTCCTCCATCGACTGTC 60
 Db 1 CTCGAGTCTGGCCCGAGAGCTGTGTAAGCCTTCAAGACCTTCCTCCATCGACTGTC 60
 Qy 61 TCTGAGTCTCCATCCGAGTGTGTATTATCTGAGATTGAGTCCGACGCTCCAGGG 120
 Db 61 TCTGAGTCTCCATCCGAGTGTGTATTATCTGAGATTGAGTCCGACGCTCCAGGG 120
 Qy 121 AAGGCTCTGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 Db 121 AAGGCTCTGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 Qy 181 CTCGAGTCTGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Db 181 CTCGAGTCTGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Qy 241 AGCTCTGTGACTGCGCGGAGACGCGCGGTATTATGATGATGATGATGATGATGATGAT 300
 Db 241 AGCTCTGTGACTGCGCGGAGACGCGCGGTATTATGATGATGATGATGATGATGATGAT 300

QY 301 TTGGACAATTGGGGCCAGGAAACCTTGTCACCGTCTCTCTCA 342
DB 301 TTGGACAATTGGGGCCAGGAAACCTTGTCACCGTCTCTCTCA 342

RESULT 4
ADC99786
ID ADC99786 standard; DNA, 352 BP.
AC ADC99786;
XX
XX
DT 01-JAN-2004 (first entry)
XX
XX
DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 15.
XX
XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KM cytostatic; melanoma; oesophageal; pancreatic; colorectal tumor;
KM cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KM lung cancer; human; ds; gene.
XX
XX Homo sapiens.
OS
XX WO2003057838-A2.
PN 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041581.
PF 28-DEC-2001; 2001US-0346299P.
PR
XX
XX (ABGE-) ABGENIX INC.
PA
XX
XX Gudas J;
PI
XX
XX WPI; 2003-587113/55.
DR P-PSDB; ADC99784.
XX
XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
XX
PS Claim 8; SEQ ID NO 15; 78pp; English.

CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumors, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumors, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain variable domain DNA of the invention.

XX
SQ Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;

Query Match 83.2%; Score 284.6; DB 10; Length 352;
Best Local Similarity 92.0%; Pred. No. 3.1e-70;
Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY 4 GAGTCTGAGCCAGAGACTGTGAAGCCTTGACAGACCTGTCCTGACCTGACTGTCTCT 63
DB 16 GAGTCTGAGCCAGAGACTGTGAAGCCTTGACAGACCTGTCCTGACCTGACTGTCTCT 75
QY 64 GGTGGCTCCACATCCAGAGGTGTGTTATTAATGAGAGTGGACCCGACGCGGAGAG 123
DB 76 GTGGCTCCACATCCAGAGGTGTGTTATTAATGAGAGTGGACCCGACGCGGAGAG 135
QY 124 GGCCTGAGTGGATCGGGTATCATATCAAGTGGACCAACCTCAACACCCGTCCTC 183
DB 136 GGCCTGAGTGGATCGGGTATCATATTAACGTGGAGCACTACTACAAACCCGTCCTC 195

QY 184 AAGAGTGAAGTACCATGTGATGACAGACGTCTTAAGAACCACTTCTCCCTGAGCTGAGC 243
DB 196 AAGAGTGAAGTACCATGTGATGACAGACGTCTTAAGAACCACTTCTCCCTGAGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACAGCGCGGTATTAATGAGAGTGGATGAGTGGATGAGTGG 303
DB 256 TCTGTGACTGCGCGGACACAGCGCGGTATTAATGAGAGTGGATGAGTGGATGAGTGG 312
QY 304 GACAACTGGGGCCAGGAAACCTTGTCACCGTCTCTCTCA 342
DB 313 GACTACTGGGGCCAGGAAACCTTGTCACCGTCTCTCTCA 351

RESULT 5
ADD05390
ID ADD05390 standard; DNA, 352 BP.
AC ADD05390;
XX
XX
DT 01-JAN-2004 (first entry)
XX
XX
DE Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID No 15.
XX
XX monoclonal antibody; tumor; MUC18; proliferation; cytostatic; vaccine;
KM antigen; tumor metastasis; melanoma; metastatic; human; heavy chain;
KM gene; ds.
XX
XX Homo sapiens.
OS
XX WO2003057006-A2.
PN 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041582.
PF 28-DEC-2001; 2001US-0346460P.
PR
XX
XX (ABGE-) ABGENIX INC.
PA
XX
XX Gudas J, Bar-Eli M;
PI
XX
XX WPI; 2003-577496/54.
DR P-PSDB; ADD05388.
XX
XX
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.

XX
XX
PS Disclosure; SEQ ID NO 15; 87pp; English.

CC The invention relates to a novel monoclonal antibody used for inhibiting
CC tumor growth in an animal. The tumor inhibition process comprises
CC selecting an animal in need of treatment for a tumor, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumor with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumors, inhibiting tumor growth (e.g. melanoma, lung tumor or
CC tumor metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumor. This
CC polynucleotide sequence represents the DNA encoding an anti-MUC18
CC antibody heavy chain, variable region, protein of the invention.

XX
SQ Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;

Query Match 83.2%; Score 284.6; DB 10; Length 352;
Best Local Similarity 92.0%; Pred. No. 3.1e-70;
Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGAGCTGTGTAAGCCCTTACAGACCCCTGTCTCACTGTGACTGTCTCT 63
DB 16 GAGTCTGGCCAGGAGCTGTGTAAGCCCTTACAGACCCCTGTCTCACTGTGACTGTCTCT 75
QY 64 GGTGGCTTCATCCGCACTGTGTGTATTAATCTGAGATTGGATCCGCCAGCGTCCAGGGAG 123
DB 76 GGTGGCTTCATCCGCACTGTGTGTATTAATCTGAGATTGGATCCGCCAGCGTCCAGGGAG 135
QY 124 GGCCTGGAGTGGATGGGTTACATCTATCAAGTGGCAACACTTAACAACCCGTCCTC 183
DB 136 GGCCTGGAGTGGATGGGTTACATCTATTAATCAAGTGGCAACACTTAACAACCCGTCCTC 195
QY 184 AAGAGTGAAGTTACATATCACTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 196 AAGAGTGAAGTTACATATCACTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTAATCTGTGAGAGTCAATGAGTGTG 303
DB 256 TCTGTGACTGCGCGGACACGCGCGTGTATTAATCTGTGAGAGTCAATGAGTGTG 312
QY 304 GACAACCTGGGGCCAGGGAACCCGTGTCAACCGTCTCTCA 342
DB 313 GACTACTGGGGCCAGGGAACCCGTGTCAACCGTCTCTCA 351

RESULT 6

ADP09828
ID ADF09828 standard; DNA; 352 BP.

AC ADF09828;

DT 12-FEB-2004 (first entry)

DE Human anti-MUC18 monoclonal antibody heavy chain coding sequence #4.

XX cell proliferation inhibitor; MUC18 tumour antigen;

KW anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;

KW carcinoma; cancer; malignancy; heavy chain; human; de; gene.

OS Homo sapiens.

XX WO2003057837-A2.

PN 17-JUL-2003.

PD 26-DEC-2002; 2002WO-US041580.

PR 28-DEC-2001; 2001US-0346414P.

PA (ABGE-) ABGENIX INC.

PI Gudas J;

DR WPI; 2003-598367/56.

DR P-PSDB; ADF09826.

PT Inhibiting cell proliferation associated with expression of MUC18 tumor

PT antigen, involves incubating and inhibiting cell by administering anti-

PT MUC18 monoclonal antibody.

PS Disclosure: SEQ ID NO 15; 83bp; English.

XX The invention comprises a method for inhibiting cell proliferation

CC associated with expression of MUC18 tumour antigen. The method involves

CC administering anti-MUC18 monoclonal antibody. The method of the invention

CC is useful for inhibiting cell (e.g. melanoma or tumour cell)

CC proliferation associated with the expression of MUC18 tumour antigen, the

CC method is preferably useful for inhibiting tumour metastasis. The method

CC is useful for inhibiting cell proliferation in patients with tumours,

CC carcinoma, cancer and other malignancies. The present DNA sequence

CC encodes a heavy chain from an MUC18 tumour antigen-specific monoclonal

CC antibody.

50 Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;
Query Match 83.2%; Score 284.6; DB 10; Length 352;
Best Local Similarity 92.0%; Pred. No. 3.1e-70;
Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGAGCTGTGTAAGCCCTTACAGACCCCTGTCTCACTGTGACTGTCTCT 63
DB 16 GAGTCTGGCCAGGAGCTGTGTAAGCCCTTACAGACCCCTGTCTCACTGTGACTGTCTCT 75
QY 64 GGTGGCTTCATCCGCACTGTGTGTATTAATCTGAGATTGGATCCGCCAGCGTCCAGGGAG 123
DB 76 GGTGGCTTCATCCGCACTGTGTGTATTAATCTGAGATTGGATCCGCCAGCGTCCAGGGAG 135
QY 124 GGCCTGGAGTGGATGGGTTACATCTATCAAGTGGCAACACTTAACAACCCGTCCTC 183
DB 136 GGCCTGGAGTGGATGGGTTACATCTATTAATCAAGTGGCAACACTTAACAACCCGTCCTC 195
QY 184 AAGAGTGAAGTTACATATCACTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 196 AAGAGTGAAGTTACATATCACTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTAATCTGTGAGAGTCAATGAGTGTG 303
DB 256 TCTGTGACTGCGCGGACACGCGCGTGTATTAATCTGTGAGAGTCAATGAGTGTG 312
QY 304 GACAACCTGGGGCCAGGGAACCCGTGTCAACCGTCTCTCA 342
DB 313 GACTACTGGGGCCAGGGAACCCGTGTCAACCGTCTCTCA 351

RESULT 7

AAF29076
ID AAF29076 standard; DNA; 360 BP.

AC AAF29076;

DT 03-APR-2001 (first entry)

DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 32.

XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;

KW envelope glycoprotein; gp120; diagnosis; de.

OS Homo sapiens.

XX WO200100678-A1.

PN 04-JAN-2001.

PD 23-JUN-2000; 2000WO-US017327.

PR 30-JUN-1999; 99US-0141701P.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Watkins BA, Reitz MS;

DR WPI; 2001-112438/12.

DR P-PSDB; AAB62775.

PT Novel human monoclonal antibody immunoreactive with human

PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1

PT in biological sample and providing passive immunotherapy to HIV-1

PT infected mammal.

PS Claim 4; Page 45; 81bp; English.

XX The present invention provides the protein and coding sequences for the

CC variable regions of human monoclonal antibodies which are immunoreactive

CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.

CC These can be used in diagnosis and therapy of HIV-1 infection

KW spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain;
 KM variable region; ds.
 OS Homo sapiens.
 XX US2004175379-A1.
 XX 09-SEP-2004.
 XX 10-OCT-2003; 2003US-00684109.
 XX 14-OCT-2002; 2002US-0418031P.
 XX (DEVIR/) DEVIRIES P J.
 XX (OSTR/) OSTROW D H.
 XX (REIL/) REILLY E B.
 XX (GREEN/) GREEN L J.
 XX (WIELER/) WIELER J.
 XX Devires PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;
 XX WPI; 2004-661369/64.
 XX P-PSDB; ADR68546.
 XX New antibody or its antibody fragment that activates an endogenous
 PT activity or is capable of binding to a human erythropoietin receptor in a
 PT mammal, useful for treating a mammal suffering aplasia or anemia.
 PS Claim 47; SEQ ID NO 42; 156pp; English.
 XX The invention describes an antibody or its fragment that activates an
 CC endogenous activity or capable of binding to a human erythropoietin
 CC receptor in a mammal, or that comprises at least one heavy or light chain
 CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
 CC given in the specification. Also described are: a method of activating or
 CC modulating an endogenous activity of a human erythropoietin receptor in a
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an
 CC isolated and purified polynucleotide sequence selected from 28 sequences
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
 CC the specification, and their fragments, complements, and degenerate codon
 CC equivalents; and an isolated and purified amino acid sequence selected
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
 CC their fragments. The antibody or its antibody fragment that activates or
 CC modulates the activity of the receptor is useful in a method of treating
 CC a mammal suffering aplasia or anaemia. The antibodies are also useful for
 CC treating disorders characterised by decreased or subnormal levels of
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue
 CC hypoxia and/or diseases characterised by inadequate blood circulation or
 CC reduced blood flow. They are also useful for promoting wound healing or
 CC for protecting against neural cell and/or tissue damage, resulting from
 CC brain/spinal cord injury, stroke and the like. The antibodies are also
 CC useful for identifying or diagnosing mammals having dysfunctional
 CC erythropoietin receptor. This sequence encodes an anti-EPO-R-antibody
 CC heavy chain variable region.
 XX
 XX Sequence 354 BP; 76 A; 105 C; 97 G; 76 T; 0 U; 0 Other;
 SQ
 Query Match 80.9%; Score 276.6; DB 13; Length 354;
 Best Local Similarity 88.5%; Fred. No. 5.5e-68;
 Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
 QY 4 GAGTGTGGCCGAGGAGCTGTGAAGCTTACAGAGACCCCTGCTCACTGACGTGTCTCT 63
 DB 16 GAGTGTGGCCGAGGAGCTGTGAAGCTTACAGAGACCCCTGCTCACTGACGTGTCTCT 75
 QY 64 GGTGGCTTCATCCGAGTGTGTGTATTACTGAGATTGATTCGCCAGCTGCCAGGAAG 123
 DB 76 GGTGGCTTCATCCGAGTGTGTGTATTACTGAGATTGATTCGCCAGCTGCCAGGAAG 135

QY 124 GGCTGTGAGTGTGATCGGATCATCTATACAGTGGCAACACCTTAACAACCCGCTCC 183
 DB 136 GGCTGTGAGTGTGATCGGATCATCTATTAAGATGAGACCTCTCTAACAACCCGCTCC 195
 QY 184 AAGAGTGAATTACCATGTCAGTACGACGCTCTAAGAACCTTCTCCCTGAGGTGAGC 243
 DB 196 AAGAGTGAATTACCATGTCAGTACGACGCTCTAAGAACCTTCTCCCTGAGGTGAGC 255
 QY 244 TCTGTGACTGCGCGGACGACGCGCGGTGATTAATGTCGAGGTGAGTACACTTTCG 303
 DB 256 TCTGTGACTGCGCGGACGACGCGCGGTGATTAATGTCGAGGTGAGTACACTTTCG 315
 QY 304 GACAACTGGGGCCGAGGAAACCTGTGATCACTCTCTCTCA 342
 DB 316 GACTACTGGGGCCGAGGAAACCTGTGATCACTCTCTCTCA 354
 RESULT 10
 ADS84454/c
 ID ADS84454 standard; DNA; 1996 BP.
 XX
 XX ADS84454;
 XX
 XX 18-NOV-2004 (first entry)
 XX
 XX Human anti-EPO-R antibody Ab412 heavy chain complementary DNA SEQ ID:93.
 XX
 XX human; erythropoietin receptor; EPO receptor;
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;
 KW antianaemic; neuroprotective; vulnery; gene therapy; aplasia; anaemia;
 KW wound healing; neural cell damage protection;
 KW neural tissue damage protection; brain injury; spinal cord injury;
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;
 KW ds.
 KW Homo sapiens.
 XX
 XX US2004035603-A2.
 XX
 XX 29-APR-2004.
 XX
 XX 14-OCT-2003; 2003WO-US032243.
 XX
 XX 14-OCT-2002; 2002US-00269711.
 XX 10-OCT-2003; 2003US-00684109.
 XX
 XX (ABBOTT LAB.
 XX
 XX Devires PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;
 XX WPI; 2004-348433/32.
 XX P-PSDB; ADS84455.
 XX
 XX New antibodies that bind to or activate an endogenous human
 PT erythropoietin receptor, useful for diagnosing, preventing or treating
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.
 PT anemia.
 PT
 XX
 XX Disclosure; SEQ ID NO 93; 192pp; English.
 PS
 XX The present invention describes an antibody or its fragment that binds to
 CC or activates an endogenous activity of a human erythropoietin (EPO)
 CC receptor in a mammal, but does not interact with a peptide having a
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)
 CC methods of modulating or activating an endogenous activity of a human EPO
 CC receptor in a mammal, comprising administering to the mammal a
 CC therapeutic amount of the above antibody or its fragment to modulate or
 CC activate the receptor; (2) a method of treating a mammal suffering from
 CC aplasia, comprising administering to the mammal a therapeutic amount of
 CC the above antibody or its fragment to modulate or activate the receptor;
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)
 CC an isolated and purified polynucleotide sequence, and their fragments,

CC	complements and degenerate codon equivalents; and (5) an isolated and
CC	purified amino acid sequence, and their fragments. The EPO receptor
CC	binding antibody has antianaemic, neuroprotective and vulnary
CC	activities, and can be used in gene therapy. The compositions and methods
CC	from the present invention can be used for modulating an endogenous
CC	activity of a human EPO receptor or for treating mammals suffering from
CC	aplasia or anaemia. They may also be used for identifying mammals having
CC	a dysfunctional EPO receptor. The composition may also be used in
CC	promoting wound healing or in protecting against neural cell and/or
CC	tissue damage resulting from brain/spinal cord injury, stroke and the
CC	like. The present sequence represents a human anti-EPO-R antibody heavy
CC	chain complementary DNA sequence, which is given in the exemplification
CC	of the present invention.
XX	
XX	Sequence 1996 BP; 351 A; 537 C; 686 G; 422 T; 0 U; 0 Other;
QQ	
Query Match	80.9%; Score 276.6; DB 13; Length 1996;
Best Local Similarity	88.5%; Pred. No. 8,6e-68;
Matches	300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY	4 GAGTCTGGCCCGAGACTGATGAAAGCCTTCACAGACCCTGCTCCACCTGCATGTCCTCT
DB	1924 GAGTCGGGCCAGGACTGTGTAAGCCTTCACAGACCCTGCTCCACCTGCATGTCCTCT
QY	64 GGTGGCTCATCCGACGTGTGTTATTACTGGAATGGATCCGACGCTTCAGGGAAG
DB	1864 GGTGGCTCATCAGACGATGTGTCTTACTACGTAAGTGTGATCCGACACCCAGGGAAG
QY	124 GGCCCTGAGTGGATGGGGTACTCATCTACAGGTGGCAACCTTACAAACCCGTCCTC
DB	1804 GGCCCTGAGTGGATGGGGTACTCATCTACAGGTGGCAACCTTACAAACCCGTCCTC
QY	184 AAGAGTCAGTTACCATGTCAGTAGACACGTCCTAAGAACCACTTCCCTGAGGCTGAGC
DB	1744 AAGAGTCAGTTACCATGTCAGTAGACACGTCCTAAGAACCACTTCCCTGAGGCTGAGC
QY	244 TCTGTGATGCCCGCGGACACGGCCGTGTATTACTGTGCGAGGTGATGGTCACTTTG
DB	1684 TCTGTGATGCCCGCGGACACGGCCGTGTATTATTGTGCGAGGATGAACCTGGGATCGCG
QY	304 GACAACTGGGGCCAGGGAAACCTGTGTACCCGTCCTCA 342
DB	1624 GACTACTGGGGCCAGGGAAACCTGTGTACCCGTCCTCA 1586
RESULT 11	
AD584453	
ID	AD584453 standard; DNA; 1996 BP.
AC	
AC	AD584453;
DT	18-NOV-2004 (first entry)
XX	
DE	Human anti-EPO-R antibody Ab412 heavy chain DNA SEQ ID NO:92.
XX	
KW	human; erythropoietin receptor; EPO receptor;
KW	erythropoietin receptor binding antibody; EPO receptor binding antibody;
KW	antianaemic; neuroprotective; vulnary; gene therapy; aplasia; anaemia;
KW	wound healing; neural cell damage protection;
KW	neural tissue damage protection; brain injury; spinal cord injury;
KW	stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;
ds.	
XX	
OS	Homo sapiens.
XX	
FN	WO2004035603-A2.
XX	
PD	29-APR-2004.
XX	
PF	14-OCT-2003; 2003WO-US032243.
XX	
PR	14-OCT-2002; 2002US-00269711.
PR	10-OCT-2003; 2003US-00684109.

(ABBO) ABBOTT LAB.

Devries PJ, Green IL, Ostrow DH, Reilly EB, Wiewler J;
WPI: 2004-348433/32.
P-PSDBJ, ADS844455.

New antibodies that bind to or activate an endogenous human erythropoietin receptor, useful for diagnosing, preventing or treating disorders associated with dysfunctional erythropoietin receptor, e.g. anemia.

Disclosure; SEQ ID NO 92; 192pp; English.

The present invention describes an antibody or its fragment that binds to or activates an endogenous activity of a human erythropoietin (EPO) receptor in a mammal, but does not interact with a peptide having a sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1) methods of modulating or activating an endogenous activity of a human EPO receptor in a mammal, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (2) a method of treating a mammal suffering from aplasia, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (3) a pharmaceutical composition comprising a therapeutic amount of the above antibody or antibody fragment, and a pharmaceutical excipient; (4) an isolated and purified polynucleotide sequence, and their fragments, complements and degenerate codon equivalents; and (5) an isolated and purified amino acid sequence, and their fragments. The EPO receptor binding antibody has antianaemic, neuroprotective and vulnerrary activities, and can be used in gene therapy. The compositions and methods from the present invention can be used for modulating an endogenous activity of a human EPO receptor or for treating mammals suffering from aplasia or anaemia. They may also be used for identifying mammals having a dysfunctional EPO receptor. The composition may also be used in promoting wound healing or in protecting against neural cell and/or tissue damage resulting from brain/spinal cord injury, stroke and the like. The present sequence encodes a human anti-EPO-R antibody heavy chain, which is given in the exemplification of the present invention.

Sequence 1996 BP, 422 A, 686 C, 537 G, 351 T, 0 U, 0 Other;

Query Match 80.9%; Score 276.6; DB 13; Length 1996;
Best Local Similarity 88.5%; Pred. No. 8.6e-68;
Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0

4 GAGTGTGGCCCAAGACTGTGTGAAGCTTTCACAGACCCGTGTCTCCTCACTGCAGTGTCT 63
|||
73 GAGTGGGGCCCAAGACTGTGTGAAGCTTTCACAGACCCGTGTCTCCTCACTGCAGTGTCT 132
|||
64 GGTGGCTCATCCCGAGTGGTGTATATATACGTGGATTGGATTCGCGACACCCAGGAG 123
133 GGTGGCTCATCCCGAGTGGTGTATATATACGTGGATTGGATTCGCGACACCCAGGAG 192
124 GGCCGTGAGTGGATGGGTATCATCTATACAGAGTGGCAACACTCAACAAACCCGTCCCTC 183
193 GGCCGTGAGTGGATGGGTATCATCTATACAGAGTGGCAACACTCTACTAACAACCCGTCCCTC 252
184 AAGAGTCAGTTACCATGTGTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
253 AAGAGTCAGTTACCATGTGTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 312
244 TCTGTGATCGCCCGGAGACAGGCGGTGTATTAATCTGTGGAGGTCAAGATGGGTACCTTTG 303
313 TCTGTGATCGCCCGGAGACAGGCGGTGTATTAATCTGTGGAGGTCAAGATGGGTACCTTTG 372
304 GACAACTGGGGCAAGGAACCTGGTGCACCGTCTCTCA 342
373 GACTACTGGGGCAAGGAACCTGGTGCACCGTCTCTCA 411

RESULT 12

ADR68595
ID ADR68595 standard; DNA; 1996 BP.
AC ADR68595;
XX
DT 02-DEC-2004 (first entry)
XX
XX Human antibody Ab412 heavy chain polynucleotide seqid 92.
DE
XX
XX antihaemic; respiratory; vulnery; gene therapy; vaccine;
KM erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
KM hypoxemia; chronic tissue hypoxia; blood circulation; blood flow;
KM wound healing; neural cell damage; tissue damage; brain injury;
KM spinal cord injury; stroke; human; anti-EPO-R-antibody; heavy chain;
KM Ab412; ds.
XX
OS Homo sapiens.
XX
XX US2004175379-A1.
XX
XX 09-SEP-2004.
XX
XX 10-OCT-2003; 2003US-00684109.
XX
XX 14-OCT-2002; 2002US-0418031P.
XX
XX (DEVIR/) DEVRIES P J.
PA (OSTR/) OSTROW D H.
PA (REIL/) REILLY E B.
PA (GREE/) GREEN L L.
PA (WIEL/) WIELER J.
XX
PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;
XX
XX WPI; 2004-661369/64.
DR P-PSDB; ADR68597, ADR68576, ADR68577.
XX
XX New antibody or its antibody fragment that activates an endogenous
PT activity or is capable of binding to a human erythropoietin receptor in a
PT mammal, useful for treating a mammal suffering aplasia or anemia.
PT
XX
XX Disclosure; SEQ ID NO 92; 156pp; English.
XX
XX The invention describes an antibody or its fragment that activates an
CC endogenous activity or capable of binding to a human erythropoietin
CC receptor in a mammal, or that comprises at least one heavy or light chain
CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
CC ID NO: 3 or 5) given in the specification or its fragment, but does not
CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
CC given in the specification. Also described are: a method of activating or
CC modulating an endogenous activity of a human erythropoietin receptor in a
CC mammal; a pharmaceutical composition comprising a therapeutic amount of
CC an antibody or antibody fragment above and a pharmaceutical excipient; an
CC isolated and purified polynucleotide sequence selected from 28 sequences
CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
CC the specification, and their fragments, complements, and degenerate codon
CC equivalents; and an isolated and purified amino acid sequence selected
CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
CC their fragments. The antibody or its antibody fragment that activates or
CC modulates the activity of the receptor is useful in a method of treating
CC a mammal suffering aplasia or anaemia. The antibodies are also useful for
CC treating disorders characterised by decreased or subnormal levels of
CC oxygen in the blood or tissue such as hypoxemia or chronic tissue
CC hypoxia and/or diseases characterised by inadequate blood circulation or
CC reduced blood flow. They are also useful for promoting wound healing or
CC for protecting against neural cell and/or tissue damage, resulting from
CC brain/spinal cord injury, stroke and the like. The antibodies are also
CC useful for identifying or diagnosing mammals having dysfunctional
CC erythropoietin receptor. This sequence represents a human Ab412 antibody
CC heavy chain polynucleotide.
XX
XX Sequence 1996 BP; 422 A; 686 C; 537 G; 351 T; 0 U; 0 Other;
XX
XX

Query Match 80.9%; Score 276.6; DB 13; Length 1996;
Best Local Similarity 88.5%; Pred. No. 8.66-68;
Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
OY 4 GAGTCTGGCCCAAGAGCTGTGTAAGCCCTTCACAGACCTGTCTCCCTGACCTGACTGTCTCT 63
DB 73 GAGTCTGGCCCAAGAGCTGTGTAAGCCCTTCACAGACCTGTCTCCCTGACCTGACTGTCTCT 132
OY 64 GGTGCTCCATCCGACGAGTGTGTTATTACTGTGAGTTGATGCCGACGCTCCAGGGAG 123
DB 133 GGTGCTCCATCCGACGAGTGTGTTATTACTGTGAGTTGATGCCGACGCTCCAGGGAG 192
OY 124 GGCCTGAGTGTGATCGGCTATCATCAAGTGGCAACCTTCAACCAACCCGCTCC 183
DB 193 GGCCTGAGTGTGATCGGCTATCATCAAGTGGCAACCTTCAACCAACCCGCTCC 252
OY 184 AAGAGTGGAGTTTACATGTCAGTACACGCTTAAAGAACCTTCTCCCTGAGGCTGAGC 243
DB 253 AAGAGTGGAGTTTACATGTCAGTACACGCTTAAAGAACCTTCTCCCTGAGGCTGAGC 312
OY 244 TCTGTGACTGCGGCGGACACGCGCTGTATTACTGTGAGAGTACAGATGGTACCTTG 303
DB 313 TCTGTGACTGCGGCGGACACGCGCTGTATTACTGTGAGAGTAACTGGGATCGCG 372
OY 304 GACAACCTGGGCGGAGGAGACCTGTGACCGTCTCCTCA 342
DB 373 GACTTCTGGGCGGAGGAGACCTGTGACCGTCTCCTCA 411
RESULT 13
ADR68596/c
ID ADR68596 standard; DNA; 1996 BP.
XX
XX ADR68596;
XX
XX 02-DEC-2004 (first entry)
XX
XX Human antibody Ab412 heavy chain polynucleotide seqid 93.
XX
XX
XX antihaemic; respiratory; vulnery; gene therapy; vaccine;
KM erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
KM hypoxemia; chronic tissue hypoxia; blood circulation; blood flow;
KM wound healing; neural cell damage; tissue damage; brain injury;
KM spinal cord injury; stroke; human; anti-EPO-R-antibody; heavy chain;
KM Ab412; ds.
XX
XX Homo sapiens.
XX
XX US2004175379-A1.
XX
XX 09-SEP-2004.
XX
XX 10-OCT-2003; 2003US-00684109.
XX
XX 14-OCT-2002; 2002US-0418031P.
XX
XX (DEVIR/) DEVRIES P J.
PA (OSTR/) OSTROW D H.
PA (REIL/) REILLY E B.
PA (GREE/) GREEN L L.
PA (WIEL/) WIELER J.
XX
PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;
XX
XX WPI; 2004-661369/64.
XX
XX New antibody or its antibody fragment that activates an endogenous
PT activity or is capable of binding to a human erythropoietin receptor in a
PT mammal, useful for treating a mammal suffering aplasia or anemia.
PT
XX
XX Disclosure; SEQ ID NO 93; 156pp; English.
XX
XX

CC The invention describes an antibody or its fragment that activates an
 CC endogenous activity or capable of binding to a human erythropoietin
 CC receptor in a mammal, or that comprises at least one heavy or light chain
 CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
 CC given in the specification. Also described are: a method of activating or
 CC modulating an endogenous activity of a human erythropoietin receptor in a
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an
 CC isolated and purified polynucleotide sequence selected from 28 sequences
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
 CC the specification, and their fragments, complements, and degenerate codon
 CC equivalents; and an isolated and purified amino acid sequence selected
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
 CC their fragments. The antibody or its antibody fragment that activates or
 CC modulates the activity of the receptor is useful in a method of treating
 CC a mammal suffering aplasia or anaemia. The antibodies are also useful for
 CC treating disorders characterised by decreased or subnormal levels of
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue
 CC hypoxia and/or diseases characterised by inadequate blood circulation or
 CC reduced blood flow. They are also useful for promoting wound healing or
 CC for protecting against neural cell and/or tissue damage, resulting from
 CC brain/spinal cord injury, stroke and the like. The antibodies are also
 CC useful for identifying or diagnosing mammals having dysfunctional
 CC erythropoietin receptor. This sequence represents a human Ab412 antibody
 CC heavy chain polynucleotide.

XX Sequence 1996 BP, 351 A; 537 C; 686 G; 422 T; 0 U; 0 Other;

Query Match 80.9%; Score 276.6; DB 13; Length 1996;

Best Local Similarity 88.5%; Pred. No. 8.6e-68;

Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 4 GAGCTGAGCCAGGACTGGTGAACCTTACAGACCCGTGCTCCACCTGACGCTGCTCT 63
 DB 1924 GAGTCGGAGCCAGGACTGGTGAACCTTACAGACCCGTGCTCCACCTGACGCTGCTCT 1865
 QY 64 GGTGGCTCCATCCGACGTGTGTATTACTGAGATTGATCCGCCAGCGTCCAGGGAG 123
 DB 1864 GGTGCTCCATCCAGGAGTGTGTATTACTGAGATTGATCCGCCAGCGTCCAGGGAG 1805
 QY 124 GGCTTGAGTGAATCGGATGATCTATATCAGTGGCAACACTTAACAACCCGTCCCTC 183
 DB 1804 GGCTTGAGTGAATGATGATGATCTATATCAGTGGCAACACTTAACAACCCGTCCCTC 1745
 QY 184 AAGAGTGAGTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243
 DB 1744 AAGAGTGAGTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1685
 QY 244 TCTGTGACTGCGCGGACACGCGCGTATTAATCTGTGCGAGGTGAGATGGGTACACTTGG 303
 DB 1684 TCTGTGACTGCGCGGACACGCGCGTATTAATCTGTGCGAGGTGAGATGGGTACACTTGG 1625
 QY 304 GACAACTGGGGCCAGGGAACCTTGATGATGATGATGATGATGATGATGATGATGATGATG 342
 DB 1624 GACTACTGGGGCCAGGGAACCTTGATGATGATGATGATGATGATGATGATGATGATGATG 1586

RESULT 14

ADJ32125 standard; DNA; 663 BP.

ADJ32125;

22-APR-2004 (first entry)

Human interferon-gamma antibody heavy chain gene SeqID79.

XX antibody; antigen binding domain; interferon-gamma; INF-gamma;
 KM antagonist antibody; anti-inflammatory; immunosuppressive;
 KW autoimmune disease; inflammatory condition; human; gene; ds; heavy chain.

XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH CDS 8..663
 FT /*tag= a
 FT /product= "Human interferon-gamma antibody heavy chain"
 FT /partial
 FT /note= "No start or stop codon"

US2003099647-A1.

29-MAY-2003.

05-OCT-2001; 2001US-00972656.

05-OCT-2001; 2001US-00972656.

(DESH/) DESHPANDE R V.

(TSAI/) TSAI M.

Deehpande RV, Tsai M;

WPI: 2003-696068/66.

P-PSDB; ADJ32126.

PT New antibody or antigen binding domain, or its fragment, variant or
 PT derivative, which binds to an interferon-gamma protein, useful for
 PT preparing a composition for preventing or treating inflammatory or
 PT autoimmune disorders.

XX Example 3; SEQ ID NO 79; 113bp; English.

CC This invention relates to a novel antibody or antigen binding domain, or
 CC its fragment, variant or derivative, which binds to an interferon-gamma
 CC (INF-gamma) protein, and is an antagonist antibody. The invention may be
 CC useful for the development of compounds with an anti-inflammatory or
 CC immunosuppressive activity through action as interferon-gamma agonists. A
 CC composition containing the antibody is useful for preventing or treating
 CC an autoimmune disease and an inflammatory condition. The present sequence
 CC is that of a gene which encodes an antibody heavy chain of a human INF-
 CC gamma antibody which may be part of the invention.

XX Sequence 663 BP, 133 A; 216 C; 188 G; 126 T; 0 U; 0 Other;

Query Match 80.6%; Score 275.8; DB 10; Length 663;

Best Local Similarity 89.0%; Pred. No. 1.1e-67;

Matches 298; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 4 GAGCTGGCCAGGACTGGTGAACCTTACAGACCCGTGCTCCACCTGACGCTGCTCT 63
 DB 16 GAGTCGGAGCCAGGACTGGTGAACCTTACAGACCCGTGCTCCACCTGACGCTGCTCT 75
 QY 64 GGTGGCTCCATCCGACGTGTGTATTACTGAGATTGATCCGCCAGCGTCCAGGGAG 123
 DB 76 GGTGCTCCATCCAGGAGTGTGTATTACTGAGATTGATCCGCCAGCGTCCAGGGAG 135
 QY 124 GGCTTGAGTGAATCGGATGATCTATATCAGTGGCAACACTTAACAACCCGTCCCTC 183
 DB 136 GGCTTGAGTGAATGATGATGATCTATATCAGTGGCAACACTTAACAACCCGTCCCTC 195
 QY 184 AAGAGTGAGTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243
 DB 196 AAGAGTGAGTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 255
 QY 244 TCTGTGACTGCGCGGACACGCGCGTATTAATCTGTGCGAGGTGAGATGGGTACACTTGG 303
 DB 256 TCTGTGACTGCGCGGACACGCGCGTATTAATCTGTGCGAGGTGAGATGGGTACACTTGG 315
 QY 304 GACAACTGGGGCCAGGGAACCTTGATGATGATGATGATGATGATGATGATGATGATGATG 338
 DB 316 GACTACTGGGGCCAGGGAACCTTGATGATGATGATGATGATGATGATGATGATGATGATG 350

RESULT 15

ADCC97778 ID ADC99778 standard; DNA; 352 BP.

AC ADC99778;

DT 01-JAN-2004 (first entry)

DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 7.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
 XX cytosolic; melanoma; oesophageal; pancreatic; colorectal tumour;
 KM cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
 KM lung cancer; human; ds; gene.
 XX Homo sapiens.

XX MO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudus J;

XX WPI; 2003-587113/55.

XX P-PSDB; ADC99776.

PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease
 PT or condition associated with expression of MUC18 in a patient, e.g.
 PT tumors, cancers, and other malignancies.

PS Claim 8; SEQ ID NO 7; 78bp; English.

CC The invention relates to a novel isolated monoclonal antibody comprising
 CC a heavy or light chain amino acid or a heavy or light chain variable
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the
 CC invention demonstrates cytostatic activity and may be useful for treating
 CC a disease or condition associated with the expression of MUC18 on the
 CC cell surface such as tumours, specifically melanoma, oesophageal,
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical
 CC carcinomas and cervical intraepithelial neoplasia and cancers including
 CC colorectal, breast or lung cancer, as well as other malignancies. The
 CC current sequence is that of the anti-human MUC18 monoclonal antibody
 CC heavy chain variable domain DNA of the invention.

XX Sequence 352 BP; 76 A; 102 C; 103 G; 71 T; 0 U; 0 Other;

Query Match 80.4%; Score 275; DB 10; Length 352;

Best Local Similarity 90.3%; Pred. No. 1.6e-67;

Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTGTGCCCCAGAGCTGGTGAAGCTTCAACAGACCTGTGCTCACTGCACTGTCT 63
 DB 16 GAGTGGGCCCCAGAGCTGGTGAAGCTTCAACAGACCTGTGCTCACTGCACTGTCT 75
 QY 64 GGTGCTCCATCCGAGAGGTGTGTTATTAACGAGATTGGATCCGACAGCCGAGGAG 123
 DB 76 GGTGCTCCATCCGAGAGGTGTGTTATTAACGAGATTGGATCCGACAGCCGAGGAG 135
 QY 124 GGCCTGAGTGGATCGGTATCATCTATCAACAGTGGCAACCTTACAAACCCGTCCTC 183
 DB 136 GGCCTGAGTGGATCGGTATCATCTATTAACAGTGGGAGACCTTACAAACCCGTCCTC 195
 QY 184 AAGAGTCCAGTTACATGTCATGATAGACAGAGTGAAGAACCACTTCTCCCTGAGGCTGAGC 243
 DB 196 AAGAGTCCAGTTACATGTCATGATAGACAGAGTGAAGAACCACTTCTCCCTGAGGCTGAGC 255

QY 244 TCTGTGACTGCGCGGACACAGCGCGGTATTAACGAGAGTGAAGTGGTACACTTG 303
 DB 256 TCTGTGACTGCGCGGACACAGCGCGGTATTAACGAGAGTGGTACACTTG 312
 QY 304 GACAACTGGGAGCCAGGGAACCTGTGTCACCGTCTCTCA 342
 DB 313 AAGTACTGGGAGCCAGGGAACCTGTGTCACCGTCTCTCA 351

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 Job time : 322.618 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 09:08:49 ; Search time 512.827 Seconds
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4312.305 Million cell updates/sec

Title: US-10-027-725a-3
Perfect score: 342
Sequence: 1 ctcgagctgcagccagcact.....ccctgcacgcctcctca 342

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 7277826 seqs, 323339505 residues

Total number of hits satisfying chosen parameters: 14555652

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	324.4	99.9	342	14	US-10-027-725a-2
3	310	96.6	342	14	US-10-027-725a-1
4	284.6	83.2	352	15	US-10-330-613-15
5	284.6	83.2	352	16	US-10-330-530-15
6	284.6	83.2	352	19	US-10-660-357-15
7	276.6	80.9	354	19	US-10-684-109-42

8	276.6	80.9	1996	19	US-10-684-109-92	Sequence 92, Appl
9	276.6	80.9	1996	19	US-10-684-109-93	Sequence 99, Appl
10	275.8	80.6	663	10	US-09-972-656-79	Sequence 7, Appl
11	275	80.4	352	15	US-10-330-613-7	Sequence 7, Appl
12	275	80.4	352	15	US-10-330-530-7	Sequence 7, Appl
13	275	80.4	352	19	US-10-660-357-7	Sequence 7, Appl
14	274.2	80.2	360	21	US-10-644-777-93	Sequence 99, Appl
15	272.2	79.6	366	22	US-10-984-960A-19	Sequence 99, Appl
16	271.8	79.5	355	19	US-10-684-109-54	Sequence 54, Appl
17	271.8	79.5	1996	19	US-10-684-109-110	Sequence 110, Appl
18	271.8	79.5	1996	19	US-10-684-109-111	Sequence 111, Appl
19	271.2	79.3	420	21	US-10-893-576-18	Sequence 18, Appl
20	270.8	79.2	370	17	US-10-309-762-186	Sequence 186, Appl
21	270	78.9	1338	21	US-10-644-277-61	Sequence 61, Appl
22	268.4	78.5	358	15	US-10-330-613-27	Sequence 27, Appl
23	268.4	78.5	358	16	US-10-330-530-27	Sequence 27, Appl
24	268.4	78.5	358	19	US-10-660-357-110	Sequence 110, Appl
25	267.8	78.3	429	17	US-10-309-762-110	Sequence 110, Appl
26	267.6	78.2	370	17	US-10-309-762-189	Sequence 189, Appl
27	267.2	78.1	516	20	US-10-612-497-33	Sequence 33, Appl
28	267.2	78.1	361	17	US-10-776-649-33	Sequence 33, Appl
29	267	78.1	361	17	US-10-309-762-191	Sequence 191, Appl
30	265.8	77.7	366	22	US-10-984-960A-55	Sequence 55, Appl
31	265	77.5	370	17	US-10-309-762-185	Sequence 185, Appl
32	264.2	77.3	367	17	US-10-309-762-195	Sequence 195, Appl
33	263.8	76.8	1392	21	US-10-910-901-9	Sequence 9, Appl
34	263.8	76.8	352	15	US-10-330-613-35	Sequence 35, Appl
35	263.8	76.8	352	16	US-10-330-530-35	Sequence 35, Appl
36	262.8	76.8	352	19	US-10-660-357-35	Sequence 35, Appl
37	261.6	76.5	376	17	US-10-309-762-184	Sequence 184, Appl
38	261.6	76.5	376	17	US-10-309-762-197	Sequence 197, Appl
39	261.6	76.5	376	17	US-10-309-762-199	Sequence 199, Appl
40	261.2	76.4	370	17	US-10-309-762-200	Sequence 200, Appl
41	260.6	76.2	352	17	US-10-309-762-203	Sequence 203, Appl
42	260	76.0	376	17	US-10-309-762-187	Sequence 187, Appl
43	259.6	75.9	519	17	US-10-309-762-174	Sequence 174, Appl
44	258.6	75.6	382	17	US-10-309-762-194	Sequence 194, Appl
45	258.6	75.6	1443	21	US-10-910-901-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-10-027-725a-3
Sequence 3, Application US/10027725A
Publication No. US20030082639A1
GENERAL INFORMATION:
APPLICANT: Flicker, Sabine
TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
FILE REFERENCE: 25401-4
CURRENT APPLICATION NUMBER: US/10/027,725A
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/259,436
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 342
TYPE: DNA
ORGANISM: Homo sapiens
US-10-027-725a-3

Query Match	100.0%	Score 342	DB 14	Length 342
Best Local Similarity	100.0%	Pred. No. 1.4e-101	Indels 0	Gaps 0
Matches 342	Conservative 0	Mismatches 0		
QY	1	CTCGAGTGTGCGCAGACCTGTAAGCTTCACAGACCTGTCCTGACCTGACCTGTC	60	
DB	1	CTCGAGTGTGCGCAGACCTGTAAGCTTCACAGACCTGTCCTGACCTGACCTGTC	60	
QY	61	TCGTGTCCTGTCATCCGACGAGTGTGTTATTAATGAGATTGATCCGACGTCGACGG	120	

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Db      61  TCTGTCGCTCCATCCGAGTGTGTTATTACTGAGTTGGATCCGCCAGCTCCAGGG 120
Qy      121  AAGGCGCTGAGTGAGTGGGTATCATCTATACAGATGGCAACACTACAAACCCGCTC 180
Db      121  AAGGCGCTGAGTGAGTGGGTATCATCTATACAGATGGCAACACTACAAACCCGCTC 180
Qy      181  CTCAAGAGTGCAGTTACATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTG 240
Db      181  CTCAAGAGTGCAGTTACATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTG 240
Qy      241  AGCTCTGAGTGCAGGAGACAGCGCGGTATTACTGTGAGAGGTGAGATGGGTACACT 300
Db      241  AGCTCTGAGTGCAGGAGACAGCGCGGTATTACTGTGAGAGGTGAGATGGGTACACT 300
Qy      301  TTGGACAACCTGGGGCCAGGGAACCTGTGTCAACCGTCTCTCA 342
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RESULT 2
US-10-027-725a-2
; Sequence 2, Application US/10027725a
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725a
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259, 436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725a-2

Query Match      94.9%; Score 324.4; DB 14; Length 342;
Best Local Similarity 96.8%; Pred. No. 8.3e-96;
Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy      1  CTCGAGTCTGGCCCAAGACTGTGTAAGCTTTCACAGACCTGTGCTCCATCCTGCATGTC 60
Db      1  CTCGAGTCTGGCCCAAGACTGTGTAAGCTTTCACAGACCTGTGCTCCATCCTGCATGTC 60
Qy      61  TCTGTCGCTCCATCCGAGTGTGTTATTACTGAGTTGGATCCGCCAGCTCCAGGG 120
Db      61  TCTGTCGCTCCATCCGAGTGTGTTATTACTGAGTTGGATCCGCCAGCTCCAGGG 120
Qy      121  AAGGCGCTGAGTGAGTGGGTATCATCTATACAGATGGCAACACTACAAACCCGCTC 180
Db      121  AAGGCGCTGAGTGAGTGGGTATCATCTATACAGATGGCAACACTACAAACCCGCTC 180
Qy      181  CTCAAGAGTGCAGTTACATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTG 240
Db      181  CTCAAGAGTGCAGTTACATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTG 240
Qy      241  AGCTCTGAGTGCAGGAGACAGCGCGGTATTACTGTGAGAGGTGAGATGGGTACACT 300
Db      241  AGCTCTGAGTGCAGGAGACAGCGCGGTATTACTGTGAGAGGTGAGATGGGTACACT 300
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Db      301  TTGGACAACCTGGGGCCAGGGAACCTGTGTCAACCGTCTCTCA 342

RESULT 3
US-10-027-725a-1
; Sequence 1, Application US/10027725a
; Publication No. US20030082659A1
; GENERAL INFORMATION:
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; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725a
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259, 436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725a-1

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Matches 322; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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Qy      61  TCTGTCGCTCCATCCGAGTGTGTTATTACTGAGTTGGATCCGCCAGGCTCCAGGG 120
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Qy      181  CTCAAGAGTGCAGTTACATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTG 240
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Qy      241  AGCTCTGAGTGCAGGAGACAGCGCGGTATTACTGTGAGAGGTGAGATGGGTACACT 300
Db      241  AGCTCTGAGTGCAGGAGACAGCGCGGTATTACTGTGAGAGGTGAGATGGGTACACT 300
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Db      301  TTGGACAACCTGGGGCCAGGGAACCTGTGTCAACCGTCTCTCA 342

RESULT 4
US-10-330-613-15
; Sequence 15, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Guéas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330, 613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-15

Query Match      83.2%; Score 284.6; DB 15; Length 352;
Best Local Similarity 92.0%; Pred. No. 8.9e-83;
Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

Qy      4  GAGTCTGGCCCAAGACTGTGTAAGCTTTCACAGACCTGTGCTCCATCCTGCATGTCCT 63
Db      16  GAGTCTGGCCCAAGACTGTGTAAGCTTTCACAGACCTGTGCTCCATCCTGCATGTCCT 75
Qy      64  GGTGCTTCATCCGAGTGTGTTATTACTGAGTTGGATCCGCCAGGCTCCAGGGAAG 123
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D _b	76	GATGGCTCCATTACGACAGTGGTGTTAACTACTGGA	CTTGGATCCCGCAGCACCCAGGAAAG	135
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D _b	136	GGCCTGGAGTAGATGGGTTCACTATAATACAGGGAGCA	CCCTACTACAAACCCGTCCCTC	195
O _y	184	AAGAAGTCAGTTAACCATGTCAGTAGACACGTC	TAAAGACCATCTTCCTCTGAGCTTGAGC	243
D _b	196	AAGAGTCAAGTTAACCATATCACTATGACAGGT	CTAAGAAACAAGTTCTCCCTGAAGCTGAGC	255
O _y	244	TCTGTGACTGCAGCGGACACGGCCCGTATTTA	CTGTGCAGAGTCAAGATGGGTACATTTTG	303
D _b	256	TCTGTGACTGCAGCGGACACGGCCCGTATTTA	CTGTGCAG--ACAGGAGATGGCTTT	312
O _y	304	GACAACCTGGGCGCAGGAAACCTTGGACACCGTCTCTCA		342
D _b	313	GACTAATGGGCGCAGGAAACCTTGGACACCGTCTCTCA		351

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US-10-330-530-15
; Sequence 15, Application US/10330530
; Publication No. US2003015251A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: AGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIORITY APPLICATION NUMBER: US 60/346414
; PRIORITY FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-530-15

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Query Match	83.2%;	Score 284.6;	DB 16;	Length 352;
Best Local Similarity	92.0%;	Pred. No. 8.9e-83;		
Matches 312;	Conservative 0;	Mismatches 24;	Indels 3;	Gaps 1;

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QY	64	GATGGCTCCATCCGACGATGATGATTTATCTGAGATTTGATATCCGACGCTCCAGGGAG	123
Db	76	GATGGCTCCATCAGACGATGATGATTTCTATCGACATTTGATATCCGACGACCCAGGGAG	135
QY	124	GAGCTGAGATGATGGGGTACATCTATCAACGAGGACAAACCTAACAAACCCGCTCTC	183
Db	136	GAGCTGAGATGATGGGGTTCATCTATTACAGTGGGAGCACTTACATCAACCCGCTCTC	195
QY	184	AAGAGTCGATTCACCATGTCACTAGACACAGCTCTAAGAACCATCTTCTCCCTGAGGCTGAGC	243
Db	196	AAGAGTCGATTCACCATATCAGTAGACAGCTCAAAACACAGTCTCTCCCTGAAGCTGAGC	255
QY	244	TCTGTGACGACCGCGGACACGGCCGATTTATATGAGCGAGGTCAATGGGTCACTTTG	303
Db	256	TCTGTGACGACCGCGGACACGGCCGATTTATATGATCTGATCGAG--AGAGGAGATGGCTTT	312
QY	304	GACAACTGGGGCCAGGGAAACCTGTGATCCGCTCTCTCA	342
Db	313	GACTACTGGGGCCAGGGAAACCTGTGATCCGCTCTCTCA	351

RESULT 6
US-10-660-357-15
; Sequence 15, Application US/10660357
; Publication No. US20040115205A1

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: GENERAL INFORMATION:
: APPLICANT: Bar-Eli, Menashe
: APPLICANT: Green, Larry B.
: TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
: TITLE OF INVENTION: ANTIGEN
: FILE REFERENCE: AGENIX. 030C1
: CURRENT APPLICATION NUMBER: US/10/660,357
: CURRENT FILING DATE: 2003-09-10
: PRIOR APPLICATION NUMBER: 10/330,580
: PRIOR FILING DATE: 2002-12-26
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 15
: LENGTH: 352
: TYPE: DNA
: ORGANISM: Homo Sapiens
US-10-660-357-15

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Query Match	93.24%	Score 284.6	DB 19	Length 352
Best Local Similarity	82.04%	Pred. No. 8.9e-83		
Matches 312	Conservative	0	Mismatches 24	Indels 3
				Gaps 11
QY	4	GAGTCTGGCCCGAGCACTGGTGAAGCCCTTTCACAGACCCCTGCTCCTCACTGCTCTCT	63	
DB	16	GAGTCTGGGCCCGAGCACTGGTGAAGCCCTTTCACAGACCCCTGCTCCTCACTGCTCTCT	75	
QY	64	GGTGGCTTCATCCGCACTGGTGGTTATTACTTGGAGTTGGATTCGGCAAGCTTCACGGGAAG	123	
DB	76	GGTGGCTTCATCAACAGAGTGGTTACTTACCTGGACTTGGATTCGGCAACCCACGGGAAG	135	
QY	124	GGCCGTGAGTGGAGTCCGGTACATCTATACAGTGGCAACACCTTCAACACCCGTCCTC	183	
DB	136	GGCCGTGAGTGGATTTGGTTTCATCTATTACAGTGGCAACCTTCAACACCCGTCCTC	195	
QY	184	AAGAGTCAGATTACCATGTCAGTAGACACGTCTAAGAACCTTCTCCCTGAGGCTGAGC	243	
DB	196	AAGAGTCAGATTACCATATCAGTAGACACGTCTAAGAACCAAGTCTCCTGAGGCTGAGC	255	
QY	244	TCTGTGACTGCCGGGAGACACGGCCGTGTATTACTGTGGAGAGTCAGATGGGTACACTTTG	303	
DB	256	TCTGTGACTGCCGGGAGACACGGCCGTGTATTACTGTGGAGGAGGAGGAGGAGGAGGAGG	312	
QY	304	GACAACTGGGGGCGAGGAACCTGTGTCAACCGTCTCCCTCA	342	
DB	313	GACTACTGGGGGCGAGGAACCTGTGTCAACCGTCTCCCTCA	351	

```

RESULT 7
US-10-684-109-42
; Sequence 42, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devities, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Rellly, Edward B.
; APPLICANT: Waieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989, US, 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/259,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-684-109-42

```

Query Match	80.9%;	Score 276.6;	DB 19;	Length 354;
-------------	--------	--------------	--------	-------------

Best Local Similarity 88.5%; Pred. No. 3.7e-80;
Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

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QY 4 GAGTCTGGCCAGAGACTGTGTAAGCCCTTCAACAGCCCTGTCTCTCACTGACCTGTCTCT 63
Db 16 GAGTCGGGCCAGAGACTGTGTAAGCCCTTCAACAGCCCTGTCTCTCACTGACCTGTCTCT 75
QY 64 GGTGGCTCCATCCGCACTGGTGTATTACTGAGATTGAGTCCGCCAGCTCCAGGGAG 123
Db 76 GGTGGCTCCATCCGCACTGGTGTATTACTGAGATTGAGTCCGCCAGCTCCAGGGAG 135
QY 124 GGCTTGAGAGAGATCGGGTACATCTATCAAGTGGCAACCTTCAACACCCGCTCCCTC 183
Db 136 GGCTTGAGAGAGATCGGGTACATCTATCAAGTGGCAACCTTCAACACCCGCTCCCTC 195
QY 184 AAGAGTCGAGTTACCATGTGATGAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAGTTACCATGTGATGAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGGCCGTGTATTACTGTGCGAGGTCAATGGGTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGGCCGTGTATTACTGTGCGAGATTAACCTGGGATCGCG 315
QY 304 GACAACTGGGGCCAGGGAAACCTGTGTCACCGTCTCTCTCA 342
Db 316 GACTACTGGGGCCAGGGAAACCTGTGTCACCGTCTCTCTCA 354
```

RESULT 8

```
US-10-684-109-92
; Sequence 92; Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wielef, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989, US. 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-684-109-92
```

Query Match 80.9%; Score 276.6; DB 19; Length 1996;

Best Local Similarity 88.5%; Pred. No. 5.5e-80;
Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

```
QY 4 GAGTCTGGCCAGAGACTGTGTAAGCCCTTCAACAGCCCTGTCTCTCACTGACCTGTCTCT 63
Db 73 GAGTCGGGCCAGAGACTGTGTAAGCCCTTCAACAGCCCTGTCTCTCACTGACCTGTCTCT 132
QY 64 GGTGGCTCCATCCGCACTGGTGTATTACTGAGATTGAGTCCGCCAGCTCCAGGGAG 123
Db 133 GGTGGCTCCATCCGCACTGGTGTATTACTGAGATTGAGTCCGCCAGCTCCAGGGAG 192
QY 124 GGCTTGAGAGAGATCGGGTACATCTATCAAGTGGCAACCTTCAACACCCGCTCCCTC 183
Db 193 GGCTTGAGAGAGATCGGGTACATCTATCAAGTGGCAACCTTCAACACCCGCTCCCTC 252
QY 184 AAGAGTCGAGTTACCATGTGATGAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 253 AAGAGTCGAGTTACCATGTGATGAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 312
```

```
QY 244 TCTGTGACTGCGCGGACACAGCCCGTGTATTACTGTGCGAGGTCAATGGGTACACTTTG 303
Db 313 TCTGTGACTGCGCGGACACAGCCCGTGTATTACTGTGCGAGATTAACCTGGGATCGCG 372
QY 304 GACAACTGGGGCCAGGGAAACCTGTGTCACCGTCTCTCTCA 342
Db 373 GACTACTGGGGCCAGGGAAACCTGTGTCACCGTCTCTCTCA 411
```

RESULT 9

```
US-10-684-109-93/c
; Sequence 93; Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wielef, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989, US. 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-684-109-93
```

Query Match 80.9%; Score 276.6; DB 19; Length 1996;

Best Local Similarity 88.5%; Pred. No. 5.5e-80;
Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

```
QY 4 GAGTCTGGCCAGAGACTGTGTAAGCCCTTCAACAGCCCTGTCTCTCACTGACCTGTCTCT 63
Db 1924 GAGTCGGGCCAGAGACTGTGTAAGCCCTTCAACAGCCCTGTCTCTCACTGACCTGTCTCT 1865
QY 64 GGTGGCTCCATCCGCACTGGTGTATTACTGAGATTGAGTCCGCCAGCTCCAGGGAG 123
Db 1864 GGTGGCTCCATCCGCACTGGTGTATTACTGAGATTGAGTCCGCCAGCTCCAGGGAG 1805
QY 124 GGCTTGAGAGAGATCGGGTACATCTATCAAGTGGCAACCTTCAACACCCGCTCCCTC 183
Db 1804 GGCTTGAGAGAGATCGGGTACATCTATCAAGTGGCAACCTTCAACACCCGCTCCCTC 1745
QY 184 AAGAGTCGAGTTACCATGTGATGAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 1744 AAGAGTCGAGTTACCATGTGATGAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 1685
QY 244 TCTGTGACTGCGCGGACACAGCCCGTGTATTACTGTGCGAGGTCAATGGGTACACTTTG 303
Db 1684 TCTGTGACTGCGCGGACACAGCCCGTGTATTACTGTGCGAGATTAACCTGGGATCGCG 1625
QY 304 GACAACTGGGGCCAGGGAAACCTGTGTCACCGTCTCTCTCA 342
Db 1624 GACTACTGGGGCCAGGGAAACCTGTGTCACCGTCTCTCTCA 1586
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RESULT 10

```
US-09-972-656-79
; Sequence 79; Application US/09972656
; Publication No. US20030093647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Teal, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
```

CURRENT APPLICATION NUMBER: US/09/972,656
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn version 3.0
SEQ ID NO 79
LENGTH: 663
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(663)
US-09-972-656-79

Query Match 80.6%; Score 275.8; DB 10; Length 663;
Best Local Similarity 89.0%; Pred. No. 7.8e-80;
Matches 298; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCCGAGAGCTGTGAAGCTTTCACAGACCTTCTCCCTCACTGCACTGTCTCT 63
DB 16 GAGTCTGGCCCGAGAGCTGTGAAGCTTTCACAGACCTTCTCCCTCACTGCACTGTCTCT 75
QY 64 GGTGGCTCATCCGAGTGTGTGTTTACTGAGTTGATCCGCGACGTCAGGGAG 123
DB 76 GGTGGCTCATCCGAGTGTGTGTTTACTGAGTTGATCCGCGACGTCAGGGAG 135
QY 124 GGCCTGAGTGGATCGGTATCATCTATCAAGTGGCAACCTTACAAACCCGTCCTC 183
DB 136 GGCCTGAGTGGATCGGTATCATCTATCAAGTGGCAACCTTACAAACCCGTCCTC 195
QY 184 AAGAGTCGATTACCATCTAGTAGACACGCTTAAAGAACCTTCTCCCTGAGCTGAGC 243
DB 196 AAGAGTCGATTACCATCTAGTAGACACGCTTAAAGAACCTTCTCCCTGAGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATCTGTGAGAGTGCAGATGGGTACCTTGG 303
DB 256 TCTGTGACTGCGCGGACACGCGCTGTATCTGTGAGAGTGCAGATGGGTACCTTGG 315
QY 304 GACAACCTGGGGCCAGGAGAACCTTGTACACCGTCTC 338
DB 316 GACTACTGGGGCCAGGAGAACCTTGTACACCGTCTC 350

RESULT 11
US-10-330-613-7
Sequence 7, Application US/10330613
Publication No. US20030147809A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: AGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 352
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-330-613-7

Query Match 80.4%; Score 275; DB 15; Length 352;
Best Local Similarity 90.3%; Pred. No. 1.2e-79;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCGAGAGCTGTGAAGCTTTCACAGACCTTCTCCCTCACTGCACTGTCTCT 63
DB 16 GAGTCTGGCCCGAGAGCTGTGAAGCTTTCACAGACCTTCTCCCTCACTGCACTGTCTCT 75
QY 64 GGTGGCTCATCCGAGTGTGTGTTTACTGAGTTGATCCGCGACGTCAGGGAG 123
DB 76 GGTGGCTCATCCGAGTGTGTGTTTACTGAGTTGATCCGCGACGTCAGGGAG 135

QY 124 GGCCTGAGTGGATCGGTATCATCTATCAAGTGGCAACCTTACAAACCCGTCCTC 183
DB 136 GGCCTGAGTGGATCGGTATCATCTATCAAGTGGCAACCTTACAAACCCGTCCTC 195
QY 184 AAGAGTCGATTACCATCTAGTAGACACGCTTAAAGAACCTTCTCCCTGAGCTGAGC 243
DB 196 AAGAGTCGATTACCATCTAGTAGACACGCTTAAAGAACCTTCTCCCTGAGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATCTGTGAGAGTGCAGATGGGTACCTTGG 303
DB 256 TCTGTGACTGCGCGGACACGCGCTGTATCTGTGAGAGTGCAGATGGGTACCTTGG 312
QY 304 GACAACCTGGGGCCAGGAGAACCTTGTACACCGTCTCTCA 342
DB 313 AAGTACTGGGGCCAGGAGAACCTTGTACACCGTCTCTCA 351

RESULT 12
US-10-330-530-7
Sequence 7, Application US/10330530
Publication No. US20030152514A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
FILE REFERENCE: AGENIX.031A
CURRENT APPLICATION NUMBER: US/10/330,530
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: US 60/346414
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 352
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-330-530-7

Query Match 80.4%; Score 275; DB 16; Length 352;
Best Local Similarity 90.3%; Pred. No. 1.2e-79;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCGAGAGCTGTGAAGCTTTCACAGACCTTCTCCCTCACTGCACTGTCTCT 63
DB 16 GAGTCTGGCCCGAGAGCTGTGAAGCTTTCACAGACCTTCTCCCTCACTGCACTGTCTCT 75
QY 64 GGTGGCTCATCCGAGTGTGTGTTTACTGAGTTGATCCGCGACGTCAGGGAG 123
DB 76 GGTGGCTCATCCGAGTGTGTGTTTACTGAGTTGATCCGCGACGTCAGGGAG 135
QY 124 GGCCTGAGTGGATCGGTATCATCTATCAAGTGGCAACCTTACAAACCCGTCCTC 183
DB 136 GGCCTGAGTGGATCGGTATCATCTATCAAGTGGCAACCTTACAAACCCGTCCTC 195
QY 184 AAGAGTCGATTACCATCTAGTAGACACGCTTAAAGAACCTTCTCCCTGAGCTGAGC 243
DB 196 AAGAGTCGATTACCATCTAGTAGACACGCTTAAAGAACCTTCTCCCTGAGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATCTGTGAGAGTGCAGATGGGTACCTTGG 303
DB 256 TCTGTGACTGCGCGGACACGCGCTGTATCTGTGAGAGTGCAGATGGGTACCTTGG 312
QY 304 GACAACCTGGGGCCAGGAGAACCTTGTACACCGTCTCTCA 342
DB 313 AAGTACTGGGGCCAGGAGAACCTTGTACACCGTCTCTCA 351

RESULT 13
US-10-660-357-7
Sequence 7, Application US/10660357
Publication No. US20040115205A1
GENERAL INFORMATION:
APPLICANT: Bar-Eli, Menashe

```

; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX .030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-7

Query Match      80.4%; Score 275; DB 19; Length 352;
Best Local Similarity 90.3%; Pred. No. 1.2e-79;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGAGCCAGAGCTGTGAGACCTTTCACAGACCTGTCTCTACCTGACCTGTCTCT
DB 16 GAGTCGGGCCCCAGAGCTGTGAGACCTTTCACAGACCTGTCTCTCTCTCTCTCTCT
QY 64 GGTGGCTCCATCCGACAGTGTGTATTATTAATGAGTTGGATCCGCGACGCTCCAGGAG
DB 76 GGTGGCTCCATCCGACAGTGTGTATTATTAATGAGTTGGATCCGCGACGCTCCAGGAG
QY 124 GGCCTGAGTGTGATCGGTATCATCTATCATGAGCAACCTTCAACAAACCCGTCTCTC
DB 136 GGCCTGAGTGTGATCGGTATCATCTATCATGAGCAACCTTCAACAAACCCGTCTCTC
QY 184 AAGAGTGAAGTTACATGTCAGTAGACAGCTCTAAGAACCTTCTCTGAGGCTGAGC
DB 196 AAGAGTGAAGTTACATGTCAGTAGACAGCTCTAAGAACCTTCTCTGAGGCTGAGC
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTAATCTGTGAGAGTCAAGTGGTACACTT
DB 256 TCTGTGACTGCGCGGACACGCGCTGTATTAATCTGTGAGAGTCAAGTGGTACACTT
QY 304 GACAACTGGGGGCGAGGAGACCTGTGATCAACCTGTCTCTCA 342
DB 313 AAGTACTGGGGGCGAGGAGACCTGTGATCAACCTGTCTCTCA 351

RESULT 14
US-10-644-277-93
; Sequence 93, Application US/10644277
; Publication No. US2005058639A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean M.
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Foord, Oric
; APPLICANT: Liang, Meina L.
; APPLICANT: Ahluwalia, Kiran
; APPLICANT: Bhakta, Sunil
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
; TITLE OF INVENTION: CHEMO-ATTRACTANT PROTEIN-1 (MCP-1) AND USES THEREOF
; FILE REFERENCE: ABGENIX 091A
; CURRENT APPLICATION NUMBER: US/10/644,277
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 60/404,802
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homosapien
US-10-644-277-93

Query Match      80.2%; Score 274.2; DB 21; Length 560;
Best Local Similarity 89.1%; Pred. No. 2.5e-79;
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```

Matches 311; Conservative 0; Mismatches 28; Indels 10; Gaps 1;

QY 4 GAGTCTGAGCCAGAGCTGTGAGACCTTTCACAGACCTGTCTCTACCTGACCTGTCTCT
DB 16 GAGTCGGGCCCCAGAGCTGTGAGACCTTTCACAGACCTGTCTCTCTCTCTCTCTCTCT
QY 64 GGTGGCTCCATCCGACAGTGTGTATTATTAATGAGTTGGATCCGCGACGCTCCAGGAG
DB 76 GGTGGCTCCATCCGACAGTGTGTATTATTAATGAGTTGGATCCGCGACGCTCCAGGAG
QY 124 GGCCTGAGTGTGATCGGTATCATCTATCATGAGCAACCTTCAACAAACCCGTCTCTC
DB 136 GGCCTGAGTGTGATCGGTATCATCTATCATGAGCAACCTTCAACAAACCCGTCTCTC
QY 184 AAGAGTGAAGTTACATGTCAGTAGACAGCTCTAAGAACCTTCTCTGAGGCTGAGC
DB 196 AAGAGTGAAGTTACATGTCAGTAGACAGCTCTAAGAACCTTCTCTGAGGCTGAGC
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTAATCTGTGAGAGTCAAGTGGTACACTT
DB 256 TCTGTGACTGCGCGGACACGCGCTGTATTAATCTGTGAGAGTCAAGTGGTACACTT
QY 294 GTACACTTGTGACAACTGGGCGAGGAGACCTGTGATCAACCTGTCTCTCA 342
DB 316 CCACTGTTGACCCCTGTGGGCGAGGAGACCTGTGATCAACCTGTCTCTCA 364

RESULT 15
US-10-984-960A-19
; Sequence 19, Application US/10984960A
; Publication No. US20050142137A1
; GENERAL INFORMATION:
; APPLICANT: Gallo, Michael
; APPLICANT: Chui, Daniel
; APPLICANT: Zhong, Hailong
; APPLICANT: Ary, Gulehan
; APPLICANT: Laroche, William J.
; TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
; FILE REFERENCE: Cura 970
; CURRENT APPLICATION NUMBER: US/10/984,960A
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: 60/518,275
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 19
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(366)
US-10-984-960A-19

Query Match      79.6%; Score 272.2; DB 22; Length 366;
Best Local Similarity 88.6%; Pred. No. 1e-78;
Matches 311; Conservative 0; Mismatches 28; Indels 12; Gaps 1;

QY 4 GAGTCTGAGCCAGAGCTGTGAGACCTTTCACAGACCTGTCTCTACCTGACCTGTCTCT
DB 16 GAGTCGGGCCCCAGAGCTGTGAGACCTTTCACAGACCTGTCTCTCTCTCTCTCTCTCT
QY 64 GGTGGCTCCATCCGACAGTGTGTATTATTAATGAGTTGGATCCGCGACGCTCCAGGAG
DB 76 GGTGGCTCCATCCGACAGTGTGTATTATTAATGAGTTGGATCCGCGACGCTCCAGGAG
QY 124 GGCCTGAGTGTGATCGGTATCATCTATCATGAGCAACCTTCAACAAACCCGTCTCTC
DB 136 GGCCTGAGTGTGATCGGTATCATCTATTAATGAGCAACCTTCAACAAACCCGTCTCTC
QY 184 AAGAGTGAAGTTACATGTCAGTAGACAGCTCTAAGAACCTTCTCTGAGGCTGAGC
DB 196 AAGAGTGAAGTTACATGTCAGTAGACAGCTCTAAGAACCTTCTCTGAGGCTGAGC
```


QY 244 TCTGTGACTGCCCGGACACGCGCGTGTATTACTGTGGAG-----GTCAGAT 291
 Db 256 TCTGTGACTGCCCGGACACGCGCGTGTATTACTGTGGAGAGAGGGGAGTACTACGAT 315
 QY 292 GGGTACACTTTGGACCACTGGGGCCAGGAACTGTGTCAACCGTCTCTCA 342
 Db 316 GAGGGGGGTTTGACTACTGGGGCCAGGAACTGTGTCAACCGTCTCTCA 366

Search completed: July 27, 2005, 18:58:28
 Job time : 512.827 secs

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QY 301 TTGACACCTGGGGCCAGGAAACCTGTGACCTCTCTCTCA 342
Db 301 ATAGACGTCTGGGGCCAGGAAACGATCACCGTCTCTCTCA 342

RESULT 2

US-08-360-125-3

Sequence 3, Application US/08360125
Patent No. 5767246
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246ihiko ITO
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:

CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-3

Query Match

Best Local Similarity 85.1%; Pred. No. 3,1e-68;

Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGAGCTGTGAAGCCTTCAAGACCTGCTCTCACTGCTCT 63
Db 16 GAGTGGGGCCAGAGCTGTGAAGCCTTCAAGACCTGCTCTCACTGCTCT 75
QY 64 GGTGGCTTCCATCCGCACTGCTGTATTATTGAGTTGGTCCGCGCCTCCAGGGAAG 123
Db 76 GGTGGCTTCCATCCGCACTGCTGTATTATTGAGTTGGTCCGCGCCTCCAGGGAAG 135
QY 124 GGCCTGGAGTGATCCGCAATCTATCAAGTGGCAACCTTAACAACCCGCTC 183
Db 136 GGCCTGGAGTGATCCGCAATCTATCAAGTGGCAACCTTAACAACCCGCTC 195
QY 184 AAGAGTGAATTACATGTCAGTAGACACGCTTAAGAACCTTCTCTGAGACTGACC 243
Db 196 AAGAGTGAATTACATGTCAGTAGACACGCTTAAGAACCTTCTCTGAGACTGACC 255
QY 244 TCTGTACTGCGCGGACACAGCGCGTATTATTACTGTGCGGCTCAAGTGGTATCTTTG 303
Db 256 TCTGTACTGCGCGGACACAGCGCGTATTATTACTGTGCGGCTCAAGTGGTATCTTTG 315
QY 304 ---GACAACTGGGGCCAGGAAACCTGTACCGCTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGAAACATGTCACCGCTCTCTCA 357

RESULT 3

US-08-450-578-3

Sequence 3, Application US/08450578
Patent No. 5837845
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845ihiko ITO
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Mordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL LINE: antibody GAH
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-3

Query Match 72.9%; Score 249.2; DB 2; Length 357;
Best Local Similarity 85.1%; Pred. No. 3,1e-68;
Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCAAGACTGTGTGAAGCCCTTCACAGACCTGTCCCTCAGCTGTCTCT 63
|||
Db 16 GAGTCGGGCCCAAGACTGTGTGAAGCCCTTCACAGACCTGTCCCTCAGCTGTCTCT 75
QY 64 GGTGGCTCCATCCGCGAGTGTGTATTATTTAGATTGGGTCCGCCAGCCCTCCAGGAG 123
|||
Db 76 GGTGGCTCCATCCGCGAGTGTGTATTATTTAGATTGGGTCCGCCAGCCCTCCAGGAG 135
QY 124 GGCCTGGAGTGAATCCGCAACATCTATACAGATGGCAACCTAACAACCCGTCCCTC 183
|||
Db 136 GGCCTGGAGTGAATCCGCAACATCTATACAGATGGCAACCTAACAACCCGTCCCTC 195
QY 184 AAGAGTGAATTAACATGTACATGATGACACGCTTAAGAACCACTTCTCTGAGCTGAC 243
|||
Db 196 AAGAGTGAATTAACATGTACATGATGACACGCTTAAGAACCACTTCTCTGAGCTGAC 255
QY 244 TCTGTACTGCCCCGAGACAGCGCGTATTATTACTGTGCGGGGTCAATGGTATCTTGG 303
|||
Db 256 TCTGTACTGCCCCGAGACAGCGCGTATTATTACTGTGCGGGGTCAATGGTATCTTGG 315
QY 304 ---GACAACTGGGGCCAGGGAACCCGTGTCACCGTCTCTCA 342
|||
Db 316 GCTGACTACTGGGGCCAGGGAACATGTGTCACCGTCTCTCA 357

RESULT 4
US-09-017-628-3
Sequence 3, Application US/09017628
Patent No. 5990287
GENERAL INFORMATION:
APPLICANT: HOSOKAWA, Saiko
APPLICANT: TAGAWA, Toshiaki
APPLICANT: HIRAKAWA, Yoko
APPLICANT: ITO, No. 5990287:hiko
APPLICANT: NAGAIKE, Kazuhiro
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
FILE REFERENCE: 177/527361KH
CURRENT APPLICATION NUMBER: US/09/017,628
CURRENT FILING DATE: 1998-02-02
EARLIER APPLICATION NUMBER: 08/360,125
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 357
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-3

Query Match 72.9%; Score 249.2; DB 2; Length 357;
Best Local Similarity 85.1%; Pred. No. 3,1e-68;
Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCAAGACTGTGTGAAGCCCTTCACAGACCTGTCCCTCAGCTGTCTCT 63
|||
Db 16 GAGTCGGGCCCAAGACTGTGTGAAGCCCTTCACAGACCTGTCCCTCAGCTGTCTCT 75
QY 64 GGTGGCTCCATCCGCGAGTGTGTATTATTTAGATTGGGTCCGCCAGCCCTCCAGGAG 123
|||
Db 76 GGTGGCTCCATCCGCGAGTGTGTATTATTTAGATTGGGTCCGCCAGCCCTCCAGGAG 135
QY 124 GGCCTGGAGTGAATCCGCAACATCTATACAGATGGCAACCTAACAACCCGTCCCTC 183
|||
Db 136 GGCCTGGAGTGAATCCGCAACATCTATACAGATGGCAACCTAACAACCCGTCCCTC 195
QY 184 AAGAGTGAATTAACATGTACATGATGACACGCTTAAGAACCACTTCTCTGAGCTGAC 243
|||
Db 196 AAGAGTGAATTAACATGTACATGATGACACGCTTAAGAACCACTTCTCTGAGCTGAC 255
QY 244 TCTGTACTGCCCCGAGACAGCGCGTATTATTACTGTGCGGGGTCAATGGTATCTTGG 303
|||
Db 256 TCTGTACTGCCCCGAGACAGCGCGTATTATTACTGTGCGGGGTCAATGGTATCTTGG 315

Db 256 TCTGTGACTGCGGAGACGCGCGTGTATTACTGTGAGAGTCTTACCCGACTAGGGGG 315
Qy 304 ---GACAACTGGGGCCAGGAAACCTGGTACCGTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGAAACATGTGTACCGTCTCTTCA 357

RESULT 5
US-09-014-880-3
; Sequence 3, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Menderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,880
; FILING DATE: January 28, 1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,578
; FILING DATE: May 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody G4H
; US-09-014-880-3

Query Match 72.9%; Score 249.2; DB 2; Length 357;
Best Local Similarity 85.1%; Pred. No. 3.1e-68;
Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

Qy 4 GAGTCTGGCCCGAGACTGTGAAGCTTCAAGACCTGTCTCTCACTGACTGTCTCT 63
Db 16 GAGTCTGGCCCGAGACTGTGAAGCTTCAAGACCTGTCTCTCACTGACTGTCTCT 75
Qy 64 GGTGGCTCCATCCGACAGTGGTATTATATGAGTTGGGGCCGACACCCCGAGGAG 123
Db 76 GGTGGCTCCATCCGACAGTGGTATTATATGAGTTGGGGCCGACACCCCGAGGAG 135

Qy 124 GGCCTGAGTGGATCGGCAACATCTATACAGTGGCAACCTTACAAACCCGCTCC 183
Db 136 GGCCTGAGTGGATCGGCAACATCTATACAGTGGCAACCTTACAAACCCGCTCC 195
Qy 184 AAGAGTGAATTAACATGTCAGTATGACAGTCTTAAGAACCACTTCTCCGAGCTAAC 243
Db 196 AAGAGTGAATTAACATGTCAGTATGACAGTCTTAAGAACCACTTCTCCGAGCTAAC 255
Qy 244 TCTGTGACTGCGCGGACAGCGCGTATTACTGTGCGCGTCAATGGTATACCTTTG 303
Db 256 TCTGTGACTGCGCGGACAGCGCGTATTACTGTGCGCGTCAATGGTATACCTTTG 315
Qy 304 ---GACAACTGGGGCCAGGAAACCTGGTACCGTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGAAACATGTGTACCGTCTCTTCA 357

RESULT 6
US-08-450-363-3
; Sequence 3, Application US/08450363
; Patent No. 6436434
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 6436434Ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Menderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,363
; FILING DATE: May 25, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:


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IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 3
US-09-467-903-3

Query Match      72.9%; Score 249.2; DB 4; Length 357;
Best Local Similarity 85.1%; Pred. No. 3.1e-68;
Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCCAGAGACTGTGTAAGCCCTTCAACAGACCCCTGCTCCTCAGCTGCTCT 63
DB 16 GAGTCGGGCCCGAGACTGTGTAAGCCCTTCAACAGACCCCTGCTCCTCAGCTGCTCT 75
QY 64 GGTGGCTCCATCCGCACTGTGTTATTATTGAGTTGGTCCGCGCAGCTCCAGGGAG 123
DB 76 GGTGGCTCCATCCGCACTGTGTTATTATTGAGTTGGTCCGCGCAGCTCCAGGGAG 135
QY 124 GGCCTGAGTGGATCGGCAACATCTATCAAGTGGCAACCTTCAACACCCGCTCC 183
DB 136 GGCCTGAGTGGATCGGCAACATCTATCAAGTGGCAACCTTCAACACCCGCTCC 195
QY 184 AAGAGTGAATTACCATGTCAAGTGAACAGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 196 AAGAGTGAATTACCATGTCAAGTGAACAGCTTAAGAACCACTTCTCCCTGAGACTGACC 255
QY 244 TCTGTACTGCCCCGAGACAGCGCGCTTATTACTGTGCGCGCTGAGATGGTATACCTTTG 303
DB 256 TCTGTACTGCCCCGAGACAGCGCGCTTATTACTGTGCGCGCTGAGATGGTATACCTTTG 315
QY 304 ---GACAACCTGGGGCGAGGGAACCTGTGTCACCGTCTCCCTCA 342
DB 316 GCTGACTACTGGGGCGAGGGAACATGTGTACCGTCTCTTCA 357

RESULT 8
US-09-471-276-100
Sequence 100, Application US/09471276
Patent No. 6822072
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclet A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6822072
FILE REFERENCE: GENSET.025CPI
CURRENT APPLICATION NUMBER: US/09/471.276
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: 09/057,719
EARLIER FILING DATE: 1998-04-09
EARLIER APPLICATION NUMBER: 09/069,047
EARLIER FILING DATE: 1998-04-28
EARLIER APPLICATION NUMBER: PCT/IB99/00712
EARLIER FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 1622
SOFTWARE: Patent.pm
SEQ ID NO 100
LENGTH: 504
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
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LOCATION: 39..503
NAME/KEY: sig_peptide
LOCATION: 39..95
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 9.3000019073486
OTHER INFORMATION: seq FULLVAGPRWVL5/QV
US-09-471-276-100

Query Match      71.6%; Score 244.8; DB 4; Length 504;
Best Local Similarity 83.4%; Pred. No. 8.6e-67;
Matches 287; Conservative 3; Mismatches 51; Indels 3; Gaps 1;

QY 1 CTGAGCTTGCCCCAGAGACTGTGTAAGCCCTTCAACAGACCCCTGCTCCTCAGCTGTC 60
DB 108 SDRAGATCGGGCCCGAAGACTGTGTAAGCCCTTCAACAGACCCCTGCTCCTCAGCTGTA 167
QY 61 TCTGTGGCTCCATCCGCACTGTGTTATTATTGAGTTGGTCCGCGCAGCTCCAGGG 120
DB 168 TCTGTGGCTCCATCCGCACTGTGTTATTATTGAGTTGGTCCGCGCAGCTCCAGGG 227
QY 121 AAGGCGCTGAGTGGATCGGCAACATCTATCAAGTGGCAACCTTCAACACCCGCTCC 180
DB 228 AAGGCGCTGAGTGGATCGGCAACATCTATCAAGTGGCAACCTTCAACACCCGCTCC 287
QY 181 CTGAAGTGAATTACCATGTCAAGTGAACAGCTTAAGAACCACTTCTCCCTGAGACTG 240
DB 288 CTGAAGTGAATTACCATGTCAAGTGAACAGCTTAAGAACCACTTCTCCCTGAGACTG 347
QY 241 ACCTGTGACTGCGCGGAGACAGCGCGCTTATTACTGTGCGCGTCAATGGGTATAC 300
DB 348 AGTCTGTGACTGCGCGGAGACAGCGCGCTTATTACTGTGCGCGTCAATGGGTATAC 407
QY 301 ---TTGACAACCTGGGGCGAGGGAACCTGTGTCTCTC 341
DB 408 CTATTGACCCCTGGGGCGAGGGAACCTGTGTCTCTC 451

RESULT 9
US-09-582-337-13
Sequence 13, Application US/09582337
Patent No. 6562618
GENERAL INFORMATION:
APPLICANT: Japan Tobacco, Inc.
TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
FILE REFERENCE: JI-009PCT
CURRENT APPLICATION NUMBER: US/09/582.337
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: JP P1997-367699
PRIOR FILING DATE: 1997-12-25
PRIOR APPLICATION NUMBER: JP P1998-356183
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 450
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(450)
NAME/KEY: sig_peptide
LOCATION: (1)..(58)
NAME/KEY: V region
LOCATION: (59)..(353)
US-09-582-337-13

Query Match      71.1%; Score 243; DB 4; Length 450;
Best Local Similarity 84.9%; Pred. No. 3e-66;
Matches 303; Conservative 0; Mismatches 35; Indels 19; Gaps 2;

QY 4 GAGTCTGCCCCAGAGACTGTGTAAGCCCTTCAACAGACCCCTGCTCCTCAGCTGCTCT 63
```


Db 74 GAGTCGGCCAGAGCTGTGAAGCCTTCAACAGCCCTGT-CCTACCTGCACTGTCTT 132
QY 64 GGTGGCTCCATCCGACAGTGGTATTATTATTTAGATTGGTCCGACAGCTCCAGGAG 123
Db 133 GGTGGCTCCATCCGACAGTGGTATTATTATTTAGATTGGTCCGACAGCTCCAGGAG 192
QY 124 GGCCTGAGTGAATGCGCAACATCTATCAAGTGGCAACCTTAACAACCCGTCCTC 183
Db 193 GGCCTGAGTGAATGCGTATCATTTATTAAGTGGAGCACTTAACAACCCGTCCTC 252
QY 184 AAGAGTGAATTTACATGTCATGTAACAAGTCTTAAGAACCACTTCTCCCTGAGACTGAC 243
Db 253 AAGAGTGAATTTACATGTCATGTAACAAGTCTTAAGAACCACTTCTCCCTGAGACTGAC 312
QY 244 TCTGTGACTGCGCGGACAGCGCGTATTACTGTGCGGGTCAATGGTATTAATCT--- 300
Db 313 TCTGTGACTGCGCGGACAGCGCGTATTACTGTGCGGGTCAATGGTATTAATCT--- 372
QY 301 -----TTGACAACTGGGCGGAGAACTGTGTCACCGTCTCTCA 342
Db 373 GGTATTAGACACTTGTGACTGACTGGGGCCAGGAACTGTGTCACCGTCTCTCA 429

RESULT 10
US-08-545-809A-31
; Sequence 31, Application US/08545809A
; Patent No. 6096878

GENERAL INFORMATION:

APPLICANT: Honjo, Tasuku

APPLICANT: Matsumoto, Fumihiko

TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

NUMBER OF SEQUENCES: 145

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/545,809A

FILING DATE: 27-MAR-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/00603

FILING DATE: 10-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Freeman, John W.

REGISTRATION NUMBER: 29,066

REFERENCE/DOCKET NUMBER: 06501/004001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 631 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

CELL TYPE: human lymphoblast

CELL LINE: CEM1

US-08-545-809A-31

Query Match 70.9%; Score 242.6; DB 3; Length 631;

Best Local Similarity 91.5%; Pred. No. 4,6e-66;
Matches 257; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 4 GAGTCGGCCAGAGCTGTGAAGCCTTCAACAGCCCTGT-CCTACCTGCACTGTCTT 63
Db 305 GAGTCGGCCAGAGCTGTGAAGCCTTCAACAGCCCTGT-CCTACCTGCACTGTCTT 364
QY 64 GGTGGCTCCATCCGACAGTGGTATTATTATTTAGATTGGTCCGACAGCTCCAGGAG 123
Db 365 GGTGGCTCCATCCGACAGTGGTATTATTATTTAGATTGGTCCGACAGCTCCAGGAG 424
QY 124 GGCCTGAGTGAATGCGCAACATCTATCAAGTGGCAACCTTAACAACCCGTCCTC 183
Db 425 GGCCTGAGTGAATGCGTATCATTTATTAAGTGGAGCACTTAACAACCCGTCCTC 484
QY 184 AAGAGTGAATTTACATGTCATGTAACAAGTCTTAAGAACCACTTCTCCCTGAGACTGAC 243
Db 485 AAGAGTGAATTTACATGTCATGTAACAAGTCTTAAGAACCACTTCTCCCTGAGACTGAC 544
QY 244 TCTGTGACTGCGCGGACAGCGCGTATTACTGTGCGGGTCAATGGTATTAATCT--- 284
Db 545 TCTGTGACTGCGCGGACAGCGCGTATTACTGTGCGGGTCAATGGTATTAATCT--- 585

RESULT 11
US-09-471-276-51
; Sequence 51, Application US/09471276
; Patent No. 6822072

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Ducleit A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6822072

FILE REFERENCE: GENSET.025CPI

CURRENT APPLICATION NUMBER: US/09/471,276

CURRENT FILING DATE: 1999-12-21

EARLIER APPLICATION NUMBER: 09/057,719

EARLIER FILING DATE: 1998-04-09

EARLIER APPLICATION NUMBER: 09/069,047

EARLIER FILING DATE: 1998-04-28

EARLIER APPLICATION NUMBER: PCT/IB99/00712

EARLIER FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 1622

SOFTWARE: Patent.pm

SEQ ID NO 51

LENGTH: 466

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: 38..466

NAME/KEY: sig_peptide

LOCATION: 38..94

OTHER INFORMATION: Von Heijne matrix

OTHER INFORMATION: score 10.8999996185303

OTHER INFORMATION: seq FLVLVAAPRWLS/QV

FEATURE:

NAME/KEY: misc_feature

LOCATION: 423

OTHER INFORMATION: n=a, g, c or t

OTHER INFORMATION: Oligonucleotide

US-09-471-276-51

Query Match 69.5%; Score 237.8; DB 4; Length 466;

Best Local Similarity 81.2%; Pred. No. 1.3e-64;

Matches 281; Conservative 7; Mismatches 51; Indels 7; Gaps 1;

QY 4 GAGTCGGCCAGAGCTGTGAAGCCTTCAACAGCCCTGT-CCTACCTGCACTGTCTT 63
Db 110 GAGTCGGCCAGAGCTGTGAAGCCTTCAACAGCCCTGT-CCTACCTGCACTGTCTT 169
QY 64 GGTGGCTCCATCCGACAGTGGTATTATTATTTAGATTGGTCCGACAGCTCCAGGAG 123

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Db 170 GGTGGCTCCATCAGCACTGGTGTACTTCTTGGAGTTGGATCCGCCAGCCCAAGGCGG 229
Qy 124 GGCCTGAGTGAATCGGCAACATCTATCAGATGGCAACCTAACAAACCCGCTCC 183
Db 230 GGCCTGAGTGAATCGGCAACATCTATCAGATGGCAACCTAACAAACCCGCTCC 289
Qy 184 AAGAGTCGAGTTACATGTCAGTAGAGACGCTTAAAGAACCTTCTCCCTGAGACTACC 243
Db 290 AAGAGTCGAGTTACATGTCAGTAGAGACGCTTAAAGAACCTTCTCCCTGAGACTACC 349
Qy 244 TCTGTGACTCCCGGAGACGCGCGTCTATTACTGTGCGG-----GTCAAGTGGATA 236
Db 350 TCTGTGACTCCCGGAGACGCGCGTCTATTACTGTGCGGAGAGTCCGCGAGCGCTTGGC 409
Qy 297 TACTTGGACAACCTGGGCGGAGGAAACCTGTGTCACGCTCTCTCA 342
Db 410 TGGTTCASHMCTNNGGGMCAAGGACCAAGGTACCGTCTCA 455

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RESULT 12
US-09-672A-17
Sequence 17, Application US/09049672A
Patent No. 6135941

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Marian R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANTCTU01
CLONE: 1513264
US-09-049-672A-17

Query Match 69.4%; Score 237.4; DB 3; Length 1567;
Best Local Similarity 82.1%; Pred. No. 2,9e-64;
Matches 293; Conservative 0; Mismatches 46; Indels 18; Gaps 1;
Qy 4 GAGTCTGGCCAGAGAGTGTGAAGCCTTCAAGACCCCTGTCCCTCACTGCTCT 63
Db 150 GAGTCTGGCCAGAGAGTGTGAAGCCTTCAAGACCCCTGTCCCTCACTGCTCT 209
Qy 64 GGTGGCTCCATCCGCACTGGTGTATTTATGAGTTGGTCCGCAAGCTCCAGGAG 123
Db 210 GGTGGCTCCATCCGCACTGGTGTATTTATGAGTTGGTCCGCAAGCTCCAGGAG 269
Qy 124 GGCCTGAGTGAATCGGCAACATCTATCAGATGGCAACCTAACAAACCCGCTCC 183
Db 270 GGCCTGAGTGAATCGGCAACATCTATCAGATGGCAACCTAACAAACCCGCTCC 329
Qy 184 AAGAGTCGAGTTACATGTCAGTAGAGACGCTTAAAGAACCTTCTCCCTGAGACTACC 243
Db 330 AAGAGTCGAGTTACATGTCAGTAGAGACGCTTAAAGAACCTTCTCCCTGAGACTACC 389
Qy 244 TCTGTGACTCCCGGAGACGCGCGTCTATTACTGTGCGGAGATG----- 232
Db 390 TCTGTGACTCCCGGAGACGCGCGTCTATTACTGTGCGGAGATGAGGTTAAGG 449
Qy 293 -----GCTATCTTGGACAACCTGGGCGGAGGAAACCTGTGTCACGCTCTCTCA 342
Db 450 GGGGGAACCTACGCTATGACGCTGTGGGCGGAGGAAACCTGTGTCACGCTCTCTCA 506

RESULT 13

US-09-720-493-1

Sequence 1, Application US/09720493
Patent No. 6827925

GENERAL INFORMATION:

APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Williams, Andrew J
APPLICANT: Tempest, Philip R
APPLICANT: Holte, Thor L
APPLICANT: Main, Sarah H
APPLICANT: Jackson, Helen
APPLICANT: Darmon, Oleksan
TITLE OF INVENTION: Improvements relating to antibodies
FILE REFERENCE: AHB/CP577533
CURRENT APPLICATION NUMBER: US/09/720,493
CURRENT FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: GB 9814383.7
PRIOR FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 351
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(351)
US-09-720-493-1

Query Match 69.2%; Score 236.6; DB 4; Length 351;
Best Local Similarity 83.2%; Pred. No. 2.7e-64;
Matches 282; Conservative 0; Mismatches 54; Indels 3; Gaps 1;

Qy 4 GAGTCTGGCCAGAGAGTGTGAAGCCTTCAAGACCCCTGTCCCTCACTGCTCT 63
Db 16 GAGTCTGGCCAGAGAGTGTGAAGCCTTCAAGACCCCTGTCCCTCACTGCTCT 75
Qy 64 GGTGGCTCCATCCGCACTGGTGTATTTATGAGTTGGTCCGCAAGCTCCAGGAG 123
Db 76 GGTGGCTCCATCCGCACTGGTGTATTTATGAGTTGGTCCGCAAGCTCCAGGAG 132
Qy 124 GGCCTGAGTGAATCGGCAACATCTATCAGATGGCAACCTAACAAACCCGCTCC 183
Db 133 GGCCTGAGTGAATCGGCAACATCTATCAGATGGCAACCTAACAAACCCGCTCC 192

QY 184 AAGAGTGAATTACATGCTGAGTACAGCCTTCTAAGAACCACTTCTCCCTGAGACTGACC 243
| | | | |
Db 193 AAGAGTGAAGTACACCATATCATGATGACACGCTCAAGAACCAAGTCTCCCTGAGACTGAGC 252
QY 244 TCTGTGACTGCGCGGAGACGCGCGCTCATATCATGCTGCGCGCTGAGATGGTATACCTTTG 303
| | | | |
Db 253 TCTGTGACCGCGGAGACGCGCGCTCATATCATGCTGCGAGAGGAGAGTGTGCGAAGTTT 312
QY 304 GACAACCTGGGGGCGAGGAAACCTGTGTCACCGTCTCTCTCA 342
| | | | |
Db 313 GACTATTGGGGGCGAGGAAACCTGTGTCACCGTCTCTCTCA 351

RESULT 14

US-09-720-493-21/c
; Sequence 21. Application US/09720493
; Patent No. 6827925
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Williams, Andrew J
; APPLICANT: Tempest, Philip R
; APPLICANT: Holter, Thor L
; APPLICANT: Main, Sarah H
; APPLICANT: Jackson, Helen
; APPLICANT: Daromola, Olalekan
; TITLE OF INVENTION: Improvements relating to antibodies
; FILE REFERENCE: AHB/CP5775333
; CURRENT APPLICATION NUMBER: US/09/720,493
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: GB 9814383.7
; PRIOR FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 351
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-720-493-21

Query Match 69.2%; Score 236.6; DB 4; Length 351;
Best Local Similarity 83.2%; Pred. No. 2.7e-64;
Matches 282; Conservative 0; Mismatches 54; Indels 3; Gaps 1;
QY 4 GAGCTGGCCCGAGAGCTGTGTAAGCCTTACAGACCCCTGCTCCACCTGACGTCTCT 63
| | | | |
Db 336 GAGTCCGCGCCAGAGCTGTGTAAGCCTTGGAGACCTGCTCCACCTGCGTGTCTCT 277
QY 64 GGTGGCTCCATCCGCAAGTGTGTTATATTGAGTTGGTCCGCGAGCTCCAGGGAG 123
| | | | |
Db 276 GGTACTCTCATCAGCA---GTGGTTACTACTGGGGCTGGATTCCGGCAGCCCCCAGGGAG 220
QY 124 GGCCTGAGAGTGATCGCAACATCTATCAAGTGGCAACACTTCAACAAACCGTCCCTC 183
| | | | |
Db 219 GGGCTGGAGTGATGGAGATCTATCATATGAGGAGACCTACTACAAACCGTCCCTC 160
QY 184 AAGAGTGAATTACATCATGTAGTACACGCTTAAAGAACCACTTCTCCCTGAGACTGACC 243
| | | | |
Db 159 AAGAGTGAAGTACCATATCATGTAGTACACGCTTAAAGAACCACTTCTCCCTGAGACTGAGC 100
QY 244 TCTGTGACTGCGCGGAGACGCGCGTCTATTACTGTGCGCGGTGAGATGGGTATATCTTG 303
| | | | |
Db 99 TCTGTGACCGCGCGAGACGCGCGTGTATTACTGTGTGCAAGAGGAGAGTGTGCAAGTTT 40
QY 304 GACAACCTGGGGGCGAGGAAACCTGTGTCACCGTCTCTCTCA 342
| | | | |
Db 39 GACTATTGGGGGCGAGGCAACCTGTGTCACCGTCTCTCTCA 1

RESULT 15
US-09-800-729-74
; Sequence 74. Application US/09800729
; Patent No. 6605592

; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 1543
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-800-729-74

Query Match 68.6%; Score 234.6; DB 4; Length 1543;
Best Local Similarity 81.0%; Pred. No. 2.2e-63;
Matches 273; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 4 GAGTCTGGCCCGAGAGCTGTGTAAGCCTTACAGACCCCTGCTCCACCTGACGTCTCT 63
| | | | |
Db 90 GAGTCCGCGCCAGAGCTGTGTAAGCCTTACAGACCCCTGCTCCACCTGACGTCTCT 149
QY 64 GGTGGCTCCATCCGCAAGTGTGTTATATTGAGTTGGTCCGCGAGCTCCAGGGAG 123
| | | | |
Db 150 GGTGGCTCCATCCGCAAGTGTGTTATATTGAGTTGGTCCGCGAGCTCCAGGGAG 209
QY 124 GGCCTGAGTGAATCGGCAACATCTATCAAGTGGCAACACTTCAACAAACCGTCCCTC 183
| | | | |
Db 210 GGCCTGAGTGAATGGGTATCTCTTACATGGGGTCACTACTACATTCGTTCCCTC 269
QY 184 AAGAGTGAATTACATCATGTAGTACACGCTTAAAGAACCACTTCTCCCTGAGACTGACC 243
| | | | |
Db 270 AAGAGTGAAGTACCATATCATGTAGTACACGCTTCAAGAACCAAGTCTCCCTGAGGCTGAGC 329
QY 244 TCTGTGACTGCGCGGAGACGCGCGTCTATTACTGTGCGGGGTGAGTGGTATATCTTG 303
| | | | |
Db 330 TCTGTGACTGCGCGGAGACGCGCGTCTATTACTGTGCGAAAGATCATCGAGCGACCA 389
QY 304 GACAACCTGGGGGCGAGGAAACCTGTGTCACCGTCTCTCTCA 340
| | | | |
Db 390 GACGGTACCAAGCTGGAATACCAAGGCTTTGACTACT 426

Search completed: July 27, 2005, 12:41:20
Job time : 95.3455 secs

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QY 301 TTGGACATCTGGGGCCAGGAGACCCCTGTGTCACCGTCTCTCA 342
DB 301 ATAGAGCTCTGGGGCCAGGAGACCGTCAACCGTCTCTCA 342

RESULT 2

US-08-360-125-3
Sequence 3, Application US/08360125
Patent No. 5767246
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Tochiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246hiko ITO
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL LINE: antibody GAH
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:

CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-3

Query Match 74.7%; Score 255.6; DB 1; Length 357;
Best Local Similarity 86.3%; Pred. No. 9.2e-71;
Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY 4 GAGCTTGGCCAGGAGCTGTGAAGCCTGCACAGACCCCTGCTCCTCAGCTGCGTGTCT 63
DB 16 GAGTCGGGCCCAAGACTGTGGAAGCCTTCACAGACCCCTGCTCCTCAGCTGCTCT 75
QY 64 GCGGCTCCATCCGCGAGTGTGTACTACTGAGTTGATTCGCCCAAGCCAGGGAAG 123
DB 76 GGTGGCTCCATCAGAGTGTGTCTTCTACTGGAAGTCCGCGACGACCCAGGGAAG 135
QY 124 GGCCTGAGTGAATTGGGTATCATCAAGTGGGAACACTACAAACCCGTCCTC 183
DB 136 GGCCTGAGTGAATTGGGTATCATCAAGTGGGAACACTACAAACCCGTCCTC 195
DB 184 AAGAGTGAATTGCCATGTGCTAGACACGCTGTGAGAACAGTTTCCCTGAGGCTGAAC 243
DB 196 AAGAGTGAATTGCCATGTGCTAGACACGCTGTGAGAACAGTTTCCCTGAGGCTGAAC 255
QY 244 TCTGTACTGCCCGGACACGGCCGTGTATTAATGTCGAGGTTAATGCTACACTTTC 303
DB 256 TCTGTACTGCCCGGACACGGCCGTGTATTAATGTCGAGGTTAATGCTACACTTTC 315
QY 304 ---GACATCTGGGGCCAGGAGACCCCTGTGTCACCGTCTCTCA 342
DB 316 GCTGACTACTGGGGCCAGGAGACCAATGTCAACCGTCTCTCA 357

RESULT 3

US-08-450-578-3
Sequence 3, Application US/08450578
Patent No. 5837845
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Tochiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845hiko ITO
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/450,578
 FILING DATE: May 25, 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/360,125
 FILING DATE: December 20, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/905,534
 FILING DATE: June 29, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren M. Cheek, Jr.
 REGISTRATION NUMBER: 33,367
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-8850
 TELEFAX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL:
 ANTI-SENSE:
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM:
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE:
 CELL TYPE: Hybridoma producing human
 CELL LINE: antibody GAH
 ORGANELLER:
 IMMEDIATE SOURCE:
 LIBRARY:
 CLONE:
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT:
 MAP POSITION:
 UNITS:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 PUBLICATION INFORMATION:
 AUTHORS:
 TITLE:
 JOURNAL:
 VOLUME:
 ISSUE:
 PAGES:
 DATE:
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO:
 US-08-450-578-3

Query Match 74.7%; Score 255.6; DB 2; Length 357;
 Best Local Similarity 86.3%; Pred. No. 9,2e-71;
 Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

4 GAGTCTGCCAGGAGTGTGAAGCCCTGCACAGACCCCTGTCCCTGACGTGCTCT 63
 16 GAGTCTGCCAGGAGTGTGAAGCCCTGCACAGACCCCTGTCCCTGACGTGCTCT 75
 64 GCGGCTCCATCCGAGTGTGTACTGATGATGATGATGATGATGATGATGATGAT 123
 76 GGTGGCTCCATCCGAGTGTGTACTGATGATGATGATGATGATGATGATGATGAT 135
 124 GGCCTGAGTGAATTGGGTATCTATCAAGTGGGAAACCTTAACAACCCGTCCTC 183
 136 GGCCTGAGTGAATTGGGTATCTATCAAGTGGGAAACCTTAACAACCCGTCCTC 195
 184 AAGAGTGAATTGGGTATCTATCAAGTGGGAAACCTTAACAACCCGTCCTC 243
 196 AAGAGTGAATTGGGTATCTATCAAGTGGGAAACCTTAACAACCCGTCCTC 255
 244 TCTGTGACTGCGCGGACACGCGGTATTAAGTGGGAAACCTTAACAACCCGTCCTC 303
 256 TCTGTGACTGCGCGGACACGCGGTATTAAGTGGGAAACCTTAACAACCCGTCCTC 315
 304 ---GACATCTGGGCGGACACGCGGTATTAAGTGGGAAACCTTAACAACCCGTCCTC 342
 316 GCTGACTACTGGGCGGACACGCGGTATTAAGTGGGAAACCTTAACAACCCGTCCTC 357

RESULT 4
 US-09-017-628-3
 Sequence 3, Application US/09017628
 Patent No. 5990287
 GENERAL INFORMATION:
 APPLICANT: HOSOKAWA, Saiko
 APPLICANT: TAGAWA, Toshiaki
 APPLICANT: HIRAKAWA, Yoko
 APPLICANT: ITO, No. 5990287hiko
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
 TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
 FILE REFERENCE: 177/52761KH
 CURRENT APPLICATION NUMBER: US/09/017,628
 CURRENT FILING DATE: 1998-02-02
 EARLIER APPLICATION NUMBER: 08/360,125
 EARLIER FILING DATE: 1994-12-20
 NUMBER OF SEQ ID NOS: 42
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 3
 LENGTH: 357
 TYPE: DNA
 ORGANISM: Unknown
 FEATURE:
 OTHER INFORMATION: Hybridoma producing human antibody GAH
 US-09-017-628-3

Query Match 74.7%; Score 255.6; DB 2; Length 357;
 Best Local Similarity 86.3%; Pred. No. 9,2e-71;
 Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

4 GAGTCTGCCAGGAGTGTGAAGCCCTGCACAGACCCCTGTCCCTGACGTGCTCT 63
 16 GAGTCTGCCAGGAGTGTGAAGCCCTGCACAGACCCCTGTCCCTGACGTGCTCT 75
 64 GCGGCTCCATCCGAGTGTGTACTGATGATGATGATGATGATGATGATGATGAT 123
 76 GGTGGCTCCATCCGAGTGTGTACTGATGATGATGATGATGATGATGATGATGAT 135
 124 GGCCTGAGTGAATTGGGTATCTATCAAGTGGGAAACCTTAACAACCCGTCCTC 183
 136 GGCCTGAGTGAATTGGGTATCTATCAAGTGGGAAACCTTAACAACCCGTCCTC 195
 184 AAGAGTGAATTGGGTATCTATCAAGTGGGAAACCTTAACAACCCGTCCTC 243
 196 AAGAGTGAATTGGGTATCTATCAAGTGGGAAACCTTAACAACCCGTCCTC 255
 244 TCTGTGACTGCGCGGACACGCGGTATTAAGTGGGAAACCTTAACAACCCGTCCTC 303

Db 256 TCTGTGCTGCGGCGGACAGCGCCGTGTATTAAGTGTACCCGACTACGGGGG 315
Qy 304 ---GACATCTGGGGCCAGGGAACCTGTGTACCGCTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGGAACAATGCTACCGCTCTCTCA 357

RESULT 5

US-09-014-880-3
; Sequence 3, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,880
; FILING DATE: January 28, 1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,578
; FILING DATE: May 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; US-09-014-880-3

Query Match 74.7%; Score 255.6; DB 2; Length 357;
Best Local Similarity 86.3%; Pred. No. 9.2e-71;

Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

Qy 4 GAGTCTGCCCCAGAGTGTGTAAGCTTGCACAGACCTGTCTCCCTCAAGCTGGCTGTCTCT 63
Db 16 GAGTCGGGGCCAGGAGCTGTGTAAGCTTGCACAGACCTGTCTCCCTCAAGCTGTCTCT 75
Qy 64 GGGGGCTCCATCCGACATGCTGTACTACTGAGATTGAGATCCGCCAACCAGGGGAAG 123
Db 76 GGTGGCTCCATCAGACATGTTGTGTTTCTACTGGAATGATCCGCCAGCACCCAGGGAAG 135

Qy 124 GGCCTGAGTGAATTTGGGTATCATTTACAGTGGGAACACTTAACAACCCGTCCTC 183
Db 136 GGCCTGAGTGAATTTGGGTATCATTTACAGTGGGAACACTTAACAACCCGTCCTC 195
Qy 184 AAGAGTGAATTTGGGTATCATTTACAGTGGGAACACTTAACAACCCGTCCTC 243
Db 196 AAGAGTGAATTTGGGTATCATTTACAGTGGGAACACTTAACAACCCGTCCTC 255
Qy 244 TCTGTGCTGCGGCGGACAGCGCCGTGTATTAAGTGTACCCGACTACGGGGG 303
Db 256 TCTGTGCTGCGGCGGACAGCGCCGTGTATTAAGTGTACCCGACTACGGGGG 315
Qy 304 ---GACATCTGGGGCCAGGGAACCTGTGTACCGCTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGGAACAATGCTACCGCTCTCTCA 357

RESULT 6

US-08-450-363-3
; Sequence 3, Application US/08450363
; Patent No. 6436434
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Yoshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 6436434Ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,363
; FILING DATE: May 25, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:

ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-3

Query March 74.7%; Score 255.6; DB 3; Length 357;
Best Local Similarity 86.3%; Pred. No. 9.2e-71;
Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCGAGAGCTGGTGAAGCCCTGACAGACCCCTGCTCAGCTGGCTGTCTCT 63
DB 16 GAGTCTGGCCGAGAGCTGGTGAAGCCCTGACAGACCCCTGCTCAGCTGGCTGTCTCT 75
QY 64 GCGCGCTTCATCCGAGTGGTGTACTACTGAGTTGGATCCGCAACCCGAGGAG 123
DB 76 GGTGGCTCCATCAGCAGTGTGTCTTCTACTGGAAGTGGATCCGCAACCCGAGGAG 135
QY 124 GGCCTGAGTGGATTTGGTATCATCTATCAGAGTGGGAACACTTCAACCAACCGTCCCTC 183
DB 136 GGCCTGAGTGGATTTGGTATCATCTATCAGAGTGGGAACACTTCAACCAACCGTCCCTC 195
QY 184 AAGAGTCGAATTGCGCATGTCGGTGAACAAGTCTGAGAACAGTCTCCCTGAGGCTGAC 243
DB 196 AAGAGTCGAATTGCGCATGTCGGTGAACAAGTCTGAGAACAGTCTCCCTGAGGCTGAC 255
QY 244 TCTGTACTCCGCGGAGACAGCGCGGTATTAATCTGTGAGGTTAGATGCTTACACTTTG 303
DB 256 TCTGTACTCCGCGGAGACAGCGCGGTATTAATCTGTGAGGTTAGATGCTTACACTTTG 315
QY 304 ---GACATCTGGGGCGAGGAACCGTGTCTACCGTCTCTCA 342
DB 316 GCTGACTACTGGGGCGAGGAACAGTGTCTACCGTCTCTCA 357

RESULT 7
US-09-467-903-3
Sequence 3, Application US/09467903
Patent No. 6787153
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
Toshiaki TAGAWA
Yoko HIRAKAWA

No. 6787153hiko ITO
Kazuhiko NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
Specifically Binding to Surface Antigen of Cancer
Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Menderoth, Lind & Ponack
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,903
FILING DATE: 21-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,363
FILING DATE: May 25, 1995
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER: JP158859/1991
FILING DATE: June 28, 1991
APPLICATION NUMBER: JP158860/1991
FILING DATE: June 28, 1991
APPLICATION NUMBER: JP158861/1991
FILING DATE: June 28, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: <Unknown>
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: <Unknown>
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: Hybridoma producing human
antibody GAH
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:

```
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 3
US-09-467-903-3
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Query Match 74.7%; Score 255.6; DB 4; Length 357;
Best Local Similarity 86.3%; Pred. No. 9.2e-71;
Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;
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QY 4 GAGTCTGGCCAGGAGCTGTGAAGCCCTGCACAGACCCCTGCTCAGCTGCTGCTCT 63
D 16 GAGTCGGGCCCCAGAGCTGTGAAGCCCTGCACAGACCCCTGCTCAGCTGCTGCTCT 75
QY 64 GCGCGCTCCATCCGCACTGTGTGTTACTGAGATTGATCCGCCAACACCCAGGAG 123
D 76 GGTGCTCCATCAACAGTGTGTGTTCTACTGGAAGTATCCGCCAGACCCAGGAG 135
QY 124 GGCCTGAGAGGATTGGGTATCTATCAAGTGGGAACACTTCAACAACCCCTCCCTC 183
D 136 GGCCTGAGAGGATTGGGTATCTATCAAGTGGGAACACTTCAACAACCCCTCCCTC 195
QY 184 AAGAGTCGAATTGCCATGTCGTAGACACGCTGAGAACAGTTCTCCCTGAGGCTGAA 243
D 196 AAGAGTCGAATTGCCATGTCGTAGACACGCTGAGAACAGTTCTCCCTGAGGCTGAA 255
QY 244 TCTGTACTGCGCGGACACGCGCGTATTACTGTGCGAGTTAGATGCTACACTTTG 303
D 256 TCTGTACTGCGCGGACACGCGCGTATTACTGTGCGAGTTAGATGCTACACTTTG 315
QY 304 ---GACATCTGGGGGCGAGGAAACCTGTGTCACCGTCTCCCTCA 342
D 316 GCTGACTACTGGGGCGAGGAAACATGTGTCACCGTCTCTTCA 357
```

RESULT 8

US-08-545-809A-31

Sequence 31, Application US/08545809A

Patent No. 6096878

GENERAL INFORMATION:

APPLICANT: Honjo, Tasuku

APPLICANT: Matsuda, Fumihiko

TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

NUMBER OF SEQUENCES: 145

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/545, 809A

FILING DATE: 27-MAR-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/00603

```
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 631 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: GM1
US-08-545-809A-31
```

```
Query Match 72.8%; Score 249; DB 3; Length 631;
Best Local Similarity 92.8%; Pred. No. 1.4e-68;
Matches 261; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
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QY 4 GAGTCTGGCCAGGAGCTGTGAAGCCCTGCACAGACCCCTGCTCAGCTGCTGCTCT 63
D 305 GAGTCGGGCCCCAGAGCTGTGAAGCCCTGCACAGACCCCTGCTCAGCTGCTGCTCT 364
QY 64 GCGCGCTCCATCCGCACTGTGTGTTACTGAGATTGATCCGCCAACACCCAGGAG 123
D 365 GGTGCTCCATCAACAGTGTGTGTTCTACTGGAAGTATCCGCCAGACCCAGGAG 424
QY 124 GGCCTGAGAGGATTGGGTATCTATCAAGTGGGAACACTTCAACAACCCCTCCCTC 183
D 425 GGCCTGAGAGGATTGGGTATCTATCAAGTGGGAACACTTCAACAACCCCTCCCTC 484
QY 484 AAGAGTCGAATTGCCATGTCGTAGACACGCTGAGAACAGTTCTCCCTGAGGCTGAA 243
D 485 AAGAGTCGAATTGCCATGTCGTAGACACGCTGAGAACAGTTCTCCCTGAGGCTGAA 544
QY 244 TCTGTACTGCGCGGACACGCGCGTATTACTGTGCGAG 284
D 545 TCTGTACTGCGCGGACACGCGCGTATTACTGTGCGAG 585
```

RESULT 9

US-09-049-672A-17

Sequence 17, Application US/09049672A

Patent No. 6135941

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti

APPLICANT: Tang, X. Tom

APPLICANT: Yue, Henry

APPLICANT: Au-Young, Janice

APPLICANT: Corley, Neil C.

APPLICANT: Guegler, Karl J.

APPLICANT: Baughn, Mariah R.

TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HERWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANTU01
CLONE: 1513264
US-09-049-672A-17

Query Match 72.7%; Score 248.6; DB 3; Length 1567;
Best Local Similarity 84.0%; Pred. No. 2.8e-68;
Matches 300; Conservative 0; Mismatches 39; Indels 18; Gaps 1;

QY 4 GAGCTGCCCCAGAGCTGTGAAGCCCTGACAGACCCCTGCTCAGTGGCTGTCT 63
DB 150 GAGTCGGCCCGAGAGCTGTGAAGCCCTGCGAGACCCCTGCTCAGTGGCTGTCT 209
QY 64 GCGCGCTCCATCCCGAGAGCTGTGAAGCCCTGCGAGACCCCTGCGAGAG 123
DB 210 GGTGGCTCCATCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 269
QY 124 GCGCTGAGTGAGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 183
DB 270 GCGCTGAGTGAGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 329
QY 184 AAGAGTGAATTCGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 243
DB 330 AAGAGTGAATTCGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 389
QY 244 TCTGTGACTGCGCGGAGACGCGCGTGTATTACTGTGTGTGTGTGTGTGTGTGTGTGTGT 292
DB 390 TCTGTGACTGCGCGGAGACGCGCGTGTATTACTGTGTGTGTGTGTGTGTGTGTGTGTGT 449
QY 293 -----GCTACACTTGTGACATCTGGGCGCAGGGAACCTGTGACCGTCTCTCA 342
DB 450 GGGGGGAACCTACGATGAGACGTCTGGGGCGCAGGGAACCTGTGACCGTCTCTCA 506

RESULT 10
US-09-582-337-13
Sequence 13, Application US/09582337
Patent No. 6562618
GENERAL INFORMATION:
APPLICANT: Japan Tobacco, Inc.
TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
FILE REFERENCE: J1-009PCT
CURRENT APPLICATION NUMBER: US/09/582,337
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: JP P1997-367699
PRIOR FILING DATE: 1997-12-25
PRIOR APPLICATION NUMBER: JP P1998-356183
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patent Ver. 2.0

SEQ ID NO 13
LENGTH: 450
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(450)
NAME/KEY: sig_peptide
LOCATION: (1)..(58)
NAME/KEY: V region
LOCATION: (59)..(353)
US-09-582-337-13

Query Match 72.5%; Score 247.8; DB 4; Length 450;
Best Local Similarity 85.7%; Pred. No. 2.9e-68;
Matches 306; Conservative 0; Mismatches 32; Indels 19; Gaps 2;

QY 4 GAGCTGCCCCAGAGCTGTGAAGCCCTGACAGACCCCTGCTCAGTGGCTGTCT 63
DB 74 GAGTCGGCCCGAGAGCTGTGAAGCCCTTCAAGACCCCTGCTCAGTGGCTGTCT 132
QY 64 GCGCGCTCCATCCCGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 123
DB 133 GGTGGCTCCATCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 192
QY 124 GCGCTGAGTGAGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 183
DB 193 GCGCTGAGTGAGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 252
QY 184 AAGAGTGAATTCGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 243
DB 253 AAGAGTGAATTCGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 312
QY 244 TCTGTGACTGCGCGGAGACGCGCGTGTATTACTGTGTGTGTGTGTGTGTGTGTGTGTGT 286
DB 313 TCTGTGACTGCGCGGAGACGCGCGTGTATTACTGTGTGTGTGTGTGTGTGTGTGTGTGT 372
QY 287 -TAGATGCTACACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 342
DB 373 GGTATTACAGACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 429

RESULT 11
US-09-471-276-51
Sequence 51, Application US/09471276
Patent No. 6822072
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6822072
FILE REFERENCE: GENSET.025CP1
CURRENT APPLICATION NUMBER: US/09/471,276
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: 09/057,719
EARLIER FILING DATE: 1998-04-09
EARLIER APPLICATION NUMBER: 09/069,047
EARLIER FILING DATE: 1998-04-28
EARLIER APPLICATION NUMBER: PCT/IB99/00712
EARLIER FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 1622
SOFTWARE: Patent .pm
SEQ ID NO 51
LENGTH: 466
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 38..466
NAME/KEY: sig_peptide
LOCATION: 38..94
OTHER INFORMATION: Von Heijne matrix

OTHER INFORMATION: score 10.899996185303
OTHER INFORMATION: seq FLILVABRWLS/QV
FEATURE:
NAME/KEY: misc_feature
LOCATION: 423
OTHER INFORMATION: n=a, g, c or t
OTHER INFORMATION: Oligonucleotide
US-09-471-276-51

Query Match 70.5%; Score 241; DB 4; Length 466;
Best Local Similarity 81.8%; Pred. No. 4,1e-66;
Matches 283; Conservative 7; Mismatches 49; Indels 7; Gaps 1;

QY 4 GAGTCTGAGCCAGGACTGGTGAAGCCCTGACAGACCCCTGCTCAAGCTGGCTGTCTCT 63
DB 110 GAGTCGGGCCCCAGACTGGTGAAGCCCTTCAAGACCCCTGCTCAAGCTGGCTGTCTCT 169
QY 64 GGGCGCTCCACCCGACATGGTGTACTACTGAGATTGAGATCCGCCAACCCGAGAG 123
DB 170 GGTGGCTCCACACAGAGGTGGTACTCTGAGATTGATCCGCCACACCCAGGCGG 229
QY 124 GGCCTGAGATGATGGTGTATCATATCAAGTGGAAACCTTCAACAAACCCGCTCC 183
DB 230 GGCCTGAGATGATGGTGTATCATATCAATGGAGACCTTCAACAAACCCGCTCC 289
QY 184 AAGAGTCGAATGGCATGTGCGTGAACAAGCTTGAAGAAAGATTCTCCCTGAGGCTGAAC 243
DB 290 AGGAGTCGAGTTACATGTCAATGAGACAGCTTAAGAAACAGTTCTCCCTGAACCTGAAC 349
QY 244 TCTGTGACTGCGCGGACACGCGCGTATATCTGTGAGAGTTAGATGCTAC----- 297
DB 350 TCTGTACTGCGCGGACACGCGSCATGTATTACTGTGSAGAGGTGCGGACGCGCTTGGC 409
QY 298 -ACTTTGACATCTGGGCGCAGGAAACCTGTGACCGCTCTCTCA 342
DB 410 TGGTTCAASHMCTTNGGGMCAGGACCCAGGTACCCCTTCATCA 455

RESULT 12
US-09-800-729-74
Sequence 74, Application US/09800729
Patent No. 6605592
GENERAL INFORMATION:
APPLICANT: NI et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 74
LENGTH: 1543
TYPE: DNA
ORGANISM: Homo sapiens
US-09-800-729-74

Query Match 70.5%; Score 241; DB 4; Length 1543;
Best Local Similarity 82.2%; Pred. No. 7e-66;
Matches 277; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GAGTCTGAGCCAGGACTGGTGAAGCCCTGCTCAAGCTGGCTGTCTCT 63
DB 90 GAGTCGGGCCCCAGACTGGTGAAGCCCTTCAAGACCCCTGCTCAAGCTGGCTGTCTCT 149
QY 64 GGCCTGAGATGATGGTGTATCATATCAAGTGGAAACCTTCAACAAACCCGCTCC 123
DB 150 GGTGGCTCCACACAGAGGTGGTACTCTGAGATTGAGATCCGCCAACCCGAGAG 209
QY 124 GGCCTGAGATGATGGTGTATCATATCAAGTGGAAACCTTCAACAAACCCGCTCC 183

DB 210 GGCCTGAGATGATGGTGTATCATATCTTACAAATGGGGTCACTTAACAATCCGTCCTC 269
QY 184 AAGAGTCGAATGGCATGTGCTAGACACGCTGAGAACAAAGTTTCCCTGAGGCTGAAC 243
DB 270 AAGAGTCGAATTTACATATCTGTAGACAGCTTCAAGAACAGTTTCCCTGAGGCTGAGC 329
QY 244 TCTGTGACTGCGCGGACACAGCGCGTATATCTGTGCGAGATTAGATGAGCTACATTTC 303
DB 330 TCTGTGACTGCGCGGACACAGCGCGTCTATTACTGTGCGAAGATCATGAGGACGACGA 389
QY 304 GACATCTGGGGCCAGGGAACCTGTGTACCGTCTCTCT 340
DB 390 GACGGGTACCACTGGAATACCAAGGCTTGTGACTACT 426

RESULT 13
US-09-471-276-100
Sequence 100, Application US/09471276
Patent No. 6822072
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PATENT NO. 6822072
FILE REFERENCE: GENSET.025CP1
CURRENT APPLICATION NUMBER: US/09/471,276
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: 09/057,719
EARLIER FILING DATE: 1998-04-09
EARLIER APPLICATION NUMBER: 09/069,047
EARLIER FILING DATE: 1998-04-28
EARLIER APPLICATION NUMBER: PCT/IB99/00712
NUMBER OF SEQ ID NOS: 1622
SOFTWARE: Patent.pm
SEQ ID NO 100
LENGTH: 504
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 39..503
NAME/KEY: sig_peptide
LOCATION: 39..95
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 9.30000019073486
OTHER INFORMATION: seq FLILVABRWLS/QV
US-09-471-276-100

Query Match 70.2%; Score 240; DB 4; Length 504;
Best Local Similarity 82.6%; Pred. No. 8,9e-66;
Matches 284; Conservative 3; Mismatches 54; Indels 3; Gaps 1;

QY 1 CTCGAGTCTGAGCCAGGACTGGTGAAGCCCTGACAGACCCCTGCTCAAGCTGGCTGTCT 60
DB 108 SDKAGTCGGGCCCCAGACTGGTGAAGCCCTTCAAGACCCCTGCTCAAGCTGGCTGTCT 167
QY 61 TCTGGCGGCTCCATCCGACATGGTGTACTACTGAGATTGAGATCCGCCAACCCGAGG 120
DB 168 TCTGGCGGCTCCGACAGATGTGGGTACTATTGACCTGGAGATCCGCCAGCTCCAGGG 227
QY 121 AAGGCTGAGATGATGGTGTATCATATCAAGTGGAAACCTTCAACAAACCCGCTCC 180
DB 228 AAGGCTGAGATGATGGTGTATCATATCAAGTGGAAACCTTCAACAAACCCGCTCC 287
QY 181 CTCGAAGTCGAATGGCATGTGCGTGAACAAGCTTGAAGAAAGTTCTCCCTGAGGCTG 240
DB 288 CTCGAAGTCGAATTAACATATCAATGAGACAGCTTAAGATCAAGTTCCTCCGAACTTG 347
QY 241 AACTCTGACTGCGCGGACACGCGCGTATTAATCTGTGCGAGTTAGATGCTACTACT 300

Db 348 AGGCTGTGACTACCGCGGACACGCGCGTCTATTACTGTGAGAGACCATTTGATCTT 407
QY 301 ---TTGACATCTGGGGCCAGGAGACCTGTCTACCGTCTCTC 341
Db 408 TACTGACCCCTGGGGCCAGGAGAACCTGTCTACCGTCTCTC 451

RESULT 14
US-08-360-125-9
Sequence 9, Application US/08360125
Patent No. 5767246
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Tohiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246ihiko ITO
TITLE OF INVENTION: Human Monoclonal Antibody
SPECIFICALLY BINDING TO SURFACE ANTIGEN OF CANCER
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:

POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
JOURNAL:
TITLE:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-9

Query Match 69.3%; Score 237; DB 1; Length 366;
Best Local Similarity 82.3%; Pred. No. 6, 8e-65;
Matches 289; Conservative 0; Mismatches 50; Indels 12; Gaps 1;

QY 4 GAGCTGTGCGCCAGAGCTGTGAGACCTGACAGACCTGTCTCTGCTCTCT 63
Db 16 GAGTGGGGCCAGAGCTGTGAGACCTGCGAGACCTGTCTCTCTCTCTCT 75
QY 64 GGGGCTTCCATCCGCACTGTGTACTACTGAGTTGATCCGCCAACCCAGGAG 123
Db 76 GGTGGCTCCATCAGCAGTACTGTACTGTGGGCTGATCCGCCAGGCCAGGAG 135
QY 124 GGCTGTGAGTGAATTGGGTATCTATCAAGTGGGAAACCTTCAACAACCCGCTCTC 183
Db 136 GGGCTGAGTGAATTGGGATATCTATTATAGTGGAGCACTTACTCAACCCGCTCTC 195
QY 184 AAGAGTGAATTGCCATGTGAGACAGCTGTGAGAAAGTTCTCTGAGGCTGAG 243
Db 196 AAGAGTGAATCAACATATCCGTAGACAGTCCAAAGACGTTCTCTGAGGCTGAG 255
QY 244 TCTGTACTGCGCCGAGCAGGCGCTGTATTACTGTGCGA-----GGTTGAT 291
Db 256 TCTGTACCGCCGAGCAGGCTGTATTACTGTGCGAGGCGGAGCTACGCGGCTAC 315
QY 292 GGCTACCTTGGACATCTGGGGCAGGAAACCTGTCAACCGTCTCTCA 342
Db 316 TACTACGATGAGAGCTGTGGGCGCAAGGAGCAACGATCAACCGTCTCTCA 366

RESULT 15
US-08-450-578-9
Sequence 9, Application US/08450578
Patent No. 5837845
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Tohiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5837845ihiko ITO
TITLE OF INVENTION: Human Monoclonal Antibody
SPECIFICALLY BINDING TO SURFACE ANTIGEN OF CANCER
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-9

Query Match 69.3%; Score 237; DB 2; Length 366;
Best Local Similarity 82.3%; Pred. No. 6,8e-65;
Matches 289; Conservative 0; Mismatches 50; Indels 12; Gaps 1;

QY 4 GAATCTGGCCCCAGAGACTGTGTAAGCCTGCACAGACCCTGTCTCTCACTGCGCTGTCT 63
|||
Db 16 GAGTCGGGCCCCAGAGACTGTGTAAGCCTTCGAGAACCTGTCCCTCACTGCACTGTCTCT 75
|||
QY 64 GGGGGCTCCATCCGCACTGGTGTACTACTGAGTTGATCCGCCAACCAGGGAAG 123
|||
Db 76 GGTGGCTCCATCAGCAGTAGTAGTACTACTGAGGCTGGATCCGCAAGCCCCAGGGGAAG 135
|||
QY 124 GGCCTGGAGTGAATTGGGTACATCTATCAGTGGGNAACACTAACAACCCGTCCTC 183
|||
Db 136 GGGCTGAGTGAATTGGGAGTATCTATTAAGTGGAGCACTACTAACAACCCGTCCTC 195
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QY 184 AAGATCGAATTGCCATGTGCTGTAACACGCTCTGAACAAGTTTCCTCTGAGGCTGAAC 243
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Db 196 AAGATCGAAGTCAACATATCCGTAGAACGTCGAAGAACAGTTCTCTGGAAGCTGAGC 255
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QY 244 TCTGTAGCTGCCCGGACACGGCGGTATTAATCTGTGCCA-----GTTAGAT 291
|||
Db 256 TCTGTACCGCCGACAGACAGCGCTGTGTATTAATCTGTGCGAGGGGGAAGTACGGGGGCTAC 315
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QY 292 GGCTACACTTTGGACATCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342
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Db 316 TACTACGGTATGACGCTCTGGGGCCAAGGACCAAGGTCACCGTCTCTCA 366
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Search completed: July 27, 2005, 12:41:20
Job time : 96.3455 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:09:06 ; Search time 1956.83 Seconds
(without alignments)
8468.649 Million cell updates/sec

Title: US-10-027-725A-2
Perfect score: 342
Sequence: 1 ctcgagctctgcccagact.....ccctgctcaccgtctctca 342

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmbl:1:
1: gb ba:*
2: gb bta:*
3: gb in:*
4: gb om:*
5: gb ov:*
6: gb pat:*
7: gb ph:*
8: gb pl:*
9: gb pr:*
10: gb ro:*
11: gb sts:*
12: gb sy:*
13: gb un:*
14: gb vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	340.4	99.5	342	9	HSA458383
2	324.4	94.9	342	9	HSA458384
3	297.2	86.9	342	9	HSA458382
4	286.2	83.7	355	9	AY640487
5	284.6	83.2	355	9	AY640580
6	281.4	82.3	355	9	AY640509
7	281.4	82.3	355	9	AY640579
8	279.8	81.8	355	9	AY640564
9	275	80.4	355	9	AY640507
10	275	80.4	432	9	HSA491911
11	273.4	79.9	432	9	HSA491912
12	271.8	79.5	354	9	HSA245064
13	271.8	79.5	414	9	AF062112
14	270.8	79.2	411	9	HST22X1
15	269	78.7	403	12	AF452917
16	268.6	78.5	351	9	HSA245020
17	268.4	78.5	351	9	HSA244930
18	268.4	78.5	358	9	AF021954
19	268.4	78.5	360	6	AX061463

20	267	78.1	360	9	HSU80129	U80129 Human immun
21	267	78.1	360	9	HSU80130	U80130 Human immun
22	266	77.8	354	9	HSA244955	AJ244955 Homo sapi
23	266	77.8	355	9	AY640551	AY640551 Homo sapi
24	265.8	77.7	341	9	AY607380	AY607380 Homo sapi
25	265.8	77.7	400	12	AF452909	AF452909 Synthetic
26	265.6	77.7	357	9	HSA244949	AJ244949 Homo sapi
27	265.4	77.6	354	9	HSA579125	AJ579125 Homo sapi
28	264.2	77.3	414	9	HST14X13	Z75365 H. sapiens m
29	264.2	77.3	414	9	HST14X4	Z75378 H. sapiens m
30	264	77.2	363	9	HSU80131	U80131 Human immun
31	263	76.9	412	12	AF452912	AF452912 Synthetic
32	262.8	76.8	411	9	HST14X10	Z75363 H. sapiens m
33	262.4	76.7	409	12	AF452947	AF452947 Synthetic
34	262	76.6	357	9	HSA279523	AJ279523 Homo sapi
35	261.8	76.5	362	9	HSU80166	U80166 Human immun
36	261.4	76.4	351	9	AY607364	AY607364 Homo sapi
37	260.8	76.3	363	9	HSU80128	U80128 Human immun
38	260.6	76.2	406	12	AF453047	AF453047 Synthetic
39	260.4	76.1	357	9	HSA279541	AJ279541 Homo sapi
40	259.6	75.9	417	9	HST14X9	Z75383 H. sapiens m
41	259	75.7	339	9	AY607360	AY607360 Homo sapi
42	259	75.7	340	9	AY607366	AY607366 Homo sapi
43	259	75.7	384	9	AY640529	AY640529 Homo sapi
44	258.8	75.7	357	9	HSA244934	AJ244934 Homo sapi
45	258.8	75.7	357	9	HSA244964	AJ244964 Homo sapi

ALIGNMENTS

RESULT 1
HSA458383
LOCUS
DEFINITION
Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 60.
ACCESSION
AJ458383.1 GI:20387065
VERSION
KEYWORDS
IGHV gene, immunoglobulin heavy chain; variable region.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1
AUTHORS
Flicker, S., Steinberger, P., Norderhaug, L., Sperry, W.R., Majlesi, Y., Valent, P., Kratt, D. and Valente, R.
TITLE
Conversion of grass allergen-specific human IGH into a protective IgG1 antibody
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 342)
AUTHORS
Flicker, S.
TITLE
Direct Submission
JOURNAL
Submitted (24-APR-2002) Flicker S., Department of Pathophysiology, General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090 Vienna, AUSTRIA
FEATURES
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/product="immunoglobulin heavy chain variable region"

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Query Match 99.5%; Score 340.4; DB 9; Length 342;
Best Local Similarity 99.7%; Pred. No. 1.9e-89;
Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCGAGCACTGTGTAAGCCTTCACAGACCCCTGTCCCTCAGCTGACGTGC 60
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QY 61 TCTGTGGCTCCATCCGACGTGTGTTATTATTGAGTTGGGTCCGCGACGCTCCAGGG 120
Db 61 TCTGTGGCTCCATCCGACGTGTGTTATTATTGAGTTGGGTCCGCGACGCTCCAGGG 120

QY 121 AAGGCGCTGGAGTGGATCGGCAACATCTATACAGTGGCAACACCTTACAAACCCGCTCC 180
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QY 181 CTCAGAGTGGATTTACATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGACTG 240
Db 181 CTCAGAGTGGATTTACATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGACTG 240

QY 241 ACCTCTGTACTGCGCGGACACGCGCGTCTATTACTGTGCGGCGTCAAGATGGGTATACT 300
Db 241 ACCTCTGTACTGCGCGGACACGCGCGTCTATTACTGTGCGGCGTCAAGATGGGTATACT 300

QY 301 TTGGACAACCTGGGGCCAGGGAACCCCTGTGTCACCGTCTCCCTCA 342
Db 301 TTGGACAACCTGGGGCCAGGGAACCCCTGTGTCACCGTCTCCCTCA 342

RESULT 2
HSA458384 342 bp mRNA linear PRI 30-APR-2002
LOCUS HSA458384
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 100.
ACCESSION AJ458384.1 GI:20387067
VERSION IGHV gene; immunoglobulin heavy chain; variable region.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Flicker, S., Steinberger, P., Norderhaug, L., Sperm, W.R., Majlesi, Y., Valent, P., Kraft, D. and Valenta, R.
TITLE Conversion of grass allergen-specific human IGB into a protective IgG1 antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 342)
AUTHORS Flicker, S.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2002) Flicker S., Department of Pathophysiology, General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090 Vienna, AUSTRIA

FEATURES
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/db_xref="GI:20387068"

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ORIGIN

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Best Local Similarity 96.8%; Pred. No. 1e-84;
Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCGAGCACTGTGTAAGCCTTCACAGACCCCTGTCCCTCAGCTGACGTGC 60
Db 1 CTCGAGTCTGGCCGAGCACTGTGTAAGCCTTCACAGACCCCTGTCCCTCAGCTGACGTGC 60

QY 61 TCTGTGGCTCCATCCGACGTGTGTTATTATTGAGTTGGGTCCGCGACGCTCCAGGG 120
Db 61 TCTGTGGCTCCATCCGACGTGTGTTATTATTGAGTTGGGTCCGCGACGCTCCAGGG 120

QY 121 AAGGCGCTGGAGTGGATCGGCAACATCTATACAGTGGCAACACCTTACAAACCCGCTCC 180
Db 121 AAGGCGCTGGAGTGGATCGGCAACATCTATACAGTGGCAACACCTTACAAACCCGCTCC 180

QY 181 CTCAGAGTGGATTTACATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGACTG 240
Db 181 CTCAGAGTGGATTTACATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGACTG 240

QY 241 ACCTCTGTACTGCGCGGACACGCGCGTCTATTACTGTGCGGCGTCAAGATGGGTATACT 300
Db 241 ACCTCTGTACTGCGCGGACACGCGCGTCTATTACTGTGCGGCGTCAAGATGGGTATACT 300

QY 301 TTGGACAACCTGGGGCCAGGGAACCCCTGTGTCACCGTCTCCCTCA 342
Db 301 TTGGACAACCTGGGGCCAGGGAACCCCTGTGTCACCGTCTCCCTCA 342

RESULT 3
HSA458382 342 bp mRNA linear PRI 30-APR-2002
LOCUS HSA458382
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 94.
ACCESSION AJ458382.1 GI:20387063
VERSION IGHV gene; immunoglobulin heavy chain; variable region.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Flicker, S., Steinberger, P., Norderhaug, L., Sperm, W.R., Majlesi, Y., Valent, P., Kraft, D. and Valenta, R.
TITLE Conversion of grass allergen-specific human IGE into a protective IgG1 antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 342)
AUTHORS Flicker, S.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2002) Flicker S., Department of Pathophysiology, General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090 Vienna, AUSTRIA

FEATURES
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gene
CDS

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Query Match 86.9%; Score 297.2; DB 9; Length 342;
Best Local Similarity 91.8%; Pred. No. 1.1e-76;
Matches 314; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCCAAGAGCTGTGAAGCTTCACAGACCTCTGCTACCTGCACTGTC 60
DB 1 CTCGAGTCTGGCCCAAGAGCTGTGAAGCTTCACAGACCTCTGCTACCTGCACTGTC 60
QY 61 TCTGTGGCTCCATCCGAGTGTGTATTATTGAGATTGAGTCCGCGCAGCTCCAGGG 120
DB 61 TCTGTGGCTCCATCCGAGTGTGTATTATTGAGATTGAGTCCGCGCAGCTCCAGGG 120
QY 121 AAGGCTGTGAGTGTGAGTGTGCAATCTATGACAGTGGCAACACTTACCAACCCGTC 180
DB 121 AAGGCTGTGAGTGTGAGTGTGCAATCTATGACAGTGGCAACACTTACCAACCCGTC 180
QY 181 CTCAAGAGTGAATTAATCATGTCACTGAGACAGCTGTAAAGACCACTTCTCCCTGAGACTG 240
DB 181 CTCAAGAGTGAATTAATCATGTCACTGAGACAGCTGTGTAAAGACCACTTCTCCCTGAGACTG 240
QY 241 ACCCTGTGACTGCGCGGAGCAACGCGCTGTATTACTGTGCGCGGTGCAATGGGATTA 300
DB 241 AACTGTGTGACTGCGCGGAGCAACGCGCTGTATTACTGTGCGCGGTGCAATGGGATTA 300
QY 301 TTGGACAACCTGGGCGCAGGGAACCTGTGTCAACCGTCTCTCA 342
DB 301 TTGGACAACCTGGGCGCAGGGAACCTGTGTCAACCGTCTCTCA 342

RESULT 4 355 bp mRNA linear PRI 03-JUL-2004
AY640487
LOCUS Homo sapiens clone AP immunoglobulin E variable region mRNA,
partial cds.
ACCESSION AY640487.1 GI:49354726
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Coker, H.A., Durham, S.R. and Gould, H.J.
1 (bases 1 to 355)
REFERENCE
AUTHORS Biased use of VHS IGE+ B cells in the nasal mucosa of allergic
rhinitis patients
TITLE
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 355)
AUTHORS Coker, H.A., Durham, S.R. and Gould, H.J.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St
Thomas Street, London SE1 1UL, UK

FEATURES
SOURCE
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CDS

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ORIGIN

Query Match 83.7%; Score 286.2; DB 9; Length 355;
Best Local Similarity 90.3%; Pred. No. 1.9e-73;
Matches 306; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 4 GAGTGTGCGCCCAAGAGCTGTGAAGCTTCACAGACCTGTCTGCTACCTGCACTGTC 63
DB 16 GAGTGTGCGCCCAAGAGCTGTGAAGCTTCACAGACCTGTCTGCTACCTGCACTGTC 75
QY 64 GGTGGCTTCATCCGAGTGTGTATTATTGAGATTGAGTCCGCGCAGCTCCAGGGAG 123
DB 76 GGTGGCTTCATCCGAGTGTGTATTATTGAGATTGAGTCCGCGCAGCTCCAGGGAG 135
QY 124 GAGCTGTGAGTGTGAGTGTGCAATCTATGACAGTGGCAACACTTCTCTGAGACTGAC 183
DB 136 GAGCTGTGAGTGTGAGTGTGCAATCTATGACAGTGGCAACACTTCTCTGAGACTGAC 195
QY 184 AAGAGTGAATTAATCATGTCACTGAGACAGCTGTAAAGACCACTTCTCTGAGACTGAC 243
DB 196 AAGAGTGAATTAATCATGTCACTGAGACAGCTGTAAAGACCACTTCTCTGAGACTGAC 255
QY 244 TCTGTGACTGCGCGGAGCAACGCGCTGTATTACTGTGCGCGGTGCAATGGGATTA 303
DB 256 TCTGTGACTGCGCGGAGCAACGCGCTGTATTACTGTGCGCGGTGCAATGGGATTA 315
QY 304 GACAACCTGGGCGCAGGGAACCTGTGTCAACCGTCTCTCA 342
DB 316 GACTACTGGGCGCAGGGAACCTGTGTCAACCGTCTCTCA 354

RESULT 5 355 bp mRNA linear PRI 03-JUL-2004
AY640580
LOCUS Homo sapiens clone RU immunoglobulin E variable region mRNA,
partial cds.
ACCESSION AY640580
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Coker, H.A., Durham, S.R. and Gould, H.J.
1 (bases 1 to 355)
REFERENCE
AUTHORS Biased use of VHS IGE+ B cells in the nasal mucosa of allergic
rhinitis patients
TITLE
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 355)
AUTHORS Coker, H.A., Durham, S.R. and Gould, H.J.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St
Thomas Street, London SE1 1UL, UK

FEATURES
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CDS

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ORIGIN YPBYMGQGLIVTVSS"

Query Match 83.2%; Score 284.6; DB 9; Length 355;
Best Local Similarity 90.0%; Pred. No. 5.8e-73;
Matches 305; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGAGACTGTGTGAAGCCTTCACAGACCCTGTCCCTCACCTGACTGTCTCT 63
DB 16 GAGTCGGGCCCAAGACAGTGTGTGAAGCCTTCACAGACCCTGTCCCTCACCTGACTGTCTCT 75
QY 64 GGTGGCTCCATCCGACAGTGTGTATTTATTTGAGTTGGGTGGGCGGCGACGCTCCAGGGAG 123
DB 76 GGTGGCTCCATCCGACAGTGTGTATTTATTTGAGTTGGGTGGGCGGCGACGCTCCAGGGAG 135
QY 124 GGCTGAGTGGATCGGCAACATCTATTCACAGTGGCAACACCTTCAACACCCTCCCTC 183
DB 136 GGCTGAGTGGATCGGCAACATCTATTCACAGTGGCAACACCTTCAACACCCTCCCTC 195
QY 184 AAGAGTGAATTACCATGTCTAGTACAGACGTCTAAGAACCACTTCTCTGAGACTGACC 243
DB 196 AAGAGTGAATTACCATGTCTAGTACAGACGTCTAAGAACCACTTCTCTGAGACTGACC 255
QY 244 TCTGTGACTGCCGGGACAGCGCGCTATTTACTGTGCGGGTCAAGATGGGTATACCTTG 303
DB 256 TCTGTGACTGCCGGGACAGCGCGCTATTTACTGTGCGGGTCAAGATGGGTATACCTTG 315
QY 304 GACAACTGGGGCCAGGGAACCTGTGACCGTCTCTCA 342
DB 316 GACTACTGGGGCCAGGGAACCTGTGACCGTCTCTCA 354

RESULT 6 355 bp mRNA linear PRI 03-JUL-2004
LOCUS AY640509
DEFINITION Homo sapiens clone BM immunoglobulin E variable region mRNA,
partial cds.
ACCESSION AY640509
VERSION AY640509.1 GI:49354765
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Coker,H.A., Durham,S.R. and Gould,H.J.
1 (bases 1 to 355)
REFERENCE
AUTHORS Biased use of VHS Igb+ B cells in the nasal mucosa of allergic
TITLE rhinitis patients
JOURNAL Unpublished
2 (bases 1 to 355)
REFERENCE
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St
Thomas Street, London SE1 1UL, UK
FEATURES
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rhinitis patients"
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Query Match 82.3%; Score 281.4; DB 9; Length 355;

Best Local Similarity 89.4%; Pred. No. 5.1e-72;
Matches 303; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGAGACTGTGTGAAGCCTTCACAGACCCTGTCCCTCACCTGACTGTCTCT 63
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QY 64 GGTGGCTCCATCCGACAGTGTGTATTTATTTGAGTTGGGTGGGCGGCGACGCTCCAGGGAG 123
DB 76 GGTGGCTCCATCCGACAGTGTGTATTTATTTGAGTTGGGTGGGCGGCGACGCTCCAGGGAG 135
QY 124 GGCTGAGTGGATCGGCAACATCTATTCACAGTGGCAACACCTTCAACACCCTCCCTC 183
DB 136 GGCTGAGTGGATCGGCAACATCTATTCACAGTGGCAACACCTTCAACACCCTCCCTC 195
QY 184 AAGAGTGAATTACCATGTCTAGTACAGACGTCTAAGAACCACTTCTCTGAGACTGACC 243
DB 196 AAGAGTGAATTACCATGTCTAGTACAGACGTCTAAGAACCACTTCTCTGAGACTGACC 255
QY 244 TCTGTGACTGCCGGGACAGCGCGCTATTTACTGTGCGGGTCAAGATGGGTATACCTTG 303
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QY 304 GACAACTGGGGCCAGGGAACCTGTGACCGTCTCTCA 342
DB 316 GACTACTGGGGCCAGGGAACCTGTGACCGTCTCTCA 354

RESULT 7 355 bp mRNA linear PRI 03-JUL-2004
LOCUS AY640579
DEFINITION Homo sapiens clone RT immunoglobulin E variable region mRNA,
partial cds.
ACCESSION AY640579
VERSION AY640579.1 GI:49354899
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Coker,H.A., Durham,S.R. and Gould,H.J.
1 (bases 1 to 355)
REFERENCE
AUTHORS Biased use of VHS Igb+ B cells in the nasal mucosa of allergic
TITLE rhinitis patients
JOURNAL Unpublished
2 (bases 1 to 355)
REFERENCE
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St
Thomas Street, London SE1 1UL, UK
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/organism="Homo sapiens"
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patients"
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Query Match 82.3%; Score 281.4; DB 9; Length 355;
Best Local Similarity 89.4%; Pred. No. 5.1e-72;
Matches 303; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGAGACTGTGTGAAGCCTTCACAGACCCTGTCCCTCACCTGACTGTCTCT 63

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Db 16 GAGTCGGAGCCAGAGACGTGGTAACCTTCACAGACCCTGTCCTCAGCTGCTCT 75
Qy 64 GGTGGCTCCATCCGACAGTGGTATTATATGAGTTGGGTCGCGCAGCCCTCCAGGGAG 123
Db 76 GGTGGCTCCATCAGACAGTGGTATTATGAGTTGGGTCGCGCAGCCCTCCAGGGAG 135
Qy 124 GGCCTGGAGTGGATCGGCAACATCTATCAGATGGCAACCTTCAACACCCGCTCCCTC 183
Db 136 GGCCTGGAGTGGATCGGCAACATCTATCAGATGGCAACCTTCAACACCCGCTCCCTC 195
Qy 184 AAGAGTGAATTACATGTCAGTGAACAGCTCTAAGAACCACTTCTCCTGAGACTGACC 243
Db 196 AAGAGTGAATTACATGTCAGTGAACAGCTCTAAGAACCACTTCTCCTGAGACTGACC 255
Qy 244 TCTGTGACTGCGCGGACAGCGCCGTCTATCTGTGCGGGGTGAGATGGGTATACCTTGG 303
Db 256 TCTGTGACTGCGCGGACAGCGCCGTCTATCTGTGCGGGGTGAGATGGGTATACCTTGG 315
Qy 304 GACAACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342
Db 316 GACTACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 354
RESULT 8 355 bp mRNA linear PRI 03-JUL-2004
AY640564
LOCUS Homo sapiens clone RE immunoglobulin E variable region mRNA,
DEFINITION partial cds.
ACCESSION AY640564
VERSION AY640564.1 GI:49354872
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.
TITLE Biased use of VH5 IGE+ B cells in the nasal mucosa of allergic
rhinitis patients
JOURNAL Unpublished
REFERENCE 2. (bases 1 to 355)
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St
Thomas Street, London SE1 1UL, UK
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Query Match 81.8%; Score 279.8; DB 9; Length 355;
Best Local Similarity 89.1%; Pred. No. 1.5e-71;
Matches 302; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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Db 76 GGTGGCTCCATCAGACAGTGGTATTATGAGTTGGGTCGCGCAGCCCTCCAGGGAG 135
Qy 124 GGCCTGGAGTGGATCGGCAACATCTATCAGATGGCAACCTTCAACACCCGCTCCCTC 183
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Qy 244 TCTGTGACTGCGCGGACAGCGCCGTCTATCTGTGCGGGGTGAGATGGGTATACCTTGG 303
Db 256 TCTGTGACTGCGCGGACAGCGCCGTCTATCTGTGCGGGGTGAGATGGGTATACCTTGG 315
Qy 304 GACAACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342
Db 316 GACTACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 354
RESULT 9 355 bp mRNA linear PRI 03-JUL-2004
AY640507
LOCUS Homo sapiens clone BK immunoglobulin E variable region mRNA,
DEFINITION partial cds.
ACCESSION AY640507
VERSION AY640507.1 GI:49354762
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.
TITLE Biased use of VH5 IGE+ B cells in the nasal mucosa of allergic
rhinitis patients
JOURNAL Unpublished
REFERENCE 2. (bases 1 to 355)
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St
Thomas Street, London SE1 1UL, UK
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ORIGIN
Query Match 80.4%; Score 275; DB 9; Length 355;
Best Local Similarity 88.2%; Pred. No. 4e-70;
Matches 299; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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Db      136  GGCCTGAGAGTGGATGATCATCTATTACAGGGGAGACCTTACTCAACCCGCTCCCTC 195
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Db      196  AGGAGTCGAATTAATCATGTCATTAATGACACGCTTCAATAGATGTTCTCCCTGAGGCTGACC 255
Qy      244  TCTGTGCTGCGCCGGGACACAGCGCGCTCTATTACTGTGTGCGGGGTAGATGGGTATACCTTTG 303
Db      256  TCTCTGACTGCGCCGACACAGCGCGGTATTTCTGTGCGGCTCTAATGAGGTACAGTTTG 315
Qy      304  GACAACTGGGGCCAGGAAACCTTGTCACCGTCTCTCA 342
Db      316  GACTACTGGGGCCAGGAAACCTTGTCACCGTCTCTCA 354

RESULT 10
HSA491911      432 bp  mRNA  linear  PRI 20-NOV-2003
LOCUS          Homo sapiens mRNA for immunoglobulin heavy chain V-D-J-Ce region
DEFINITION     (Clome HD17 C9) .
ACCESSION      AJ491911
VERSION        AJ491911.1 GI:24415808
KEYWORDS       constant region; epsilon chain; IGH gene; immunoglobulin heavy
SOURCE         chain; variable region.
ORGANISM       Homo sapiens (human)
REFERENCE       1
AUTHORS        Coker, H.A., Durham, S.R. and Gould, H.J.
TITLE          Local somatic hypermutation and class switch recombination in the
JOURNAL        J. Immunol. 171 (10), 5602-5610 (2003)
MEDLINE        22970235
PUBMED         14607969
REFERENCE       2 (bases 1 to 432)
AUTHORS        Coker, H.A.
TITLE          Direct Submission
JOURNAL        Submitted (26-JUN-2002) Coker H.A., Biomedical Sciences, Randall
                Centre, King's College London, Guy's Campus, London, SE1 1UL,
                UNITED KINGDOM
FEATURES       Location/Qualifiers
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Query Match      80.4%; Score 275; DB 9; Length 432;
Best Local Similarity 88.2%; Pred. No. 4e-70;
Matches 299; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
Qy      4  GAGCTTGCCCGACGACTGTGAAGCCCTTCACAGACCTGTGCTCACTGCTCTCT 63
Db      16  GAGTCGGGCCCGACGACTGTGAAGCCCTTCACAGACCTGTGCTCACTGCTCTCT 75
Qy      64  GGTGGCTCCATCCGCGTGGTGTATTATTAGTGGTGGTCCGACGCTCCAGGGAAG 123
Db      76  GGTGGCGCCATCAGTGTGTGTGTACTGTGAGCTGTGATCCGACGACCCAGGGAAG 135
Qy      124  GGCCTGAGTGTATCGGCAATCTATTCACAGTGGCAACACTTAACAACCCGTCCTC 183
Db      136  GGCCTGAGTGTATGGATATCATCTATTACAGGGGAGACACTTAACAACCCGTCCTC 195
Qy      184  AAGAGTCGAATTACCATGTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db      196  AGGAGTCGAATTAATCATGTCATTTGACAGCTGCAAAATCAGTTCCTGAGGCTGACC 255
Qy      244  TCTGTGACTGCGCCGGACACAGCGCGTCTATTACTGTGCGGGGTAGATGGGTATACCTTTG 303
Db      256  TCTCTGACTGCGCCGACACAGCGCGGTATTTCTGTGCGGCTCTAATGAGGTACAGTTTG 315
Qy      304  GACAACTGGGGCCAGGAAACCTTGTCACCGTCTCTCA 342
Db      316  GACTACTGGGGCCAGGAAACCTTGTCACCGTCTCTCA 354

RESULT 11
HSA491912      432 bp  mRNA  linear  PRI 20-NOV-2003
LOCUS          Homo sapiens mRNA for immunoglobulin heavy chain V-D-J-Ce region
DEFINITION     (Clome HD17 C37) .
ACCESSION      AJ491912
VERSION        AJ491912.1 GI:24415810
KEYWORDS       constant region; epsilon chain; IGH gene; immunoglobulin heavy
SOURCE         chain; variable region.
ORGANISM       Homo sapiens (human)
REFERENCE       1
AUTHORS        Coker, H.A., Durham, S.R. and Gould, H.J.
TITLE          Local somatic hypermutation and class switch recombination in the
JOURNAL        J. Immunol. 171 (10), 5602-5610 (2003)
MEDLINE        22970235
PUBMED         14607969
REFERENCE       2 (bases 1 to 432)
AUTHORS        Coker, H.A.
TITLE          Direct Submission
JOURNAL        Submitted (26-JUN-2002) Coker H.A., Biomedical Sciences, Randall
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                UNITED KINGDOM
FEATURES       Location/Qualifiers
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Best Local Similarity 87.9%; Pred. No. 1.2e-69;
Matches 298; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGGAGCTGGTGAAGCCTTCACAGACCCGTGTCCTCAGCTGCTCT 63
Db 16 GAGTCGGGCCAGGAGCTGGTGAAGCCTTCACAGAACCTGTCCTCAGCTGCTCT 75
QY 64 GGTGGCTCCATCCGACAGTGGTGTATTATTGAGTTGGGTCCGCCAGCCTCCAGGAAG 123
Db 76 GGTGGCCCATCATATGTTGGTGTACTACTGAGCTGGATCCGCCAGCACCCAGGAAG 135
QY 124 GGCCTGAGTGAATCGGCAACATCTATCAAGTGGCAACACCTTACAAACCCGTCCTC 183
Db 136 GGCCTGAGTGAATGATATCATCTATTAACAGGGGAGACCTTACAAACCCGTCCTC 195
QY 184 AAGAGTGAATTATCATGTGCTAGTGAACACGCTAAGAACCTTCTCCCTGAGCTAGC 243
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Db 316 GACTACTGGGGCCAGGGAACCTTGCTCAACCTCTCCCTCA 354

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RESULT 12
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LOCUS
DEFINITION Homo sapiens mRNA for immunoglobulin gamma heavy chain variable
region, partial, clone 2-D123.
ACCESSION AJ245064
VERSION AJ245064.1 GI:4995589
KEYWORDS Igg; Igg heavy chain; immunoglobulin gamma heavy chain; variable
region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS Dono, M., Zupo, S., Chiocazzi, N. and Ferrarini, M.
TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalents
JOURNAL Unpublished
2 (bases 1 to 354)
Dono, M.
REFERENCE
1
AUTHORS Direct Submission
TITLE Submitted (24-MAY-1999) Dono, M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova,
ITALY
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Best Local Similarity 87.6%; Pred. No. 3.5e-69;
Matches 297; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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QY 124 GGCCTGAGTGAATCGGCAACATCTATCAAGTGGCAACACCTTACAAACCCGTCCTC 183
Db 136 GGCCTGAGTGAATGATATCATCTATTAACAGGGGAGACCTTACAAACCCGTCCTC 195
QY 184 AAGAGTGAATTATCATGTGCTAGTGAACACGCTAAGAACCTTCTCCCTGAGCTAGC 243
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QY 244 TCTGTGACCTGCCGCGACAGCGCCCTCTATTACTGTCGGCGTCAGATGGTATACCTTG 303
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 QY 304 GACAACTGGGGCCAGGAAACCTGTCACCGTCTCTCA 342
 DB 316 GACTACTGGGGCCAGGAGCCCTGTGTACCGTCTCTCA 354
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 VERSION AF062112.1 GI:3170686
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Wang, X. and Stollar, B. D.
 TITLE Immunoglobulin VH gene expression in human aging
 JOURNAL Clin. Immunol. 93 (2), 132-142 (1999)
 MEDLINE 99459182
 PUBMED 10527689
 REFERENCE
 AUTHORS Wang, X. and Stollar, B. D.
 TITLE Direct Submission
 JOURNAL Submitted (22-APR-1998) Biochemistry Department, Tufts University
 School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
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 QY 4 GAGTCTGGCCAGAGCTGTGAAGCTTTACAGACCCGTGCTCCTGACCTGACGTCTCT 63
 DB 73 GAGTCGGGCCAGAGCTGTGAAGCTTTACAGACCCGTGCTCCTGACCTGACGTCTCT 132
 QY 64 GGTGGCTCCATCCGACGTGTGTTATTATTTGAATTGGATGGATCCGACGCTCCAGGAG 123
 DB 133 GGTGGCTCCATCCGACGTGTGTTATTATTTGAATTGGATGGATCCGACGCTCCAGGAG 192
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DB 193 GGCTGAGATGATGGATGATCATCTATTACAGTGGAGCACTTAACAACCCGCTCCTC 252
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 DB 373 GACTACTGGGGCCAGGAGCCCTGTGTACCGTCTCTCA 411
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 T22.1).
 DEFINITION 275385
 ACCESSION 275385.1 GI:2062048
 VERSION 275385
 KEYWORDS immunoglobulin; immunoglobulin heavy chain; immunoglobulin
 superfamily; variable region.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Tonnelle, C., D'Ercole, C., Deprettere, V., Metras, D., Boubli, L. and
 Fougerneau, M.
 TITLE Human thymic B cells largely overexpress the VH4 Ig gene family. A
 possible role in the control of tolerance in situ?
 JOURNAL Int. Immunol. 9 (3), 407-414 (1997)
 MEDLINE 97244170
 PUBMED 9088979
 REFERENCE
 AUTHORS Tonnelle, C.
 TITLE Direct Submission
 JOURNAL Submitted (26-JUN-1996) Cecile Tonnelle, Centre d'Immunologie
 Marseille Luminy, Marseille, 13288, France
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 Best Local Similarity 87.6%; Pred. No. 7e-69;
 Matches 296; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
 QY 4 GAGTCTGGCCAGAGCTGTGAAGCTTTACAGACCCGTGCTCCTGACCTGACGTCTCT 63
 DB 73 GAGTCGGGCCAGAGCTGTGAAGCTTTACAGACCCGTGCTCCTGACCTGACGTCTCT 132
 QY 64 GGTGGCTCCATCCGACGTGTGTTATTATTTGAATTGGATGGATCCGACGCTCCAGGAG 123
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QY 124 GGCTGGAGTGGATCGGCAACATCTATACAGTGGCAACCTTCAACAAACCCGCTCCCTC 183
DB 193 GGCTGGAGTGGATGGGTGATCATCTATTACAGTGGGAGACCTTCAACACCGCTCCCTC 252
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DB 253 AAGAGTGGAGTTACCATATCATGATAGACACCGCTAAGAACCGATTTCTCCCTGAACTGAGC 312
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DB 313 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGGCGGTGAGATGGGTATCTTGG 372
QY 304 GACCACTGGGCGCAGGAGACCGTGTGACCGCTCTCTC 341
DB 373 TCCAGCTGGGCGCAGGAGACCGTGTGACCGCTCTCTC 410

RESULT 15
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LOCUS Synthetic construct clone 7-161VH rotavirus VP7-specific antibody
DEFINITION heavy chain variable region mRNA, partial sequence.
ACCESSION AF452917
VERSION AF452917.1 GI:25988060
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 403)
AUTHORS Weikamp,J.H., Kallewaard,N., Kusuhara,K., Bures,E., Williams,J.V.,
Lapleur,B., Greenberg,H.B. and Crowe,J.E. Jr.
TITLE Infant and adult human B cell responses to rotavirus share common
immunodominant variable gene repertoires
JOURNAL J. Immunol. 171 (9), 4680-4688 (2003)
MEDLINE 22930557
PUBMED 14568943
REFERENCE 2 (bases 1 to 403)
AUTHORS Weikamp,J.H. and Crowe,J.E. Jr.
TITLE Direct Submission
SUBMITTED (28-NOV-2001) Pediatrics, Vanderbilt University Medical
Center, 1161 21st Avenue South, D-7235 Medical Center North,
Nashville, TN 37232-2581, USA
FEATURES
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sequence from Homo sapiens mRNA"
1. .>403
/note="rotavirus VP7-specific antibody heavy chain
variable region"

ORIGIN
Query Match 78.7%; Score 269, DB 12, Length 403;
Best Local Similarity 88.9%; Pred. No. 2.4e-68;
Matches 303; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

QY 5 AGTCTGGCCGAGAGTGGTGAAGCTTCAAGACCTTCCCTCAGCTGCACTGCTCTG 64
DB 42 AGTCTGGCCGAGAGTGGTGAAGCTTCAAGACCTTCCCTCAGCTGCACTGCTCTG 101
QY 65 GTGGCTCATCCGAGTGGTGTATTATTGAGTTGGGTCCGCCAGGCTCCAGGGAAG 124
DB 102 GTGGCTCATCCGAGTGGTGTATTATTGAGTTGGGTCCGCCAGGCTCCAGGGAAG 161
QY 125 GCCTGGAGTGGATGGGCAACATCTATCAGTGGCAACCTTCAACAAACCCGCTCCCTCA 184
DB 162 GCCTGGAGTGGATGGGCAACATCTATCAGTGGGAGCACTTCAACAAACCCGCTCCCTCA 221
QY 185 AGAGTGAATTACCATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACCT 244

DB 222 AGAGTGAATTACCATATTCAGTACACGCTTAAGAACCACTTCTCCCTGAGACTGACCT 281
QY 245 CTGTGACTGCGCGGACACGCGCGTCTATTACTGTGG---CGGTGAGATGGGTACTT 301
DB 282 CTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGAGTGGCTACGGCTGACT 341
QY 302 TGGACAACTGGGCGCAGGGAACCTTGTGACCGTCTCTCTCA 342
DB 342 TTGACTACTGGGCGCAGGGAACCTTGTGACCGTCTCTCTCA 382

Search completed: July 27, 2005, 09:08:38
Job time : 1956.83 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:15:56 ; Search time 2106.58 Seconds
(without alignments)
6179.670 Million cell updates/sec

Title: US-10-027-725A-2

Perfect score: 342
Sequence: 1 ctcgagctcgtgccaccagact.....ccctgacacgcctcctca 342

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hnc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_ges1.*
9: gb_ges2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	263.8	77.1	832	1	AU122174
2	250.8	73.3	509	2	AM406349
3	250.2	73.2	369	2	AM404242
4	250.2	73.2	677	4	BG686767
5	249.6	73.0	607	4	BM783015
6	248.2	72.6	490	6	CD689564
7	241.4	70.6	725	4	BG431274
8	241.2	70.5	643	1	AU134293
9	240	70.2	904	5	BQ710488
10	239.8	70.1	959	5	BQ899307
11	238.2	69.6	1108	5	BQ706579
12	238.2	69.6	1108	5	BM920469
13	237	69.3	914	4	BG757054
14	237	69.3	939	5	BQ708070
15	236.4	69.1	828	4	BF974568
16	235.2	68.8	447	2	AM402200
17	234.8	68.7	596	4	BM817833
18	234.8	68.7	813	5	BQ710364
19	234.6	68.6	582	2	AM401348
20	234.6	68.6	814	4	BG685325
21	233.6	68.3	508	7	CR747031
22	233.6	68.3	1019	5	BQ072420
23	233.6	68.3	1195	5	BQ07644
24	233.4	68.2	474	2	AM408410

25	233.4	68.2	915	5	BQ706358
26	233.2	68.2	658	5	BX505812
27	232.8	68.1	421	2	AM407630
28	232	67.8	363	2	AM403420
29	232	67.8	915	5	BQ711871
30	232	67.8	923	5	BQ707945
31	232	67.8	928	5	BQ707875
32	232	67.8	959	5	BQ709473
33	231.8	67.8	924	5	BQ708516
34	231.6	67.7	924	4	BG758027
35	231.6	67.7	987	5	BQ707970
36	231.4	67.7	650	4	BG684403
37	231.4	67.7	778	4	BF975836
38	231.4	67.7	929	4	BG341823
39	231	67.5	524	5	BU429270
40	231	67.5	856	5	BQ421299
41	230.6	67.4	661	4	BG686421
42	230.6	67.4	921	5	BQ710000
43	230.6	67.4	959	4	BG757666
44	230	67.3	542	2	AM951834
45	229.8	67.2	435	2	BF871158

ALIGNMENTS

RESULT 1	AU122174	832 bp	mRNA	linear	EST 01-AUG-2002
LOCUS	AU122174				
DEFINITION	AU122174	MAMMAL	Homo sapiens	CDNA clone	MAMMAL001802 5', mRNA
ACCESSION	AU122174				
VERSION	AU122174.1	GI:10937409			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,O., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.				
AUTHORS	Unpublished (2000)				
TITLE	HRI human CDNA project				
JOURNAL	Genomics Laboratory				
COMMENT	Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human CDNA project, 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.				
FEATURES	Location/Qualifiers				
source	1..832				
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	/tissue_type="mammary gland"				
	/clone_lib="MAMMAL"				
	/note="Vector: pME18SF13"				
ORIGIN					
Query Match	77.1%; Score 263.8; DB 1; Length 832;				
Best Local Similarity	86.1%; Pred. No. 3.2e-67;				
Matches	292; Conservative 0; Mismatches 47; Indels 0; Gaps 0;				
OY	4 GAGTCTGGCCAGGACGTGTAAGCCTTCACAGACCTTCACCTGCTCCTGACCTGCTCTCT 63				
DB	110 GAGTCTGGCCAGGACGTGTAAGCCTTCACAGACCTTCACCTGCTCCTGACCTGCTCTCT 169				

QY	64	GGTGGATCCATCCCGAGTGGGTATATATATGGAGTTGGATCGGACACTTCAGGGAA	123
Db	170	GGTGGCTCCATCAGCAGTGTGACGCCCTACTGGAGTTGGATTCGGCAGCCCCAGGAA	229
QY	124	GGCTCGAGTGGATCGGCACATCTATCAAGTGGCAACACTTACACAAACCCGCTC	183
Db	230	GGCTCGAGTGGATGGTGTACATCTATTAACAATGGGAACACTTACAAACCCGCTC	289
QY	184	AAGATCGAATTACATGTCAGTATGACACGTCCTAAGAACCACTTCCCTGAGACTGACC	243
Db	290	AAGATCGAATTACATGTCAGTATGACACGTCCTAAGAACCACTTCCCTGAGACTGAAAC	349
QY	244	TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGGTCAGATGGGTATATCTTTG	303
Db	350	TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGCAATCATATTAACAACGAGGG	409
QY	304	GACAACTGGGGCAGGGAAACCTGGTCAACCGCTCTCTCA	342
Db	410	GACTTCTGGGCGCAGGGAAACCTGGTCAACCGCTCTATCA	448

RESULT 2	AM406349	AM406349	509 bp	mRNA	linear	EST 16-FEB-2000
LOCUS						
DEFINITION		UI-HF-BL0-aco-h-03-0-UI.r1 N1H_MGC_3'				Homio sapiens cDNA clone
ACCESSION		AM406349				
VERSION		AM406349.1				GI:6925406
KEYWORDS		EST.				
SOURCE		Homio sapiens				
ORGANISM		Homio sapiens				

REFERENCE
1 (bases 1 to 509)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

ECO RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.llnl.gov/bdrip/image/image.html
Seq primer: M13 Forward.

FEATURES	Location/Qualifiers
source	1. .509

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3059933"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LT1)"
/clone_id="NH_MGC_37"
/notes="Vector: pRTT3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

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Query Match	73.3%	Score 250.8	DB 2	Length 509
Best Local Similarity	85.4%	Pred. No. 21e-63		
Matches 292	Conservative	0	Mismatches 47	Indels 3
				Gaps 1

4 GAGTGTGGCCGAGCACTGGTGAAGCTTCACAGAGCCCTGCTCTACTGTGACTGTCTCT 63
 |||||

Db	54	GAGTGGGGCCAGGACGTGTGAAGCGCTTGGGAGACCCGTGCTCCCTCACTGCACATGCTCTCTC	113
Qy	64	GGTGGCTCATCCGAGGTGGTGGTTATATTATGAGATTTGGGTGGCGCAGGCTCCAGGGAA	123
Db	114	GGTGGCTCATCAGCATGATGATGTTACTACTGGGGCTGGATTCGCCAGGCCCCAGGAAAG	173
Qy	124	GGCCTGAGTGGATCGGCAACATCTATCACTGTGCAACCTTACACAAACCCGTCTC	183
Db	174	GGCGCTGAGTGGATTGGGAGTATCTATTATAGTGGAGACCTTACTACAAACCCGTCTC	233
Qy	184	AAGATGCAATTACCATGTCACTAGTACACGCTAGAAACCATCTTCCCTGAGACTGACC	243
Db	234	AAGATCGATGACCATATTCAGTAAACACGCTCAAGAACCAAGTTCTCCCTGAAGCTGAGC	293
Qy	244	TCTGTGACTGCCCGGACACGGCGCTCTATTACTGTGCG--CGGTCAATGGGTACT	300
Db	294	TCTGTGACCGCGCGAGACACGGCGCTCTATTACTGTGCGAGAACCCCTCTTACGGA	353
Qy	301	TTTGGACACTGGGGCCAGGAAACCTTGGTCAACGCTCTCTCA	342
Db	354	TTCGACCCCTGGGGCCAGGAAACCTTGGTCAACGCTCTCTCA	395

RESULT 3	369 bp	mRNA	linear	EST 16-FEB-2000
AM404242				
LOCUS	AM404242			
DEFINITION	UI-HF-BL0-abq-f-09-0-UI.r1 NIH_MCC_37 Homo sapiens cDNA clone IMAGE:3057545 5', mRNA sequence.			
ACCESSION	AM404242			
VERSION	AM404242.1	GI:5923299		
KEYWORDS	EST.			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens (human)			
	Homo sapiens			

REFERENCE 1 (bases 1 to 369)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

PCR reaction shown at the beginning of the figure.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdnp/image/image.html
 Seq primer: M13 Forward.

FEATURES	Location/Qualifiers
source	1. .369

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/mol_type="mRNA"
/db_xref="taxon:9606"
/cclone="IMAGE:3057545"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LRI)"
/clone_lib="NH MGC 37"
/ncore="vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

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ORIGIN	Query Match	73.2%	Score 250.2	DB 2	Length 369
	Best Local Similarity	86.5%	Pred. No. 3e-63		
	Matches 276	0	Mismatches 43	Indels 0	Gaps 0
QY	4 GAGTCGTGCGCCAGAGCATGCTGAGAGCCCTTCACCTGACCTGACATGTCTCT 63				

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Db 34 GAGTCGGGCCCCAGACAGCTGTAAACCTTCACAGACCCCTGTCCTCACCCTGACCTGCTCT 93
Qy 64 GGTGGCTCCATCCGACAGTGGTGTATTTATTTAGATTGGGTGGCGGACGCCCTCAGGGAG 123
Db 94 GGTGGCTCCATCCGACAGTGGTGTATTTATTTAGATTGGGTGGCGGACGCCCTCAGGGAG 153
Qy 124 GGCCTGGAGTGGATCGGCAACATCTATACAGTGGCAACACTTAACAACCCCTCCCTC 183
Db 154 GGCCTGGAGTGGATCGGCAACATCTATACAGTGGCAACACTTAACAACCCCTCCCTC 213
Qy 184 AAGAGTGAATTACCATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGACTAGC 243
Db 214 AAGAGTGGCTTACCATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAACTAGC 273
Qy 244 TCTGTGACTGCGCGGACACGCGCTCTATCTACCTGGCGGCTCAGATGGTATACCTTG 303
Db 274 TCTGTGACTGCGCGGACACGCGCTCTATCTACCTGGCGGCTCAGATGGTATACCTTT 333
Qy 304 GACAACTGGGGCCAGGAA 322
Db 334 GATAGTAGTGTTACGGA 352

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RESULT 4 677 bp mRNA linear EST 01-MAY-2001
BG686767
LOCUS 602650737F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763217 5',
DEFINITION mRNA sequence.
ACCESSION BG686767
VERSION BG686767.1 GI:13918164
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 677)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rgs@biml.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LNCM618 row: 1 column: 10
High quality sequence stop: 675.
Location/Qualifiers
1. 677
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4763217"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 48"
/notes="Organ: B-cells; Vector: pORF7; Site 1: XhoI;
Site 2: EcoRI. cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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ORIGIN
Query Match 73.2%; Score 250.2; DB 4; Length 677;
Best Local Similarity 87.0%; Pred. No. 3.4e-63;

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Matches 300; Conservative 0; Mismatches 38; Indels 7; Gaps 2;
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Db 99 GAGTCTGGCCAGGACTGTGAAGCCCTTCAACAAGCCCTGTCCCTCACTGACTGTCT 158
Qy 64 GGTGGCTCCATCCGACAGTGGTGTATTTATTTAGATTGGGTGGCGGACGCCCTCAGGGAG 123
Db 159 GGTGGCTCCATCCGACAGTGGTGTATTTATTTAGATTGGGTGGCGGACGCCCTCAGGGAG 217
Qy 124 GGCCTGGAGTGGATCGGCAACATCTATACAGTGGCAACACTTAACAACCCCTCCCTC 183
Db 218 GGCCTGGAGTGGATCGGCAACATCTATACAGTGGCAACACTTAACAACCCCTCCCTC 277
Qy 184 AAGAGTGAATTACCATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGACTAGC 243
Db 278 AAGAGTGAATTACCATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGACTAGC 337
Qy 244 TCTGTGACTGCGCGGACACGCGCTCTATCTACCTGGCGGCTCAGATGGTAT 297
Db 338 TCTGTGACTGCGCGGACACGCGCTCTATCTACCTGGCGGCTCAGATGGTAT 397
Qy 298 ACTTGGACAACCTGGGCGCAGGGAACTTGGTCACTCTCTCTCA 342
Db 398 GGGTTGACCCCTGGGCGCAGGGAACTTGGTCACTCTCTCTCA 442

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RESULT 5 607 bp mRNA linear EST 05-MAR-2002
BM783015
LOCUS K-EST060735 S18N669761 Homo sapiens cDNA clone S18N669761-2-E06
DEFINITION 5', mRNA sequence.
ACCESSION BM783015
VERSION BM783015.1 GI:19131247
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 607)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boseun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@mail.krdb.re.kr
Plate: 2 row: E column: 06
High quality sequence stop: 607.
Location/Qualifiers
1. 607
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="S18N669761-2-E06"
/sex="F"
/lab_host="Top10P"
/clone_lib="S18N669761"
/notes="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deapped
with tobacco acid pyrophosphatase (TAP). The deapped
inact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of

```

ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells *E. coli* Top10[®] by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 73.0%; Score 249.6; DB 4; Length 607;
Best Local Similarity 84.8%; Pred. No. 5e-63;
Matches 295; Conservative 0; Mismatches 44; Indels 9; Gaps 1;

QY 4 GAGTCTGGCCAGGACGCTGGAAGCCCTTCACAGCCCTGTCCTCAGCTGCTCT 63
DB 112 GAGTCGGGCCCCAGACGCTGGAAACCTTCACAGACCTGTCCTCAGCTGCTCT 171
QY 64 GGTGGCTCCATGAAACAGTGGTATTATTTGAGTTGGGCGGCCAGCCCTCCAGGAG 123
DB 172 GGTGGCTCCATGAAACAGTGGTATTATTTGAGTTGGGCGGCCAGCCCTCCAGGAG 231
QY 124 GGCCTGGAGTGAATGGGCAACATCTATCAGAGTGGCAACCTTACAAACCCGCTCC 183
DB 232 GGCCTGGAGTGAATGGGCAACATCTATCAGAGTGGCAACCTTACAAACCCGCTCC 291
QY 184 AAGAGTGAATTTACATGCTGATGACACGCTTAAAGAACCTTCTCCCTGAGACTGAC 243
DB 292 AAGAGTGAATTTACATGCTGATGACACGCTTAAAGAACCTTCTCCCTGAGACTGAC 351
QY 244 TCTGTGACTGCGCGGACACGCGCGCTATATTACTGTCGCGG-----GTGATGGG 294
DB 352 TCTGTGACTGCGCGGACACGCGCGCTATATTACTGTCGAGATGGCAATTACGATTT 411
QY 295 TATACCTTGGACCACTGGGCGCAGGAAACCTGTGTCACCTGCTCTCA 342
DB 412 TAGCGTATGACGCTGTGGGGCAAGGACCAACGCTGACCGCTCTCTCA 459

RESULT 6 490 bp mRNA linear EST 25-JUN-2003
LOCUS CD689564
DEFINITION EST6087 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD689564
VERSION CD689564.1 GI:32209443
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 490)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 DongFeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gszsums.edu.cn.

FEATURES
source
1. .490
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="normal nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

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Best Local Similarity 85.0%; Pred. No. 1.2e-62;

Matches 290; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 5 AGTGTGCCCCAGGACGCTGGAAGCCCTTCACAGACCTGTCCTCAGCTGCTCTG 64
DB 111 AGTCGGGCCCCAGGACGCTGGAAGCCCTTCACAGACCTGTCCTCAGCTGCTCTG 170
QY 65 GTGGCTTCATCCGCAATGGTGGTATTATTTGAGTTGGGCGGCCAGCCCTCCAGGAGG 124
DB 171 GTGACTTCATCAGACAGTGGTGGTATTATTTGAGTTGGGCGGCCAGCCCTCCAGGAGG 230
QY 125 GGCCTGGAGTGAATGGGCAACATCTATCAGAGTGGCAACCTTACAAACCCGCTCC 184
DB 231 GGCCTGGAGTGAATGGGCAACATCTATCAGAGTGGCAACCTTACAAACCCGCTCC 290
QY 185 AAGTGAATTTACATGCTGATGACACGCTTAAAGAACCTTCTCCCTGAGACTGAC 244
DB 291 AAGTGAATTTACATGCTGATGACACGCTTAAAGAACCTTCTCCCTGAGACTGAC 350
QY 245 CTGTGACTGCGCGGACACGCGCGCTATATTACTGTCGCGGCTCAGAT--GGTATCTT 301
DB 351 CTGTGACTGCGCGGACACGCGCGCTATATTACTGTCGAGATGGTCCCGAGCATTA 410
QY 302 TGGACAACTGGGCGCAGGGAACCTGGTCAACCGCTCTCTCA 342
DB 411 TTGACTACTGGGGCAGGGAATCTGCTCAGCTCTCTCA 451

RESULT 7 725 bp mRNA linear EST 14-MAR-2001
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DEFINITION 60249984F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:461345 5', mRNA sequence.
ACCESSION BG431274
VERSION BG431274.1 GI:13337780
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 725)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9abps-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1CM1363 row: h column: 12
High quality sequence stop: 716.
Location/Qualifiers

FEATURES
source
1. .725
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
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/clone_lib="IMAGE:461345"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Kidney; Vector: pDNR-LTB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAAGGCAATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGACGCGGCCGACATC-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 70.6%; Score 241.4; DB 4; Length 725;
Best Local Similarity 82.0%; Pred. No. 1.4e-60;
Matches 278; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 4 GAGTCTGAGCCAGAGCTGTGAGAGCTTACAGACCTGTGCTCCTGACCTGACTGTCTCT 63
DB 109 GAGTCTGAGCCAGAGCTGTGAGAGCTTACAGACCTGTGCTCCTGACCTGACTGTCTCT 168
QY 64 GGTGGCTCCATCCGAGAGTGTGTATTTATGAGTGGTGGTCCGACGCTCCAGGGAG 123
DB 169 GGTGGCTCCATCCGAGAGTGTGTATTTATGAGTGGTGGTCCGACGCTCCAGGGAG 228
QY 124 GGCCTGAGTGTGATGCGGACATCTATCAAGTGGGACACCTTCAACAAACCCGCTCC 183
DB 229 GGCCTGAGTGTGATGCGGACATCTATCAAGTGGGACACCTTCAACAAACCCGCTCC 288
QY 184 AAGAGTCGAATTACATGTCAATGAGACAGCTCTAAGAACACTTCTCCCTGAGACTGACC 243
DB 289 GAGAGTCGAATTCATATTCGTGAGACAGCTCAAGAACAGCTTCTCCCTGAGACTGAGG 348
QY 244 TCTGTGACTGCGCGGAGACAGCGCGCTCTATCTGTGCGGCTCAGATGGGTATATCTTG 303
DB 349 CCTGTGACCGCGGAGACAGCTCTGTATATTTATGAGAGTTCGCGGGGAGATT 408
QY 304 GACAACCTGGGCGGAGAACCTGTGACCGCTCTCTCA 342
DB 409 GACTATTGGGCGGAGAACCTGTGACCGCTCTCTCA 447

RESULT 8
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LOCUS AUI34293 Homo sapiens cDNA clone OVARC1001672 5', mRNA
DEFINITION AUI34293 OVARC1 Homo sapiens cDNA clone OVARC1001672 5', mRNA
Sequence.
ACCESSION AUI34293
VERSION AUI34293.1 GI:10994832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 643)
Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y.,
Yamamoto.J., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and
Isogai.T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomic@hri.co.jp
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. 643
/organism="Homo sapiens"
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/clone_lib="OVARC1"
/note="Vector: pME188FL1"

ORIGIN
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Best Local Similarity 82.9%; Pred. No. 1.6e-60;
Matches 295; Conservative 0; Mismatches 43; Indels 18; Gaps 1;

QY 5 AGTCTGCGCCAGAGCTGTGAGAGCTTACAGACCTGTGCTCCTGACCTGACTGTCTCTG 64
DB 110 AGTCTGCGCCAGAGCTGTGAGAGCTTACAGACCTGTGCTCCTGACCTGACTGTCTCTG 169
QY 65 GTGGCTCCATCCGAGAGTGTGTATTTATGAGTGGTGGTCCGACGCTCCAGGGAGG 124
DB 170 GTGGCTCCATCCGAGAGTGTGTATTTATGAGTGGTGGTCCGACGCTCCAGGGAGG 229
QY 125 GGCCTGAGTGTGATGCGGACATCTATCAAGTGGGACACCTTCAACAAACCCGCTCC 184
DB 230 GGCCTGAGTGTGATGCGGACATCTATCAAGTGGGACACCTTCAACAAACCCGCTCC 289
QY 185 AAGATCAATTACCATGTGATGAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGACC 244
DB 290 AAGATCAATTACCATGTGATGAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGAGG 349
QY 245 CTGTGACTGCGCGGAGACAGCGCGCTCTATTAATCTGTGCGGCTCAGATGGGTACT--- 300
DB 350 CTGTGACTGCGCGGAGACAGCGCGCTCTATTAATCTGTGCGGCTCAGATGGGTACT 409
QY 301 -----TTGAGACAATCTGGGCGGAGAACCTGTGATACCGCTCTCTCA 342
DB 410 GGAACCTAAGTAACTTGAACCACTGGGCGGAGAACCTGTGATACCGCTCTCTCA 465

RESULT 9
B0710488 904 bp mRNA linear EST 16-JUL-2002
LOCUS B0710488
DEFINITION AGENCOURT 8352970 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278137
5', mRNA sequence.
ACCESSION B0710488
VERSION B0710488.1 GI:21849387
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 904)
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
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High quality sequence stop: 728.
Location/Qualifiers
1. 904
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/clone_lib="NIH MGC 113"
/note="Organ: spleen; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC library."

ORIGIN
Query Match 70.2%; Score 240; DB 5; Length 904;
Best Local Similarity 83.0%; Pred. No. 3.9e-60;

Matches 289; Conservative 0; Mismatches 50; Indels 9; Gaps 1;

QY 4 GAGCTGGCCCAAGACTGTGTAAGCCCTTCACAGACCTGTCTCCCTGACCTGACGTCTCT 63
DB 86 GAGTCGGGCCCAAGACTGTGTAAGCCCTTCACAGACCTGTCTCCCTGACCTGACGTCTCT 145
QY 64 GGTGGCTCCATCCGACGTGTGTTATTATTGAGTTGGGTCCGCCACGCTCCAGGGAG 123
DB 146 GGTGGCTCCATCCGACGTGTGTTATTATTGAGTTGGGTCCGCCACGCTCCAGGGAG 205
QY 124 GGCTGGAGTGAATCGGCAACATCTATCAAGTGGCAACCTTCAACAACCCGTCTC 183
DB 206 GGCTGGAGTGAATCGGCAACATCTATCAAGTGGCAACCTTCAACAACCCGTCTC 265
QY 184 AAGAGTGAATTCATGTCAGTAGACACGTCTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 266 AAGAGTGAATTCATGTCAGTAGACACGTCTAAGAACCACTTCTCCCTGAGACTGACC 325
QY 244 TCTGTGACTCCCGGACACGGCCGTCTATTACTGTGTGGGAGAGACGACGACCTG 294
DB 326 TCTGTGACTCCCGGACACGGCCGTCTATTACTGTGTGGGAGAGACGACGACCTG 385
QY 295 TATCTTTGACACATGGGGCCAGGAAACCTGTGACCCGTCTCTCA 342
DB 386 CATCTCTCCAGCACTGGGGCCAGGACCTGTGACCCGTCTCTCA 433

RESULT 10
BU899307 959 bp mRNA linear EST 17-OCT-2002
LOCUS ABENCOURT_8532130 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6280128
DEFINITION 5', mRNA sequence.
ACCESSION BU899307
VERSION BU899307.1 GI:24081220
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 959)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
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High quality sequence stop: 605.
Location/Qualifiers

FEATURES
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/clone="IMAGE:6280128"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

Query Match

70.1%; Score 239.8; DB 5; Length 959;

Best Local Similarity 83.2%; Pred. No. 4.5e-60;
Matches 287; Conservative 0; Mismatches 52; Indels 6; Gaps 1;

QY 4 GAGCTGGCCCAAGACTGTGTAAGCCCTTCACAGACCTGTCTCCCTGACCTGACGTCTCT 63
DB 86 GAGTCGGGCCCAAGACTGTGTAAGCCCTTCACAGACCTGTCTCCCTGACCTGACGTCTCT 145
QY 64 GGTGGCTCCATCCGACGTGTGTTATTATTGAGTTGGGTCCGCCACGCTCCAGGGAG 123
DB 146 GGTGGCTCCATCCGACGTGTGTTATTATTGAGTTGGGTCCGCCACGCTCCAGGGAG 205
QY 124 GGCTGGAGTGAATCGGCAACATCTATCAAGTGGCAACCTTCAACAACCCGTCTC 183
DB 206 GGCTGGAGTGAATCGGCAACATCTATCAAGTGGCAACCTTCAACAACCCGTCTC 265
QY 184 AAGAGTGAATTCATGTCAGTAGACACGTCTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 266 AAGAGTGAATTCATGTCAGTAGACACGTCTAAGAACCACTTCTCCCTGAGACTGACC 325
QY 244 TCTGTGACTCCCGGACACGGCCGTCTATTACTGTGTGGGAGAGACGACGACCTG 297
DB 326 TCTGTGACTCCCGGACACGGCCGTCTATTACTGTGTGGGAGAGACGACGACCTG 385
QY 298 ACTTTGACACATGGGGCCAGGAAACCTGTGACCCGTCTCTCA 342
DB 386 GCTTTGATATCTGGGGCCAGGACATGTCACCGTCTCTCA 430

RESULT 11
B0706579 903 bp mRNA linear EST 16-JUL-2002
LOCUS ABENCOURT_8487944 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6300935
DEFINITION 5', mRNA sequence.
ACCESSION B0706579
VERSION B0706579.1 GI:21845478
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 903)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
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High quality sequence stop: 584.
Location/Qualifiers

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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:6300935"
/lab_host="DH10B (phage-resistant)"
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/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

ORIGIN

Query Match 69.6%; Score 238.2; DB 5; Length 903;
Best Local Similarity 82.9%; Pred. No. 1.3e-59;
Matches 286; Conservative 0; Mismatches 53; Indels 6; Gaps 1;

QY 4 GAGTCTGCCCCAGGAGCTGTGTAAGCCCTTCACAGACCCCTGTCCTCCTGACCTGCTCTCT 63
DB 98 GAGTCGGGCCCCAGGAGCTGTGTAAGCCCTTCGAGACCCCTGTCCTCCTGACCTGCTCTCT 157
QY 64 GGTGGCTCCATCCGAGCTGTGTAAGCTGTGTAAGCTGTGTAAGCTGTGTAAGCTGTGTAAG 123
DB 158 GGTGGCTCCATCCGAGCTGTGTAAGCTGTGTAAGCTGTGTAAGCTGTGTAAGCTGTGTAAG 217
QY 124 GGCCTGAGTGTGATCGGCAATCATCTATCAAGTGGCAACCTTCAACCAACCCGCTCCTC 183
DB 218 GGCCTGAGTGTGATCGGCAATCATCTATCAAGTGGCAACCTTCAACCAACCCGCTCCTC 277
QY 184 AAGAGTGAATTTACATGTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 278 AAGAGTGAATTTACATGTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 337
QY 244 TCTGTGACTGCGCGGAGACACGCGCTGTATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 297
DB 338 TCTGTGACTGCGCGGAGACACGCGCTGTATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 397
QY 298 ACTTTGGACAATGCGGCGCAGGAAACCTGTGTCACCGCTCTCTCA 342
DB 398 TGGTTCGACCCCTGGGCGCAGGAAACCTGTGTCACCGCTCTCTCA 442

RESULT 12

LOCUS BM920469 1108 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6709612 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5750444
ACCESSION BM920469
VERSION BM920469.1 GI:19370848
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
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FEATURES

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/clone_id="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber

ORIGIN (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."

Query Match 69.6%; Score 238.2; DB 5; Length 1108;
Best Local Similarity 82.9%; Pred. No. 1.4e-59;
Matches 286; Conservative 0; Mismatches 53; Indels 6; Gaps 1;

QY 4 GAGTCTGCCCCAGGAGCTGTGTAAGCCCTTCACAGACCCCTGTCCTCCTGACCTGCTCTCT 63
DB 110 GAGTCGGGCCCCAGGAGCTGTGTAAGCCCTTCGAGACCCCTGTCCTCCTGACCTGCTCTCT 169
QY 64 GGTGGCTCCATCCGAGCTGTGTAAGCTGTGTAAGCTGTGTAAGCTGTGTAAGCTGTGTAAG 123
DB 170 GGTGGCTCCGTCAGCACTGTGTAAGCTGTGTAAGCTGTGTAAGCTGTGTAAGCTGTGTAAG 229
QY 124 GGCCTGAGTGTGATCGGCAATCATCTATCAAGTGGCAACCTTCAACCAACCCGCTCCTC 183
DB 230 GGCCTGAGTGTGATCGGCAATCATCTATCAAGTGGCAACCTTCAACCAACCCGCTCCTC 289
QY 184 AAGAGTGAATTTACATGTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 290 AAGAGTGAATTTACATGTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 349
QY 244 TCTGTGACTGCGCGGAGACACGCGCTGTATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 297
DB 350 TCTGTGACTGCGCGGAGACACGCGCTGTATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 409
QY 298 ACTTTGGACAATGCGGCGCAGGAAACCTGTGTCACCGCTCTCTCA 342
DB 410 TACATGAGACGCTGTGGGCGCAGGAAACCGCTGTCTCTCA 454

RESULT 13

LOCUS BG757054 914 bp mRNA linear EST 15-MAY-2001
DEFINITION 602710478P1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4850851 5', mRNA sequence.
ACCESSION BG757054
VERSION BG757054.1 GI:14067707
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
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High quality sequence stop: 854.

FEATURES

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/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp

/clone.lib="NIH_MGC_48"
 /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAAGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC library."

ORIGIN

```

Query Match      69.1%; Score 236.4; DB 4; Length 828;
Best Local Similarity 90.6%; Pred. No. 4.5e-59;
Matches 252; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 4 GAGCTGGCCAGAGACTGTGGAAGCCTTCAACAGACCTGTCCTGACCTGACCTGTCTCT 63
    |||||
DB 92 GAGTCGGGCCAGAGACTGTGGAAGCCTTCAACAGACCTGTCCTGACCTGACCTGTCTCT 151
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QY 64 GGTGGCTCCATCCGACGTGGTGTATTATTGAGTTGGTCCGCGACGCTCCAGGGAAG 123
    |||||
DB 152 GGTGGCTCCATCCGACGTGGTGTATTATTGAGTTGGTCCGCGACGCTCCAGGGAAG 211
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QY 124 GGCCTGGAGTGAATCGGCAACATCTATCAGATGGCAACACTTAACAACCCGTCCTC 183
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DB 212 GGCCTGGAGTGAATGTGATCATCTATTAACGTGGAGCACTTACTATAACCCGTCCTC 271
    |||||

QY 184 AAGAGTCGAATTACATGATGATGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
    |||||
DB 272 AAGAGTCGAATTACATGATGATGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 331
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QY 244 TCTGTGACTGCGCGGACACGCGCGCTATTACTGTGC 281
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DB 332 TCTGTGACTGCGCGGACACGCGCGCTATTACTGTGC 369
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XX PD 11-JUL-2002.
XX PF 27-DEC-2001; 2001WO-SE002908.
XX PR 29-DEC-2000; 2000SE-00004892.
XX PA (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX P-PSDB; ABG30446.
XX DR WPI; 2002-583604/62.
XX PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IGE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX PS Disclosure; Page 32; 45pp; English.
XX CC This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IGE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC may be used for blocking the binding of grass pollen allergic patients
CC IGE antibodies to Phi p 2. The present sequence represents the DNA
CC encoding the human IgG fab, clone 60 heavy chain protein of the invention
XX SQ Sequence 342 BP; 70 A; 105 C; 90 G; 77 T; 0 U; 0 Other;
XX
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Best Local Similarity 99.7%; Pred. No. 5.3e-87;
Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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XX DB 1 CTGAGTCTGAGCCGAGACTGTTGTAAGCTTACAGACAGCCCTGTCCTCAGCTGATGTC 60
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XX DB 61 TCTGTTGGCTTCCATCCGAGTGGTGTATTATTGAGTTGGTCCGCGACGCTCCAGGG 120
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XX DB 121 AAGGCGCTGAGTGATCGGCAACATCTATACAGTAGTGCAACACTCAACCAACCGCTCC 180
XX QY 181 CTGAAGAGTGGAAATTACATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTAGACTG 240
XX DB 181 CTGAAGAGTGGAAATTACATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTAGACTG 240
XX QY 241 ACCTCTGTACTGCGCGGAGACAGCGCGTCTATTACTGTGCGCGGTAGATGGGTAACT 300
XX DB 241 ACCTCTGTACTGCGCGGAGACAGCGCGTCTATTACTGTGCGCGGTAGATGGGTAACT 300
XX QY 301 TTGGACAACATGGGGCGAGGGAACCTGTGACCGGTCCCTCA 342
XX DB 301 TTGGACAACATGGGGCGAGGGAACCTGTGACCGGTCCCTCA 342
XX
RESULT 2
ID ABK89639 standard; DNA, 342 BP.
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XX AC ABK89639;
XX XX 21-OCT-2002 (first entry)
XX DT DNA encoding human IGE Fab clone 100 heavy chain.
XX DE
XX XX
XX KM Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;
XX KM timothy grass pollen allergen; passive immunotherapy.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..342
XX FT /*tag= a
FT /product= "Fab clone 100 heavy chain"
FT misc_feature 7..78
FT /*tag= b
FT /note= "PR1 region"
FT misc_feature 79..99
FT /*tag= c
FT /note= "CDR1 region"
FT misc_feature 100..123
FT /*tag= d
FT /note= "PR2 region"
FT misc_feature 134..141
FT /*tag= e
FT /note= "PR3 region"
FT misc_feature 142..189
FT /*tag= f
FT /note= "CDR2 region"
FT misc_feature 190..285
FT /*tag= g
FT /note= "PR3 region"
FT misc_feature 286..309
FT /*tag= h
FT /note= "CDR3 region"
FT misc_feature 310..342
FT /*tag= i
FT /note= "PR4 region"
XX
XX PN WO200253595-A1.
XX XX 11-JUL-2002.
XX PD
XX PF 27-DEC-2001; 2001WO-SE002908.
XX PR 29-DEC-2000; 2000SE-00004892.
XX XX
XX PA (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX P-PSDB; ABG30447.
XX DR WPI; 2002-583604/62.
XX XX
XX PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IGE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX PS Disclosure; Page 33; 45pp; English.
XX CC This invention relates to the DNA and protein sequences of group 2
XX allergen-specific human IGE Fabs and methods for their use. The proteins
XX of the invention may have antiallergic activities and may be used as a
XX vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
XX antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
XX 2 allergen-specific fabs of the invention may be useful for environmental
XX allergen detection and for standardisation of allergen extracts. The fabs
XX - or a vaccine against a type I allergy is useful for passive
XX immunotherapy of type I allergy, it is also useful for diagnosing a type
XX I allergy. The allergen-specific fabs of the invention are useful for
```

inter alia, diagnosis, therapy and prevention of type I allergy. They are also useful for identification of group 2 allergen-containing pollen and may be used for blocking the binding of grass pollen allergic patients IgE antibodies to Phi p 2. The present sequence represents the DNA encoding the human IgG fab, clone 100 heavy chain protein of the invention

Sequence 342 BP; 69 A; 103 C; 94 G; 76 T; 0 U; 0 Other;

Query Match 94.9%; Score 324.4; DB 6; Length 342;
Best Local Similarity 96.8%; Pred. No. 1.9e-82;
Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCCGAGACTGTGAGCCCTTCACAGACCCCTGCTCAGCTGACGTGC 60
DB 1 CTCGAGTCTGGCCCGAGACTGTGAGCCCTTCACAGACCCCTGCTCAGCTGACGTGC 60
QY 61 TCTGTGGCTCCATCCGAGTGTGTTATTATTGAGTTGGTCCGCGACCTCCAGGG 120
DB 61 TCTGTGGCTCCATCCGAGTGTGTTATTATTGAGTTGGTCCGCGACCTCCAGGG 120
QY 121 AAGGCGCTGAGTGGATTCGCAACATCTATCAGTGGCAACACTTACAAACCCGTC 180
DB 121 AAGGCGCTGAGTGGATTCGCAACATCTATCAGTGGCAACACTTACAAACCCGTC 180
QY 181 CTCAGAGTGGATTTACATGTCTAGACAGCTCTAAGAACACTTCTCCCTGAGACTG 240
DB 181 CTCAGAGTGGATTTACATGTCTAGACAGCTCTAAGAACACTTCTCCCTGAGACTG 240
QY 241 ACCTCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGCGCTCAGATGGTATACT 300
DB 241 AGCTCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGCGCTCAGATGGTATACT 300
QY 301 TTGACAACTGGGGCCGAGGAAACCTGTGTCACCGTCTCTCTA 342
DB 301 TTGACAACTGGGGCCGAGGAAACCTGTGTCACCGTCTCTCTA 342

RESULT 3

ABK89637
ID ABK89637 standard; DNA; 342 BP.

XX ABK89637;

DT 21-Oct-2002 (first entry)

XX DNA encoding human IgE Fab clone 94 heavy chain.

XX Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;

KM timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..342

FT /*tag= a

FT /product= "Fab clone 94 heavy chain"

FT /*tag= b

FT /note= "FR1 region"

FT /*tag= c

FT /note= "CDR1 region"

FT /*tag= d

FT /note= "FR2 region"

FT /*tag= e

FT /note= "FR3 region"

FT /tag= f

FT /note= "CDR2 region"

FT /*tag= g
FT /note= "FR3 region"
FT 286..309
FT /*tag= h
FT /note= "CDR3 region"
FT 310..342
FT /tag= i
FT /note= "FR4 region"

XX W0200253595-A1.

XX 11-Jul-2002.

XX 27-DEC-2001; 2001WO-SE002908.

XX 29-DEC-2000; 2000SE-00004892.

XX (PHAA) PHARMACIA DIAGNOSTICS AB.

XX Flicker S, Steinberger P, Kraft D, Valenta R;

XX WPI; 2002-583604/62.

XX P-PSDB; ABG30445.

PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising variable region of group 2 allergen specific-human IgE Fabs, useful for diagnosing or passive immunotherapy of type I allergy, for environmental allergen detection.

XX Disclosure; Page 31-32; 45pp; English.

XX This invention relates to the DNA and protein sequences of group 2 allergen-specific human IgE Fabs and methods for their use. The proteins of the invention may have antiallergic activities and may be used as a vaccine or an inhibitor of binding of grass pollen allergic patient's IgE antibodies to Phi p 2 (a major timothy grass pollen allergen). The group 2 allergen-specific Fabs of the invention may be useful for environmental allergen detection and for standardisation of allergen extracts. The Fabs - or a vaccine against a type I allergy is useful for passive immunotherapy of type I allergy, it is also useful for diagnosing a type I allergy. The allergen-specific Fabs of the invention are useful for inter alia, diagnosis, therapy and prevention of type I allergy. They are also useful for identification of group 2 allergen-containing pollen and may be used for blocking the binding of grass pollen allergic patients IgE antibodies to Phi p 2. The present sequence represents the DNA encoding the human IgG fab, clone 94 heavy chain protein of the invention

Sequence 342 BP; 69 A; 100 C; 98 G; 75 T; 0 U; 0 Other;

Query Match 96.9%; Score 297.2; DB 6; Length 342;
Best Local Similarity 91.8%; Pred. No. 1.1e-74;
Matches 314; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCCGAGACTGTGAGCCCTTCACAGACCCCTGCTCAGCTGACGTGC 60
DB 1 CTCGAGTCTGGCCCGAGACTGTGAGCCCTTCACAGACCCCTGCTCAGCTGACGTGC 60
QY 61 TCTGTGGCTCCATCCGAGTGTGTTATTATTGAGTTGGTCCGCGACCTCCAGGG 120
DB 61 TCTGTGGCTCCATCCGAGTGTGTTATTATTGAGTTGGTCCGCGACCTCCAGGG 120
QY 121 AAGGCGCTGAGTGGATTCGCAACATCTATCAGTGGCAACACTTACAAACCCGTC 180
DB 121 AAGGCGCTGAGTGGATTCGCAACATCTATCAGTGGCAACACTTACAAACCCGTC 180
QY 181 CTCAGAGTGGATTTACATGTCTAGACAGCTCTAAGAACACTTCTCCCTGAGACTG 240
DB 181 CTCAGAGTGGATTTACATGTCTAGACAGCTCTAAGAACACTTCTCCCTGAGACTG 240
QY 241 ACCTCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGCGCTCAGATGGTATACT 300
DB 241 AACTCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGCGCTCAGATGGTATACT 300

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QY      301 TTGGACAACCTGGGCGAGGAACCTGTGTCACCGTCTCTCA 342
DB      301 TTGGACAATCTGGGCGAGGAACCTGTGTCACCGTCTCTCA 342

RESULT 4
ADCC9786
ID      ADCC9786 standard; DNA; 352 BP.
XX
AC      ADCC9786;
XX
DT      01-JAN-2004 (first entry)
XX
DE      Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 15.
XX
KW      anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW      cytostatic; melanoma; oesophageal; pancreatic; colorectal tumor;
KW      cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW      lung cancer; human; ds. gene.
XX
OS      Homo sapiens.
XX
PN      WO2003057838-A2.
XX
PD      17-JUL-2003.
XX
PF      26-DEC-2002; 2002WO-US041581.
XX
PR      28-DEC-2001; 2001US-0346239P.
XX
PA      (ABGE-) ABGENIX INC.
XX
PI      Gudas J;
XX
DR      WPI; 2003-587113/55.
XX
P-PSDB; ADCC9784.
XX
PT      New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT      or condition associated with expression of MUC18 in a patient, e.g.
PT      tumors, cancers, and other malignancies.
XX
PS      Claim 8; SEQ ID NO 15; 78pp; English.
XX
CC      The invention relates to a novel isolated monoclonal antibody comprising
CC      a heavy or light chain amino acid or a heavy or light chain variable
CC      domain where the antibody binds to MUC18. The monoclonal antibody of the
CC      invention demonstrates cytostatic activity and may be useful for treating
CC      a disease or condition associated with the expression of MUC18 on the
CC      cell surface such as tumours, specifically melanoma, oesophageal,
CC      pancreatic or colorectal tumours, carcinomas, particularly cervical
CC      carcinomas and cervical intraepithelial neoplasia and cancers including
CC      colorectal, breast or lung cancer, as well as other malignancies. The
CC      current sequence is that of the anti-human MUC18 monoclonal antibody
CC      heavy chain variable domain DNA of the invention.
XX
SQ      Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;

Query Match      79.5%; Score 271.8; DB 10; Length 352;
Best Local Similarity 89.7%; Pred. No. 1.9e-67;
Matches 304; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

QY      4 GAGTCTGAGCCAGAGACTGTGAAGCCCTTACAGACCCCTGCTCCTGACCTGACTGTCTCT 63
DB      16 GAGTCGGGCGCCAGAGACTGTGAAGCCCTTACAGACCCCTGCTCCTGACCTGACTGTCTCT 75
QY      64 GGTGGCTCCACATCCCGACGTGGTGTATATATGAGAGTGGGCGCCGAGCCCTCCAGGAG 123
DB      76 GGTGGCTCCACATCCCGACGTGGTGTATATGAGAGTGGGCGCCGAGCCCTCCAGGAG 135
QY      124 GGCTTGAGTGAATCGGCAACATCTATCAAGTGGCAACCTTCAACAAACCCGCTCCTC 183
DB      136 GGCTTGAGTGAATCGGCTTCACTATTAACGTGGAGCACTTACTACAAACCCGCTCCTC 195
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QY      184 AAGAGTCGAATTACCATGTGATAGACAGCTCTTAAGAACCACTTCTCCCTGAGACTGACC 243
DB      196 AAGAGTCGAATTACCATGTGATAGACAGCTCTTAAGAACCACTTCTCCCTGAGACTGAGC 255
QY      244 TCTGTGACTGCGCGGAGCAAGCGCGTCTATTACTGTGCGCGGTCAATGAGGTATGCTT 303
DB      256 TCTGTGACTGCGCGGAGCAAGCGCGTCTATTACTGTGCGAG---AAGAGGAGATGGCTTT 312
QY      304 GACAACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342
DB      313 GACTACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 351

RESULT 5
ADD05390
ID      ADD05390 standard; DNA; 352 BP.
XX
AC      ADD05390;
XX
DT      01-JAN-2004 (first entry)
XX
DE      Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID No 15.
XX
KW      monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW      antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
KW      gene; ds.
XX
OS      Homo sapiens.
XX
PN      WO2003057006-A2.
XX
PD      17-JUL-2003.
XX
PF      26-DEC-2002; 2002WO-US041582.
XX
PR      28-DEC-2001; 2001US-0346460P.
XX
PA      (ABGE-) ABGENIX INC.
XX
PI      Gudas J, Bar-El M;
XX
DR      WPI; 2003-577496/54.
XX
P-PSDB; ADD05388.
XX
PT      Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT      treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT      associated with melanoma, or increasing survival of an animal having a
PT      metastatic tumor.
XX
PS      Disclosure; SEQ ID NO 15; 87pp; English.
XX
CC      The invention relates to a novel monoclonal antibody used for inhibiting
CC      tumor growth in an animal. The tumor inhibition process comprises
CC      selecting an animal in need of treatment for a tumour, providing a
CC      monoclonal antibody comprising a heavy chain amino acid, where the
CC      antibody consists of any one of 10 fully defined sequences of 117-123
CC      amino acids given in the specification, and where the monoclonal antibody
CC      binds MUC18, and contacting the tumour with the antibody resulting in
CC      inhibited proliferation of the cells. The monoclonal antibody has
CC      cytostatic and can be used in the production of a vaccine. The monoclonal
CC      antibodies against the MUC18 antigen are useful for diagnosing and
CC      treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC      tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC      increasing survival of an animal having a metastatic tumour. This
CC      polynucleotide sequence represents the DNA encoding an anti-MUC18
CC      antibody heavy chain, variable region, protein of the invention.
XX
SQ      Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;

Query Match      79.5%; Score 271.8; DB 10; Length 352;
Best Local Similarity 89.7%; Pred. No. 1.9e-67;
Matches 304; Conservative 0; Mismatches 32; Indels 3; Gaps 1;
```

QY 4 GAGTCTGGCCAGAGACTGTGTGAAGCCCTTCAACAGCCCTGTCTCTACCTGACTGTCTCT 63
DB 16 GAGTCGGGGCCAGAGACTGTGTGAAGCCCTTCAACAGCCCTGTCTCTACCTGACTGTCTCT 75
QY 64 GGTGGCTCCATCCCGACTGTGTGTATTATTGAGTTGGGTCCCGCCAGCCCTCCAGGAG 123
DB 76 GGTGGCTCCATCCCGACTGTGTGTATTATTGAGTTGGGTCCCGCCAGCCCTCCAGGAG 135
QY 124 GGCCTGAGTGAATCGGCAACATCTATCAAGTGGCAACCTTAAACAAACCCGCTCC 183
DB 136 GGCCTGAGTGAATCGGCAACATCTATCAAGTGGCAACCTTAAACAAACCCGCTCC 195
QY 184 AAGAGTGAATTACCATGTGAGTGAACAGCGTCTAAGAACCACTTCTCTGAGACTGACC 243
DB 196 AAGAGTGAATTACCATGTGAGTGAACAGCGTCTAAGAACCACTTCTCTGAGACTGACC 255
QY 244 TCTGTGACTGCGCGGACACGGCCGTCTATTACTGTGCGCGGTCAAGTGGTAACTTTG 303
DB 256 TCTGTGACTGCGCGGACACGGCCGTCTATTACTGTGCGAG--AGAGGAGATGGCTTT 312
QY 304 GACAACCTGGGGCCAGGGAACTGTGACCGGTCTCTCA 342
DB 313 GACTACTGGGGCCAGGGAACTGTGACCGGTCTCTCA 351

RESULT 6

ADP09828
ID ADP09828 standard; DNA, 352 BP.

AC ADF09828;

DT 12-FEB-2004 (first entry)

DE Human anti-MUC18 monoclonal antibody heavy chain coding sequence #4.

XX cell proliferation inhibitor; MUC18 tumour antigen;
KM anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KM carcinoma; cancer; malignancy; heavy chain; human; ds; gene.

OS Homo sapiens.

PN WO2003057837-A2.

PD 17-JUL-2003.

PF 26-DEC-2002; 2002WO-US041580.

PR 28-DEC-2001; 2001US-0346414P.

PA (ABGE-) ABGENIX INC.

PI Gudas J;

DR WPI; 2003-598367/56.

DR P-PSDB; ADF09826.

PT Inhibiting cell proliferation associated with expression of MUC18 tumor
PT antigen, involves incubating and inhibiting cell by administering anti-
PT MUC18 monoclonal antibody.

PS Disclosure; SEQ ID NO 15; 83bp; English.

XX The invention comprises a method for inhibiting cell proliferation
CC associated with expression of MUC18 tumour antigen. The method involves
CC administering anti-MUC18 monoclonal antibody. The method of the invention
CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
CC proliferation associated with the expression of MUC18 tumour antigen, the
CC method is preferably useful for inhibiting tumour metastasis. The method
CC is useful for inhibiting cell proliferation in patients with tumours,
CC carcinomas, cancer and other malignancies. The present DNA sequence
CC encodes a heavy chain from an MUC18 tumour antigen-specific monoclonal
CC antibody.

SQ Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;
Query Match 79.5%; Score 271.8; DB 10; Length 352;
Best Local Similarity 89.7%; Pred. No. 1,9e-67;
Matches 304; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGAGACTGTGTGAAGCCCTTCAACAGCCCTGTCTCTACCTGACTGTCTCT 63
DB 16 GAGTCGGGGCCAGAGACTGTGTGAAGCCCTTCAACAGCCCTGTCTCTACCTGACTGTCTCT 75
QY 64 GGTGGCTCCATCCCGACTGTGTGTATTATTGAGTTGGGTCCCGCCAGCCCTCCAGGAG 123
DB 76 GGTGGCTCCATCCCGACTGTGTGTATTATTGAGTTGGGTCCCGCCAGCCCTCCAGGAG 135
QY 124 GGCCTGAGTGAATCGGCAACATCTATCAAGTGGCAACCTTAAACAAACCCGCTCC 183
DB 136 GGCCTGAGTGAATCGGCAACATCTATCAAGTGGCAACCTTAAACAAACCCGCTCC 195
QY 184 AAGAGTGAATTACCATGTGAGTGAACAGCGTCTAAGAACCACTTCTCTGAGACTGACC 243
DB 196 AAGAGTGAATTACCATGTGAGTGAACAGCGTCTAAGAACCACTTCTCTGAGACTGACC 255
QY 244 TCTGTGACTGCGCGGACACGGCCGTCTATTACTGTGCGCGGTCAAGTGGTAACTTTG 303
DB 256 TCTGTGACTGCGCGGACACGGCCGTCTATTACTGTGCGAG--AGAGGAGATGGCTTT 312
QY 304 GACAACCTGGGGCCAGGGAACTGTGACCGGTCTCTCA 342
DB 313 GACTACTGGGGCCAGGGAACTGTGACCGGTCTCTCA 351

RESULT 7

AAF29076
ID AAF29076 standard; DNA, 360 BP.

AC AAF29076;

DT 03-APR-2001 (first entry)

DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 32.

XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KM envelope glycoprotein; gp120; diagnosis; ds.

OS Homo sapiens.

PN WO200100678-A1.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000WO-US017327.

PR 30-JUN-1999; 99US-0141701P.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Watkins BA, Reitz MS;

DR WPI; 2001-112438/12.

DR P-PSDB; AAB62775.

PT Novel human monoclonal antibody immunoreactive with human
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT in biological sample and providing passive immunotherapy to HIV-1
PT infected mammal.

PS Claim 4; Page 45; 81bp; English.

XX The present invention provides the protein and coding sequences for the
CC variable regions of human monoclonal antibodies which are immunoreactive
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC These can be used in diagnosis and therapy of HIV-1 infection

Sequence 360 BP; 73 A; 104 C; 107 G; 76 T; 0 U; 0 Other;

Query Match 78.5%; Score 268.4; DB 4; Length 360;
Best Local Similarity 88.6%; Pred. No. 1.8e-66;
Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 4 GAGCTGGCCCAAGACATGTTGAAGCCCTTCCACAGCCCTGCTCCTGACCTGCTCTCT 63
DB 19 GAGTGGGGCCCAAGACATGTTGAAGCCCTTCCACAGCCCTGCTCCTGACCTGCTCTCT 78
QY 64 GGTGGCTCCATCCGACAGTGGTGTATTATTGAGTTGGGCTCCGACAGCTCCAGGGAG 123
DB 79 GGTGGCTCCATCCGACAGTGGTGTATTATTGAGTTGGGCTCCGACAGCTCCAGGGAG 138
QY 124 GCGCTGAGTGGATGGGCAACATCTATCAAGTGGCAACCTTCTCCCTGACCTGCTCT 183
DB 139 GCGCTGAGTGGATGGGCAACATCTATCAAGTGGGAGACCTTCTCAACACCGCTCTCT 198
QY 184 AAGAGTGAATTTACATGTCAGTGAACAGCTCTAAGAACCTTCTCTCTGACCTGAC 243
DB 199 AAGAGTGAATTTACATGTCAGTGAACAGCTCTAAGAACCTTCTCTCTGACCTGAC 258
QY 244 TCTGTGACTGCGCGGACACGCGCGCTTATTACTGTGGG--CGGTGAGATGGTATACT 300
DB 259 TCTGTGACTGCGCGGACACGCGCGCTTATTACTGTGGAGAGGGGTAGTAGTGACTGG 318
QY 301 TTGGACAACCTGGGGCCAGGGAACTGGTGTCAACGCTCTCTCTCA 342
DB 319 TTGGACCCTGGGGCCAGGGAACTGGTGTCAACGCTCTCTCTCA 360

RESULT 8
ADS84403 standard; DNA; 354 BP.

ADS84403;

18-NOV-2004 (first entry)

Human anti-EPO-R antibody heavy chain variable region DNA SEQ ID NO:42.

human; erythropoietin receptor; EPO receptor;
erythropoietin receptor binding antibody; EPO receptor binding antibody;
antianemic; neuroprotective; vulnerrary; gene therapy; aplasia; anaemia;
wound healing; neural cell damage protection;
neural tissue damage protection; brain injury; spinal cord injury;
stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;
ds.

OS Homo sapiens.

PN WO2004035603-A2.

PD 29-Apr-2004.

PF 14-OCT-2003; 2003WO-US032243.

PR 14-OCT-2002; 2002US-00269711.

PR 10-OCT-2003; 2003US-00684109.

PA (ABBO) ABBOTT LAB.

PI Devices PJ, Green LL, Ostrow DH, Reilly EB, Wleler J;

DR WPI; 2004-348433/32.

DR P-PSDB; ADS84404.

PT New antibodies that bind to or activate an endogenous human
erythropoietin receptor, useful for diagnosing, preventing or treating
disorders associated with dysfunctional erythropoietin receptor, e.g.
anemia.

PT Claim 47; SEQ ID NO 42; 192pp; English.

XX The present invention describes an antibody or its fragment that binds to
CC or activates an endogenous activity of a human erythropoietin (EPO)
CC receptor in a mammal, but does not interact with a peptide having a
CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)
CC methods of modulating or activating an endogenous activity of a human EPO
CC receptor in a mammal, comprising administering to the mammal a
CC therapeutic amount of the above antibody or its fragment to modulate or
CC activate the receptor; (2) a method of treating a mammal suffering from
CC aplasia, comprising administering to the mammal a therapeutic amount of
CC the above antibody or its fragment to modulate or activate the receptor;
CC (3) a pharmaceutical composition comprising a therapeutic amount of the
CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)
CC an isolated and purified polynucleotide sequence, and their fragments,
CC complements and degenerate codon equivalents; and (5) an isolated and
CC purified amino acid sequence, and their fragments. The EPO receptor
CC binding antibody has antianemic, neuroprotective and vulnerrary
CC activities, and can be used in gene therapy. The compositions and methods
CC from the present invention can be used for modulating an endogenous
CC activity of a human EPO receptor or for treating mammals suffering from
CC aplasia or anaemia. They may also be used for identifying mammals having
CC a dysfunctional EPO receptor. The composition may also be used in
CC promoting wound healing or in protecting against neural cell and/or
CC tissue damage resulting from brain/spinal cord injury, stroke and the
CC like. The present sequence encodes a human anti-EPO-R antibody heavy
CC chain variable region, which is given in the exemplification of the
CC present invention.

Sequence 354 BP; 76 A; 105 C; 97 G; 76 T; 0 U; 0 Other;

Query Match 78.1%; Score 267; DB 13; Length 354;
Best Local Similarity 86.7%; Pred. No. 4.5e-66;
Matches 294; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 4 GAGCTGGCCCAAGACATGTTGAAGCCCTTCCACAGCCCTGCTCCTGACCTGCTCTCT 63
DB 16 GAGTGGGGCCCAAGACATGTTGAAGCCCTTCCACAGCCCTGCTCCTGACCTGCTCTCT 75
QY 64 GGTGGCTCCATCCGACAGTGGTGTATTATTGAGTTGGGCTCCGACAGCTCCAGGGAG 123
DB 76 GGTGGCTCCATCCGACAGTGGTGTATTATTGAGTTGGGCTCCGACAGCTCCAGGGAG 135
QY 124 GCGCTGAGTGGATGGGCAACATCTATCAAGTGGCAACCTTCTCCCTGACCTGCTCTCT 183
DB 136 GCGCTGAGTGGATGGGCAACATCTATCAAGTGGGAGACCTTCTCAACACCGCTCTCTC 195
QY 184 AAGAGTGAATTTACATGTCAGTGAACAGCTCTAAGAACCTTCTCTCTGACCTGAC 243
DB 196 AAGAGTGAATTTACATGTCAGTGAACAGCTCTAAGAACCTTCTCTCTGACCTGAC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGCTTATTACTGTGGGCTCCGACAGTGGATATCTTG 303
DB 256 TCTGTGACTGCGCGGACACGCGCGCTTATTATTGTCGAGAGATAACTGGGATGCGG 315
QY 304 GACAACCTGGGGCCAGGGAACTGGTGTACCGTCTCTCTCA 342
DB 316 GACTACTGGGGCCAGGGAACTGGTGTACCGTCTCTCTCA 354

RESULT 9
ADR68545 standard; DNA; 354 BP.

ADR68545;

02-DEC-2004 (first entry)

Anti-EPO-R-antibody heavy chain variable region DNA seqid 42.

antianemic; respiratory; vulnerrary; gene therapy; vaccine;
erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;
wound healing; neural cell damage; tissue damage; brain injury;

KW spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain;
 XX variable region; ds.
 OS Homo sapiens.
 XX US2004175379-A1.
 XX 09-SEP-2004.
 XX 10-OCT-2003; 2003US-00684109.
 XX 14-OCT-2002; 2002US-0418031P.
 XX (DEVIR/) DEVIRIES P J.
 XX (OSTRO/) OSTROW D H.
 XX (REIL/) REILLY E B.
 XX (GREE/) GREEN L L.
 XX (WIEL/) WIELER J.
 XX Devires PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;
 XX WPI; 2004-661369/64.
 XX P-PSDB; ADR68546.
 XX
 PT New antibody or its antibody fragment that activates an endogenous
 PT activity or is capable of binding to a human erythropoietin receptor in a
 PT mammal, useful for treating a mammal suffering aplasia or anemia.
 XX
 PS Claim 47; SEQ ID NO 42; 156bp; English.
 XX
 CC The invention describes an antibody or its fragment that activates an
 CC endogenous activity or capable of binding to a human erythropoietin
 CC receptor in a mammal, or that comprises at least one heavy or light chain
 CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
 CC given in the specification. Also described are: a method of activating or
 CC modulating an endogenous activity of a human erythropoietin receptor in a
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an
 CC isolated and purified polynucleotide sequence selected from 28 sequences
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
 CC the specification; and their fragments, complements, and degenerate codon
 CC equivalents; and an isolated and purified amino acid sequence selected
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
 CC their fragments. The antibody or its antibody fragment that activates or
 CC modulates the activity of the receptor is useful in a method of treating
 CC a mammal suffering aplasia or anemia. The antibodies are also useful for
 CC treating disorders characterised by decreased or subnormal levels of
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue
 CC hypoxia and/or diseases characterised by inadequate blood circulation or
 CC reduced blood flow. They are also useful for promoting wound healing or
 CC for protecting against neural cell and/or tissue damage, resulting from
 CC brain/spinal cord injury, stroke and the like. The antibodies are also
 CC useful for identifying or diagnosing mammals having dysfunctional
 CC erythropoietin receptor. This sequence encodes an anti-EPO-R-antibody
 CC heavy chain variable region.
 XX
 SQ Sequence 354 BP; 76 A; 105 C; 97 G; 76 T; 0 U; 0 Other;
 XX
 Query Match 78.1%; Score 267; DB 13; Length 354;
 Best Local Similarity 86.7%; Pred. No. 4.5e-66;
 Matches 294; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
 XX
 QY 4 GAGTGTGAGCCAGAGCTGTGAACCTTTCACAGACCTGTGCTCCACCTGACCTGTCTCT 63
 DB 16 GAGTGTGAGCCAGAGCTGTGAACCTTTCACAGACCTGTGCTCCACCTGACCTGTCTCT 75
 QY 64 GGTGCTTCATCCGACGAGTGTGTATTATTGAGTTGGTCCGACGACCTCCAGGGAG 123
 DB 76 GGTGCTTCATCCGACGAGTGTGTATTATTGAGTTGGTCCGACGACCTCCAGGGAG 135

QY 124 GGCCTGGAGTGTGATCGGCAACATCTATACAGTGGCAACACTTAACAACACCGTCCCTC 183
 DB 136 GGCCTGGAGTGTGATCGGCAACATCTATACAGTGGCAACACTTAACAACACCGTCCCTC 195
 QY 184 AAGAGTGAATTATACATGTACATGATGACACGCTTAAAGAACCACTTCTCCCTGAGACTAC 243
 DB 196 AAGAGTGAATTATACATGTACATGATGACACGCTTAAAGAACCACTTCTCCCTGAGACTAC 255
 QY 244 TCTGTGACTGCGCGGACACAGCGCGCTATTATACGTGCGGGGTGAGATGGGTATACCTTGG 303
 DB 256 TCTGTGACTGCGCGGACACAGCGCGCTATTATATGTTATGAGAGATTAACCTGGGGATGCG 315
 QY 304 GACAACTGGGGCCAGAGGAAACCTGTGATCAGCGTCTCTCA 342
 DB 316 GACTACTGGGGCCAGAGGAAACCTGTGATCAGCGTCTCTCA 354
 XX
 RESULT 10
 ADS84454/c
 ID ADS84454 standard; DNA; 1996 BP.
 XX
 AC ADS84454;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human anti-EPO-R antibody Ab412 heavy chain complementary DNA SEQ ID:93.
 XX
 KW human; erythropoietin receptor; EPO receptor;
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;
 KW anti-anemic; neuroprotective; vulnerrary; gene therapy; aplasia; anaemia;
 KW wound healing; neural cell damage protection;
 KW neural tissue damage protection; brain injury; spinal cord injury;
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;
 KW ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2004035603-A2.
 XX
 PD 29-APR-2004.
 XX
 PF 14-OCT-2003; 2003WO-US032243.
 XX
 PR 14-OCT-2002; 2002US-00269711.
 XX
 PR 10-OCT-2003; 2003US-00684109.
 XX
 PA (ABBO) ABBOTT LAB.
 PI Devires PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;
 XX
 WPI; 2004-348433/32.
 P-PSDB; ADS84455.
 DR
 XX
 PT New antibodies that bind to or activate an endogenous human
 PT erythropoietin receptor, useful for diagnosing, preventing or treating
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.
 PT anemia.
 XX
 PS Disclosure; SEQ ID NO 93; 192bp; English.
 XX
 CC The present invention describes an antibody or its fragment that binds to
 CC or activates an endogenous activity of a human erythropoietin (EPO)
 CC receptor in a mammal, but does not interact with a peptide having a
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)
 CC methods of modulating or activating an endogenous activity of a human EPO
 CC receptor in a mammal, comprising administering to the mammal a
 CC therapeutic amount of the above antibody or its fragment to modulate or
 CC activate the receptor; (2) a method of treating a mammal suffering from
 CC aplasia, comprising administering to the mammal a therapeutic amount of
 CC the above antibody or its fragment to modulate or activate the receptor;
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)
 CC an isolated and purified polynucleotide sequence, and their fragments,

CC complements and degenerate codon equivalents; and (5) an isolated and
CC purified amino acid sequence, and their fragments. The EPO receptor
CC binding antibody has antianaemic, neuroprotective and vlneryary
CC activities, and can be used in gene therapy. The compositions and methods
CC from the present invention can be used for modulating an endogenous
CC activity of a human EPO receptor or for treating mammals suffering from
CC aplasia or anaemia. They may also be used for identifying mammals having
CC a dysfunctional EPO receptor. The composition may also be used in
CC promoting wound healing or in protecting against neural cell and/or
CC tissue damage resulting from brain/spinal cord injury, stroke and the
CC like. The present sequence represents a human anti-EPO-R antibody heavy
CC chain complementary DNA sequence, which is given in the exemplification
CC of the present invention.

XX
XX
SQ Sequence 1996 BP; 351 A; 537 C; 686 G; 422 T; 0 U; 0 Other;

Query Match 78.1%; Score 267; DB 13; Length 1996;
Best Local Similarity 86.7%; Pred. No. 7e-66;
Matches 294; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 4 GAGCTGGGCCAGAGCTGTGGAACCTTCAACAGACCTGTCCTCAGCTGCTCTCT 63
DB 1924 GAGTCGGGGCCAGAGCTGTGGAACCTTCAACAGACCTGTCCTCAGCTGCTCTCT 1865

QY 64 GGTGGCTCCATCCGAGTGGTGTATTATTGGAGTGGGCGCGCCAGCCTCCAGGGAG 123
DB 1864 GGTGGCTCCATCCGAGTGGTGTATTATTGGAGTGGGCGCGCCAGCCTCCAGGGAG 1805

QY 124 GGCCTGGAGTGAATCGCAACATCTATCAGAGTGGCAACCTTCAACAAACCCGTCCTC 183
DB 1804 GGCCTGGAGTGAATCGCAACATCTATCAGAGTGGGAGAGAGTGGTCTCTCAACCCGTCCTC 1745

QY 184 AAGAGTGAATTAACATGTAGTAGACAGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 1744 AAGAGTGAATTAACATGTAGTAGACAGCTTAAGAACCACTTCTCCCTGAGACTGACC 1685

QY 244 TCTGTGACTCCCGGAGACAGCGCCGTATTAATCTGTCGGCGGTCAAGTGGTAACTTTG 303
DB 1684 TCTGTGACTCCCGGAGACAGCGCCGTATTAATCTGTCGGAGATTAAGTGGGATCGCG 1625

QY 304 GACAACCTGGGGCCAGGAGACCTGTGACCGTCTCTCA 342
DB 1624 GACAACCTGGGGCCAGGAGACCTGTGACCGTCTCTCA 1586

RESULT 11
ADS84453
ID ADS84453 standard; DNA; 1996 BP.
XX
XX ADS84453;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human anti-EPO-R antibody Ab412 heavy chain DNA SEQ ID NO:92.
XX
XX human; erythropoietin receptor; EPO receptor;
XX erythropoietin receptor binding antibody; EPO receptor binding antibody;
XX antianaemic; neuroprotective; vulneryary; gene therapy; aplasia; anaemia;
XX wound healing; neural cell damage protection;
XX neural tissue damage protection; brain injury; spinal cord injury;
XX stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;
XX db.

XX
XX Homo sapiens.
XX OS
XX PN WO2004035603-A2.
XX
XX 29-APR-2004.
XX
XX 14-OCT-2003; 2003MO-US032243.
XX
XX 14-OCT-2002; 2002US-00269711.
XX
XX 10-OCT-2003; 2003US-00684109.

XX
XX (ABBO) ABBOTT LAB.
XX
XX Devries PJ, Green JL, Ostrow DH, Reilly EB, Wieler J;
XX
XX WPI: 2004-348433/32.
XX
XX P-P-SDB; ADS84455.
XX
XX
XX New antibodies that bind to or activate an endogenous human
XX erythropoietin receptor, useful for diagnosing, preventing or treating
XX disorders associated with dysfunctional erythropoietin receptor, e.g.
XX anemia.

PS Disclosure; SEQ ID NO 92; 192pp; English.

XX
XX
XX The present invention describes an antibody or its fragment that binds to
XX or activates an endogenous activity of a human erythropoietin (EPO)
XX receptor in a mammal, but does not interact with a peptide having a
XX sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)
XX methods of modulating an endogenous activity of a human EPO
XX receptor in a mammal, comprising administering to the mammal a
XX therapeutic amount of the above antibody or its fragment to modulate or
XX activate the receptor; (2) a method of treating a mammal suffering from
XX aplasia, comprising administering to the mammal a therapeutic amount of
XX the above antibody or its fragment to modulate or activate the receptor;
XX (3) a pharmaceutical composition comprising a therapeutic amount of the
XX above antibody or antibody fragment, and a pharmaceutical excipient; (4)
XX an isolated and purified polynucleotide sequence; and (5) an isolated and
XX complements and degenerate codon equivalents; and their fragments.
XX purified amino acid sequence, and their fragments. The EPO receptor
XX binding antibody has antianaemic, neuroprotective and vulneryary
XX activities, and can be used in gene therapy. The compositions and methods
XX from the present invention can be used for modulating an endogenous
XX activity of a human EPO receptor or for treating mammals suffering from
XX aplasia or anaemia. They may also be used for identifying mammals having
XX a dysfunctional EPO receptor. The composition may also be used in
XX promoting wound healing or in protecting against neural cell and/or
XX tissue damage resulting from brain/spinal cord injury, stroke and the
XX like. The present sequence encodes a human anti-EPO-R antibody heavy
XX chain, which is given in the exemplification of the present invention.

XX
XX
SQ Sequence 1996 BP; 422 A; 686 C; 537 G; 351 T; 0 U; 0 Other;

Query Match 78.1%; Score 267; DB 13; Length 1996;
Best Local Similarity 86.7%; Pred. No. 7e-66;
Matches 294; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 4 GAGCTGGGCCAGAGCTGTGGAACCTTCAACAGACCTGTCCTCAGCTGCTCTCT 63
DB 73 GAGTCGGGGCCAGAGCTGTGGAACCTTCAACAGACCTGTCCTCAGCTGCTCTCT 132

QY 64 GGTGGCTCCATCCGAGTGGTGTATTATTGGAGTGGGCGCGCCAGCCTCCAGGGAG 123
DB 133 GGTGGCTCCATCCGAGTGGTGTATTATTGGAGTGGGCGCGCCAGCCTCCAGGGAG 192

QY 124 GGCCTGGAGTGAATCGCAACATCTATCAGAGTGGCAACCTTCAACAAACCCGTCCTC 183
DB 193 GGCCTGGAGTGAATCGCAACATCTATCAGAGTGGGAGAGTGGTCTCTCAACCCGTCCTC 252

QY 184 AAGAGTGAATTAACATGTAGTAGACAGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 253 AAGAGTGAATTAACATGTAGTAGACAGCTTAAGAACCACTTCTCCCTGAGACTGACC 312

QY 244 TCTGTGACTCCCGGAGACAGCGCCGTATTAATCTGTCGGCGGTCAAGTGGTAACTTTG 303
DB 313 TCTGTGACTCCCGGAGACAGCGCCGTATTAATCTGTCGGAGATTAAGTGGGATCGCG 372

QY 304 GACAACCTGGGGCCAGGAGACCTGTGACCGTCTCTCA 342
DB 373 GACAACCTGGGGCCAGGAGACCTGTGACCGTCTCTCA 411

RESULT 12

ID	ADR68595
AC	ADR68595 standard; DNA; 1996 BP.
XX	
DT	02-DEC-2004 (first entry)
XX	
DE	Human antibody Ab412 heavy chain polynucleotide seqid 92.
XX	
KW	antianaemic; respiratory; vulnarary; gene therapy; vaccine;
KW	erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
KW	hypoxaemic; chronic tissue hypoxia; blood circulation; blood flow;
KW	wound healing; neural cell damage; tissue damage; brain injury;
KM	spinal cord injury; stroke; human; anti-EPO-R-antibody; heavy chain;
AB412; ds.	
XX	
OS	Homo sapiens.
XX	
PN	US2004175379-A1.
PD	
XX	
PF	09-SEP-2004.
XX	
PR	10-OCT-2003; 2003US-00684109.
XX	
PA	14-OCT-2002; 2002US-0418031P.
XX	
PA	(DEVIR/) DEVRIES P J.
XX	
PI	(OSTR/) OSTROW D H.
XX	
PT	(REIL/) REILLY E B.
XX	
PT	(GREE/) GREEN L L.
XX	
PS	(WIEL/) WIELER J.
XX	
DR	Devries PJ, Ostrow DH, Reilly EB, Green LT, Wieler J;
XX	
DR	WP1: 2004-661369/64.
XX	
PT	P-FSDB; ADR68597, ADR68575, ADR68576, ADR68577.
XX	
PT	New antibody or its antibody fragment that activates an endogenous
XX	activity or is capable of binding to a human erythropoietin receptor in a
XX	mammal, useful for treating a mammal suffering aplasia or anemia.
XX	
PS	Disclosure; SEQ ID NO 92; 156bp; English.
XX	
CC	The invention describes an antibody or its fragment that activates an
CC	endogenous activity or capable of binding to a human erythropoietin
CC	receptor in a mammal, or that comprises at least one heavy or light chain
CC	variable region having a sequence comprising 116 or 107 amino acids (SEQ
CC	ID NO: 3 or 5) given in the specification or its fragment, but does not
CC	interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
CC	given in the specification. Also described are: a method of activating or
CC	modulating an endogenous activity of a human erythropoietin receptor in a
CC	mammal; a pharmaceutical composition comprising a therapeutic amount of
CC	an antibody or antibody fragment above and a pharmaceutical excipient; an
CC	isolated and purified polynucleotide sequence selected from 28 sequences
CC	comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
CC	the specification, and their fragments, complements, and degenerate codon
CC	equivalents; and an isolated and purified amino acid sequence selected
CC	from 39 sequences comprising 27-557 amino acids (odd SEQ ID NOS between
CC	SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
CC	their fragments. The antibody or its antibody fragment that activates or
CC	modulates the activity of the receptor is useful in a method of treating
CC	a mammal suffering aplasia or anaemia. The antibodies are also useful for
CC	treating disorders characterised by decreased or subnormal levels of
CC	oxygen in the blood or tissue such as hypoxaemia or chronic tissue
CC	hypoxia and/or diseases characterised by inadequate blood circulation or
CC	reduced blood flow. They are also useful for promoting wound healing or
CC	for protecting against neural cell and/or tissue damage, resulting from
CC	brain/spinal cord injury, stroke and the like. The antibodies are also
CC	useful for identifying or diagnosing mammals having dysfunctional
CC	erythropoietin receptor. This sequence represents a human Ab412 antibody
CC	heavy chain polynucleotide.
XX	
SQ	Sequence 1996 BP; 422 A; 686 C; 537 G; 351 T; 0 U; 0 Other;

Query Match	Similarity	78.1%	Score 267	DB 13	Length 1996
Best Local	Similarity	86.7%	Pred. No. 7e-66		
Matches	294	Conservative	0	Mismatches	45
				Indels	0
				Gaps	0

Query	Subject	Score	Length	Identical	Mismatch	Indel	Gap
QY	4 GAGTCTGGCCAGGACTGTGTGAAGCTTACAGACCCCTGTCCCTCACTGACTGTCTCT	63					
DB	73 GAGTGGGAGCCAGGACTGTGTGAAGCTTACAGACCCCTGTCCCTCACTGACTGTCTCT	132					
QY	64 GGTGCTTCATCCGACGTGTGTGTATTTATTTGAGTTGGGTTCGGCAGCTTCAGGGAAG	123					
DB	133 GGTGCTTCATCAGACGTGTGTGTATTTATTTGAGTTGGGTTCGGCAGCTTCAGGGAAG	192					
QY	124 GGCCCTGAGTGAATCGGCAACATCTATACAGTGGCAACACTTAACAACCCGTCCCTC	183					
DB	193 GGCCCTGAGTGAATCGGCAACATCTATACAGTGGCAACACTTAACAACCCGTCCCTC	252					
QY	184 AAGAGTCGAATTAACCATGTCTAGTAGACACGTCTTAAGAACCACTTCTCCCTGAGACTGACC	243					
DB	253 AAGAGTCGAATTAACCATGTCTAGTAGACACGTCTTAAGAACCACTTCTCCCTGAGACTGACC	312					
QY	244 TCTGTGATCTGCCGCGGACACGCGCTCTATTACTGTGGCGGTCAAGTGGTATCTTTG	303					
DB	313 TCTGTGATCTGCCGCGGACACGCGCTCTATTACTGTGGCGGTCAAGTGGTATCTTTG	372					
QY	304 GACAACCTGGGGCCAGGGAACCTGTGTCAACCGTCTCTCA	342					
DB	373 GACTACTGGGGCCAGGGAACCTGTGTCAACCGTCTCTCA	411					

Result	ID	Score	Length	Identical	Mismatch	Indel	Gap
RESULT 13	ADRe8596/C	267	1996	86.7%	45	0	0
ADRe8596	standard	DNA	1996	BP			
ADRe8596	02-DEC-2004	(first entry)					
Human antibody Ab412	heavy chain polynucleotide	seqid	93				
antianaemic; respiratory; vulnery; gene therapy; vaccine;							
erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;							
hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;							
wound healing; neural cell damage; tissue damage; brain injury;							
spinal cord injury; stroke; human; anti-EPO-R-antibody; heavy chain;							
Ab412; ds.							
Homo sapiens.							
US2004175379-A1.							
09-SEP-2004.							
10-OCT-2003; 2003US-00684109.							
14-OCT-2002; 2002US-0418031P.							
(DEVYR// DEVYRIS P J.							
(OSTR// OSTROW D H.							
(REIL// REILLY E B.							
(GREEN// GREEN L L.							
(WIEL// WIELER J.							
Devries PJ, Ostrow DH, Reilly EB, Green LL, WIELER J;							
WPI, 2004-661369/64.							
New antibody or its antibody fragment that activates an endogenous							
activity or is capable of binding to a human erythropoietin receptor in a							
mammal, useful for treating a mammal suffering aplasia or anemia.							
Disclosure: SEQ ID NO 93; 156pp; English.							

CC The invention describes an antibody or its fragment that activates an
CC endogenous activity or capable of binding to a human erythropoietin
CC receptor in a mammal, or that comprises at least one heavy or light chain
CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
CC ID NO: 3 or 5) given in the specification or its fragment, but does not
CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
CC given in the specification. Also described are: a method of activating or
CC modulating an endogenous activity of a human erythropoietin receptor in a
CC mammal; a pharmaceutical composition comprising a therapeutic amount of
CC an antibody or antibody fragment above and a pharmaceutical excipient; an
CC isolated and purified polynucleotide sequence selected from 28 sequences
CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
CC the specification, and their fragments, complements, and degenerate codon
CC equivalents; and an isolated and purified amino acids (odd SEQ ID NOS between
CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
CC their fragments. The antibody or its antibody fragment that activates or
CC modulates the activity of the receptor is useful in a method of treating
CC a mammal suffering aplasia or anaemia. The antibodies are also useful for
CC treating disorders characterised by decreased or subnormal levels of
CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue
CC hypoxia and/or diseases characterised by inadequate blood circulation or
CC reduced blood flow. They are also useful for promoting wound healing or
CC for protecting against neural cell and/or tissue damage, resulting from
CC brain/spinal cord injury, stroke and the like. The antibodies are also
CC useful for identifying or diagnosing mammals having dysfunctional
CC erythropoietin receptor. This sequence represents a human Ab412 antibody
CC heavy chain polynucleotide.

XX Sequence 1996 BP; 351 A; 537 C; 686 G; 422 T; 0 U; 0 Other;

Query Match 78.1%; Score 267; DB 13; Length 1996;

Best Local Similarity 86.7%; Pred. No. 7e-66; Mismatches 294; Conservative 0; Indels 45; Gaps 0;

4 GAGTCTGGCCAGAGCTGTGTAAGCCTTCACAGACCCGTCCTGACCTGACGTCTCT 63

1924 GAGTCGGGCCAGAGCTGTGTAAGCCTTCACAGACCCGTCCTGACCTGACGTCTCT 1865

64 GGTGGCTCCATCCGACGTGTGTTATTATTGATGGTCCGCCAGCCTCCAGGAG 123

1864 GGTGGCTCCATCCGACGTGTGTTATTATTGATGGTCCGCCAGCCTCCAGGAG 1805

124 GGCCTGAGTGTGATGCGCAACATCTATCAAGTGGCAACCTTCAACACCCTCCCTC 183

1804 GGCCTGAGTGTGATGCGCAACATCTATCAAGTGGCAACCTTCAACACCCTCCCTC 1745

184 AAGAGTGAATTAACATGATGATGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243

1744 AAGAGTGAATTAACATGATGATGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 1685

244 TCTGTGACTGCCGCGACAGCGCCGTCTATTACTGTGCGCGGTGAGATGGATATCTTTC 303

1684 TCTGTGACTGCCGCGACAGCGCCGTCTATTACTGTGCGCGGTGAGATGGATATCTTTC 1625

304 GACAACTGGGGCCAGGGAACCTCTGTCAACCGTCTCTCA 342

1624 GACAACTGGGGCCAGGGAACCTCTGTCAACCGTCTCTCA 1586

RESULT 14
ADCG9778 standard; DNA; 352 BP.

XX ADC99778;

XX 01-JAN-2004 (first entry)

DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 7.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KM cytoeslastic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;

KW lung cancer; human; ds; gene.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

XX P-PSDB; ADC99776.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
XX or condition associated with expression of MUC18 in a patient, e.g.
XX tumors, cancers, and other malignancies.

XX Claim 8; SEQ ID NO 7; 78pp; English.

CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumors, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain variable domain DNA of the invention.

XX Sequence 352 BP; 76 A; 102 C; 103 G; 71 T; 0 U; 0 Other;

Query Match 76.7%; Score 262.2; DB 10; Length 352;

Best Local Similarity 87.9%; Pred. No. 1e-64; Mismatches 298; Conservative 0; Indels 38; Gaps 1;

4 GAGTCTGGCCAGAGCTGTGTAAGCCTTCACAGACCCGTCCTGACCTGACGTCTCT 63

16 GAGTCTGGCCAGAGCTGTGTAAGCCTTCACAGACCCGTCCTGACCTGACGTCTCT 75

64 GGTGGCTCCATCCGACGTGTGTTATTATTGATGGTCCGCCAGCCTCCAGGAG 123

76 GGTGGCTCCATCCGACGTGTGTTATTATTGATGGTCCGCCAGCCTCCAGGAG 135

124 GGCCTGAGTGTGATGCGCAACATCTATCAAGTGGCAACCTTCAACACCCTCCCTC 183

136 GGCCTGAGTGTGATGCGCAACATCTATCAAGTGGCAACCTTCAACACCCTCCCTC 195

184 AAGAGTGAATTAACATGATGATGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243

196 AAGAGTGAATTAACATGATGATGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 255

244 TCTGTGACTGCCGCGACAGCGCCGTCTATTACTGTGCGCGGTGAGATGGATATCTTTC 303

256 TCTGTGACTGCCGCGACAGCGCCGTCTATTACTGTGCGCGGTGAGATGGATATCTTTC 312

304 GACAACTGGGGCCAGGGAACCTCTGTCAACCGTCTCTCA 342

313 AAGTACTGGGGCCAGGGAACCTCTGTCAACCGTCTCTCA 351

RESULT 15

ADD05382 standard; DNA; 352 BP.

AC ADD05382;

DT 01-JAN-2004 (first entry)
XX
XX Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID No 7.
XX
XX monoclonaal antibody; tumour; MUC18; proliferation; cytosstatic; vaccine;
KM antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
KW gene; ds.
XX
XX Homo sapiens.
OS
XX W02003057006-A2.
PN
XX
XX 17-JUL-2003.
PD
XX
XX 26-DEC-2002; 2002WO-US041582.
PR
XX 28-DEC-2001; 2001US-0346460P.
XX
XX (ABGE-) ABGENIX INC.
PA
XX
XX Gudas J, Bar-Eli M;
PI
XX WPI; 2003-577496/54.
DR
XX P-PSDB; ADD05380.
PT
XX Use of monoclonaal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
XX
PS Disclosure; SEQ ID NO 7; 87pp; English.
XX
XX The invention relates to a novel monoclonaal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonaal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonaal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonaal antibody has
CC cytosstatic and can be used in the production of a vaccine. The monoclonaal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC polynucleotide sequence represents the DNA encoding an anti-MUC18
CC antibody heavy chain, variable region, protein of the invention.
XX
XX
XX Sequence 352 BP; 76 A; 102 C; 103 G; 71 T; 0 U; 0 Other;

Query Match	76.7%;	Score 262.2;	DB 10;	Length 352;
Best Local Similarity	87.9%;	Pred. No. 1e-64;		
Matches 298; Conservative	0;	Mismatches 38;	Indels 3;	Gaps 1;

QY	4	GAGTGTGGCCCAAGACTGGTGAAGCCTTACAGACCCCTTCCTACCTGCACACTGTCTCT	63
Db	16	GAGTGGGGCCCAAGACTGGTGAAGCCTTACAGACCCCTTCCTACCTGCACACTGTCTCT	75
QY	64	GATGGCTCCATCCGCACTGTGTGTATTATTGGAGTGTGGGTCCGCAAGCTTCAGGGAAAG	123
Db	76	GATGGCTCCATCAGCAGTGTGTACTTACCCTGAGTGTGATCCGCGCAGCACCAGGGAAAG	135
QY	124	GAGCTGAGTGGATGGGCAACATCTATCACAGTGGCAACCTACACAAACCCTGCTCTC	183
Db	136	GAGCTGAGTGGATGGGCAACATCTATTCACGTGGAGACACTACACAAACCCTGCTCTC	195
QY	184	AAGAGTCGATTAACCATGTCAAGTAGACAGTCTAAGAACCACTTCTCCCTGAGACTGACC	243
Db	196	AAGATTCGATTAACCATATCAGTAGACAGTCTTAAGAACCAAGTCTCTCCCTGAGACTGACC	255
QY	244	TCTGTGACTGCGCGGACACGGCCGCTTATTACTGTGCGCGGTCAAGTGGGTATCTTTG	303

Db 256 TCTGTACTCGCGGGAACACGGCCGTGATTACTGTGGAG---AGGGGAGATGGCTAC 312

QY 304 GACAACTGGGGCCAGGGAAACCCCTGGTCAACGCTTCTCTCA 342

Db 313 AAGTACTGGGGCCAGGGAACCCCTGGTCAACGCTTCTCTCA 351

Search completed: July 27, 2005, 05:59:44
Job time : 322.618 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 09:08:49 ; Search time 512.827 Seconds
(without alignment)
4312.305 Million cell updates/sec

Title: US-10-027-725A-2

Perfect score: 342
Sequence: 1 ctcgagctgcgcacagact.....ccctgacccgtctctca 342

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 7277826 seqs, 3233139505 residues

Total number of hits satisfying chosen parameters: 1455652

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	342	100.0	342	14	US-10-027-725A-2
2	324.4	94.9	342	14	US-10-027-725A-1
3	298.8	87.4	342	14	US-10-027-725A-1
4	271.8	79.5	352	15	US-10-330-613-15
5	271.8	79.5	352	16	US-10-330-530-15
6	271.8	79.5	352	19	US-10-660-357-15
7	267	78.1	354	19	US-10-684-109-42

c	8	267	78.1	1996	19	US-10-684-109-92	Sequence 92, Appl
	9	267	78.1	1996	19	US-10-684-109-93	Sequence 93, Appl
	10	262.2	76.7	352	15	US-10-330-613-7	Sequence 7, Appl
	11	262.2	76.7	352	16	US-10-330-530-7	Sequence 7, Appl
	12	262.2	76.7	352	19	US-10-660-357-7	Sequence 7, Appl
	13	262.2	76.7	355	19	US-10-684-109-54	Sequence 54, Appl
	14	262.2	76.7	1996	19	US-10-684-109-110	Sequence 110, App
	15	262.2	76.7	1996	19	US-10-684-109-111	Sequence 111, App
c	16	261.4	76.4	560	21	US-10-644-277-93	Sequence 93, Appl
	17	261.4	76.4	663	10	US-09-972-656-79	Sequence 79, Appl
	18	260.4	76.1	358	15	US-10-330-613-27	Sequence 27, Appl
	19	260.4	76.1	358	16	US-10-330-530-27	Sequence 27, Appl
	20	260.4	76.1	358	19	US-10-660-357-27	Sequence 27, Appl
	21	260.4	76.1	1338	21	US-10-644-277-61	Sequence 61, Appl
	22	258.4	75.6	420	21	US-10-893-576-18	Sequence 18, Appl
	23	257.8	75.4	366	22	US-10-984-960A-19	Sequence 19, Appl
	24	256.4	75.0	370	17	US-10-309-762-186	Sequence 186, App
	25	255	74.6	429	17	US-10-309-762-110	Sequence 110, App
	26	254.8	74.5	352	15	US-10-330-613-35	Sequence 35, Appl
	27	254.8	74.5	352	16	US-10-330-530-35	Sequence 35, Appl
	28	254.8	74.5	352	19	US-10-660-357-35	Sequence 35, Appl
	29	254.6	74.4	366	22	US-10-984-960A-55	Sequence 55, Appl
	30	252.6	73.9	361	17	US-10-309-762-191	Sequence 191, App
	31	252.6	73.9	1392	21	US-10-910-901-9	Sequence 9, Appl
	32	251.6	73.6	370	17	US-10-309-762-189	Sequence 189, App
	33	251.2	73.5	516	20	US-10-612-497-33	Sequence 33, Appl
	34	251.2	73.5	516	20	US-10-776-649-33	Sequence 33, Appl
	35	250.6	73.3	370	17	US-10-309-762-185	Sequence 185, App
	36	250.4	73.2	376	17	US-10-309-762-187	Sequence 187, App
	37	249.4	72.9	352	17	US-10-309-762-203	Sequence 203, App
	38	248.8	72.7	376	17	US-10-309-762-184	Sequence 184, App
	39	248.8	72.7	376	17	US-10-309-762-197	Sequence 197, App
	40	248.8	72.7	376	17	US-10-309-762-199	Sequence 199, App
	41	248.4	72.6	519	17	US-10-309-762-174	Sequence 174, App
	42	248.2	72.6	367	17	US-10-309-762-195	Sequence 195, App
	43	245.8	71.9	467	20	US-10-478-056-16	Sequence 16, Appl
	44	245.8	71.9	384	21	US-10-727-155-1	Sequence 1, Appl
	45	245.8	71.9	384	21	US-10-727-155-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-10-027-725A-2
; Sequence 2, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific Ige-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027, 725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259, 436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-2

Query Match	100.0%	Score 342,	DB 14,	Length 342;
Best Local Similarity	100.0%	Pred. No. 1,	4e-102;	Indels 0;
Matches 342;	Conservative 0;	Mismatches 0;	Gaps 0;	
QY	1	CTCGAGCTGCGCCAGAGCTGTGAGCTTACAGACCCGTCCTGACCTGACGTC	60	
DB	1	CTCGAGCTGCGCCAGAGCTGTGAGCTTACAGACCCGTCCTGACCTGACGTC	60	
QY	61	TCGTGAGCTTCATCCGAGGTGTATTATTGAGTTGGTCCGCCACCTCCAGGG	120	

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Db      61 TCTGTGGCTCCATCCGACAGTGGTATTATTATTGAGTTGGTCCGCCACGCTCCAGGG 120
Qy      121 AAGGGCTGGAGTGGATCGGCAACATCTATTCACAGTGGCAACACCTAACAAACCCGCTCC 180
Db      121 AAGGGCTGGAGTGGATCGGCAACATCTATTCACAGTGGCAACACCTAACAAACCCGCTCC 180
Qy      181 CTCAAGAGTGAATTACATGTCTGAGACACGCTTAAAGAACCTTCTCCCTGAAGCTG 240
Db      181 CTCAAGAGTGAATTACATGTCTGAGACACGCTTAAAGAACCTTCTCCCTGAAGCTG 240
Qy      241 ACCTCTGACTGCGCGGACACGCGCTCTATTACTGTGCGCGGTCAAGATGGGTATACT 300
Db      241 ACCTCTGACTGCGCGGACACGCGCTCTATTACTGTGCGCGGTCAAGATGGGTATACT 300
Qy      301 TTGGACAACCTGGGGCCAGGGAACCTGTCTCAACCGTCTCTCA 342
Db      301 TTGGACAACCTGGGGCCAGGGAACCTGTCTCAACCGTCTCTCA 342

RESULT 2
US-10-027-725A-3
; Sequence 3, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-3

Query Match      94.9%; Score 324.4; DB 14; Length 342;
Best Local Similarity 96.8%; Pred. No. 9.2e-97;
Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy      1 CTGAGTCTGCGCCAGAGACTGTTGAAGCTTTCACAGACCTGTCTTCACCTGCATGTC 60
Db      1 CTCAGTCTGCGCCAGAGACTGTTGAAGCTTTCACAGACCTGTCTTCACCTGCATGTC 60
Qy      61 TCTGTGGCTCCATCCGACAGTGGTATTATTATTGAGTTGGTCCGCCACGCTCCAGGG 120
Db      61 TCTGTGGCTCCATCCGACAGTGGTATTATTATTGAGTTGGTCCGCCACGCTCCAGGG 120
Qy      121 AAGGGCTGGAGTGGATCGGCAACATCTATTCACAGTGGCAACACCTAACAAACCCGCTCC 180
Db      121 AAGGGCTGGAGTGGATCGGCAACATCTATTCACAGTGGCAACACCTAACAAACCCGCTCC 180
Qy      181 CTCAAGAGTGAATTACATGTCTGAGACACGCTTAAAGAACCTTCTCCCTGAAGCTG 240
Db      181 CTCAAGAGTGAATTACATGTCTGAGACACGCTTAAAGAACCTTCTCCCTGAAGCTG 240
Qy      241 ACCTCTGACTGCGCGGACACGCGCTCTATTACTGTGCGCGGTCAAGATGGGTATACT 300
Db      241 ACCTCTGACTGCGCGGACACGCGCTCTATTACTGTGCGCGGTCAAGATGGGTATACT 300
Qy      301 TTGGACAACCTGGGGCCAGGGAACCTGTCTCAACCGTCTCTCA 342
Db      301 TTGGACAACCTGGGGCCAGGGAACCTGTCTCAACCGTCTCTCA 342

RESULT 3
US-10-027-725A-1
; Sequence 1, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
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; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IGE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-1

Query Match      87.4%; Score 298.8; DB 14; Length 342;
Best Local Similarity 92.1%; Pred. No. 2.7e-88;
Matches 315; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy      1 CTGAGTCTGCGCCAGAGACTGTTGAAGCTTTCACAGACCTGTCTTCACCTGCATGTC 60
Db      1 CTGAGTCTGCGCCAGAGACTGTTGAAGCTTTCACAGACCTGTCTTCACCTGCATGTC 60
Qy      61 TCTGTGGCTCCATCCGACAGTGGTATTATTATTGAGTTGGTCCGCCACGCTCCAGGG 120
Db      61 TCTGTGGCTCCATCCGACAGTGGTATTATTATTGAGTTGGTCCGCCACGCTCCAGGG 120
Qy      121 AAGGGCTGGAGTGGATCGGCAACATCTATTCACAGTGGCAACACCTAACAAACCCGCTCC 180
Db      121 AAGGGCTGGAGTGGATCGGCAACATCTATTCACAGTGGCAACACCTAACAAACCCGCTCC 180
Qy      181 CTCAAGAGTGAATTACATGTCTGAGACACGCTTAAAGAACCTTCTCCCTGAAGCTG 240
Db      181 CTCAAGAGTGAATTACATGTCTGAGACACGCTTAAAGAACCTTCTCCCTGAAGCTG 240
Qy      241 ACCTCTGACTGCGCGGACACGCGCTCTATTACTGTGCGCGGTCAAGATGGGTATACT 300
Db      241 ACCTCTGACTGCGCGGACACGCGCTCTATTACTGTGCGCGGTCAAGATGGGTATACT 300
Qy      301 TTGGACAACCTGGGGCCAGGGAACCTGTCTCAACCGTCTCTCA 342
Db      301 TTGGACAACCTGGGGCCAGGGAACCTGTCTCAACCGTCTCTCA 342

RESULT 4
US-10-330-613-15
; Sequence 15, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Guigas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: AGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-15

Query Match      79.5%; Score 271.8; DB 15; Length 352;
Best Local Similarity 89.7%; Pred. No. 2.2e-79;
Matches 304; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

Qy      4 GAGTCTGGCCCAAGAGACTGTGAAGCTTTCACAGACCTGTCTCTCAACCTGCATGTCCT 63
Db      16 GAGTCTGGCCCAAGAGACTGTGAAGCTTTCACAGACCTGTCTCTCAACCTGCATGTCCT 75
Qy      64 GTTGCTCCATCCGACAGTGGTATTATTATTGAGTTGGTCCGCCACGCTCCAGGGAG 123
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Db      76 GGTGGCTCCATCAGCAGTGGTGTACTACTGAGCTTGATCCGCCAGCAACCCAGGGAG 135
Qy      124 GGCCTGGAGTGAATCGGCACATCTATCAGATGGGCAACCTTCAACAACCCGCTCC 183
Db      136 GGCCTGGAGTGAATCGGCATCTATTAACATGAGGAGCACTTCAACACCCGCTCC 195
Qy      184 AAGAGTGAATTAACATGATGATGAGACAGTCTAAGAACCACTTCTCCCTGAGACTGACC 243
Db      196 AAGAGTGAATTAACATGATGATGAGACAGTCTAAGAACCACTTCTCCCTGAGACTGACC 255
Qy      244 TCTGTACTGCGCGGAGACAGGCGCTTATTAATGCTGCGCGGTGAGATGGGTATCTTTG 303
Db      256 TCTGTACTGCGCGGAGACAGGCGCTTATTAATGCTGCGCGGTGAGATGGGTATCTTTG 312
Qy      304 GACAACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342
Db      313 GACTACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 351

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RESULT 5

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US-10-330-530-15
; Sequence 15, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-530-15

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Query Match 79.5%; Score 271.8; DB 16; Length 352;
 Best Local Similarity 89.7%; Pred. No. 2.2e-79;
 Matches 304; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

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Qy      4 GAGCTGGCCAGAGCTGTGTAAGCCCTTCAAGACCCCTGCTCACTGACTGTCTCT 63
Db      16 GAGTCGGGCCAGAGCTGTGTAAGCCCTTCAAGACCCCTGCTCACTGACTGTCTCT 75
Qy      64 GGTGGCTCCATCCGACAGTGTGTTATTATTGAGTGGTGGTCCGCAAGCCCTCCAGGGAG 123
Db      76 GGTGGCTCCATCCGACAGTGTGTTATTATTGAGTGGTGGTCCGCAAGCCCTCCAGGGAG 135
Qy      124 GGCCTGGAGTGAATCGGCACATCTATCAGATGGGCAACCTTCAACAACCCGCTCC 183
Db      136 GGCCTGGAGTGAATCGGCATCTATTAACATGAGGAGCACTTCAACACCCGCTCC 195
Qy      184 AAGAGTGAATTAACATGATGATGAGACAGTCTAAGAACCACTTCTCCCTGAGACTGACC 243
Db      196 AAGAGTGAATTAACATGATGATGAGACAGTCTAAGAACCACTTCTCCCTGAGACTGACC 255
Qy      244 TCTGTACTGCGCGGAGACAGGCGCTTATTAATGCTGCGCGGTGAGATGGGTATCTTTG 303
Db      256 TCTGTACTGCGCGGAGACAGGCGCTTATTAATGCTGCGCGGTGAGATGGGTATCTTTG 312
Qy      304 GACAACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342
Db      313 GACTACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 351

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RESULT 6
 US-10-660-357-15
 ; Sequence 15, Application US/10660357
 ; Publication No. US20040115205A1

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; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-15

```

Query Match 79.5%; Score 271.8; DB 19; Length 352;
 Best Local Similarity 89.7%; Pred. No. 2.2e-79;
 Matches 304; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

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Qy      4 GAGCTGGCCAGAGCTGTGTAAGCCCTTCAAGACCCCTGCTCACTGACTGTCTCT 63
Db      16 GAGTCGGGCCAGAGCTGTGTAAGCCCTTCAAGACCCCTGCTCACTGACTGTCTCT 75
Qy      64 GGTGGCTCCATCCGACAGTGTGTTATTATTGAGTGGTGGTCCGCAAGCCCTCCAGGGAG 123
Db      76 GGTGGCTCCATCCGACAGTGTGTTATTATTGAGTGGTGGTCCGCAAGCCCTCCAGGGAG 135
Qy      124 GGCCTGGAGTGAATCGGCACATCTATCAGATGGGCAACCTTCAACAACCCGCTCC 183
Db      136 GGCCTGGAGTGAATCGGCATCTATTAACATGAGGAGCACTTCAACACCCGCTCC 195
Qy      184 AAGAGTGAATTAACATGATGATGAGACAGTCTAAGAACCACTTCTCCCTGAGACTGACC 243
Db      196 AAGAGTGAATTAACATGATGATGAGACAGTCTAAGAACCACTTCTCCCTGAGACTGACC 255
Qy      244 TCTGTACTGCGCGGAGACAGGCGCTTATTAATGCTGCGCGGTGAGATGGGTATCTTTG 303
Db      256 TCTGTACTGCGCGGAGACAGGCGCTTATTAATGCTGCGCGGTGAGATGGGTATCTTTG 312
Qy      304 GACAACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 342
Db      313 GACTACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCA 351

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RESULT 7

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US-10-684-109-42
; Sequence 42, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Deviles, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; TITLE OF INVENTION: Blythtropietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989, US. 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-684-109-42

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Query Match 78.1%; Score 267; DB 19; Length 354;

Best Local Similarity 86.7%; Pred. No. 8.7e-78;
Matches 294; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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QY 4 GAGTCTGCCCCAGAGCTGTGAACCTTTACAGACCCCTGTCTCACTGTGACTGTCTCT 63
Db 16 GAGTCGGGCCCAAGAGCTGTGAACCTTTACAGACCCCTGTCTCACTGTGACTGTCTCT 75
QY 64 GGTGGCTTCCATCCGCACTGTGTGTATTATTGAGATTGGGTCCGCACTCTCAAGGAG 123
Db 76 GGTGCTTCCATCCAGAGGTGTGTATTATTGAGATTGGGTCCGCACTCTCAAGGAG 135
QY 124 GGCCTGAGTGAATGAGTGGCAATCTATCAAGTGGCAACCTTCAACCAACCCGTCTC 183
Db 136 GGCCTGAGTGAATGAGTGGTATCATCTATTAAGTGAAGACTTCTTCAACACCCGTCTC 195
QY 184 AAGAGTGAATTTACATGCTAGTGAACAGCTTAAGAACCACTTCTCCTGAGACTGACC 243
Db 196 AAGAGTGAATTTACATGCTAGTGAACAGCTTAAGAACCACTTCTCCTGAGACTGACC 255
QY 244 TCTGTGACTGCGCGGAGACGCGCGCTCTATTACTGTGCGCGGTAGATGGTATATCTTG 303
Db 256 TCTGTGACTGCGCGGAGACGCGCGCTGTATTATTGTGAGAGATTAACCTGGGATCGCG 315
QY 304 GACAACCTGGGGCCAGGGAACCTGTGATCAACCTGTCTCTCA 342
Db 316 GACTACTGGGGCCAGGGAACCTGTGATCAACCTGTCTCTCA 354
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RESULT 8

US-10-684-109-92
; Sequence 92, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Deviles, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieleter, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989, US. 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-684-109-92

Query Match 78.1%; Score 267; DB 19; Length 1996;

Best Local Similarity 86.7%; Pred. No. 1.4e-77;
Matches 294; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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QY 4 GAGTCTGCCCCAGAGCTGTGAACCTTTACAGACCCCTGTCTCACTGTGACTGTCTCT 63
Db 73 GAGTCGGGCCCAAGAGCTGTGAACCTTTACAGACCCCTGTCTCACTGTGACTGTCTCT 132
QY 64 GGTGGCTTCCATCCGCACTGTGTGTATTATTGAGATTGGGTCCGCACTCTCAAGGAG 123
Db 133 GGTGCTTCCATCCAGAGGTGTGTATTATTGAGATTGGGTCCGCACTCTCAAGGAG 192
QY 124 GGCCTGAGTGAATGAGTGGCAATCTATCAAGTGGCAACCTTCAACCAACCCGTCTC 183
Db 193 GGCCTGAGTGAATGAGTGGTATCATCTATTAAGTGAAGACTTCTTCAACACCCGTCTC 252
QY 184 AAGAGTGAATTTACATGCTAGTGAACAGCTTAAGAACCACTTCTCCTGAGACTGACC 243
Db 253 AAGAGTGAATTTACATGCTAGTGAACAGCTTAAGAACCACTTCTCCTGAGACTGACC 312
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QY 244 TCTGTGACTGCGCGGAGACAGCGCGTCTATTACTGTGCGCGGTCAAGTGGTATCTTNG 303
Db 313 TCTGTGACTGCGCGGAGACAGCGCGTGTATTATTGTGCGAGATTAACCTGGGATCGCG 372
QY 304 GACAACCTGGGGCCAGGGAACCTGTGATCAACCTGTCTCTCA 342
Db 373 GACTACTGGGGCCAGGGAACCTGTGATCAACCTGTCTCTCA 411
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RESULT 9

US-10-684-109-93/c
; Sequence 93, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Deviles, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieleter, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989, US. 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-684-109-93

Query Match 78.1%; Score 267; DB 19; Length 1996;

Best Local Similarity 86.7%; Pred. No. 1.4e-77;
Matches 294; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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QY 4 GAGTCTGCCCCAGAGCTGTGAACCTTTACAGACCCCTGTCTCACTGTGACTGTCTCT 63
Db 1924 GAGTCGGGCCCAAGAGCTGTGAACCTTTACAGACCCCTGTCTCACTGTGACTGTCTCT 1865
QY 64 GGTGGCTTCCATCCGCACTGTGTGTATTATTGAGATTGGGTCCGCACTCTCAAGGAG 123
Db 1864 GGTGCTTCCATCCAGAGGTGTGTATTATTGAGATTGGGTCCGCACTCTCAAGGAG 1805
QY 124 GGCCTGAGTGAATGAGTGGCAATCTATCAAGTGGCAACCTTCAACCAACCCGTCTC 183
Db 1804 GGCCTGAGTGAATGAGTGGTATCATCTATTAAGTGAAGACTTCTTCAACACCCGTCTC 1745
QY 184 AAGAGTGAATTTACATGCTAGTGAACAGCTTAAGAACCACTTCTCCTGAGACTGACC 243
Db 1744 AAGAGTGAATTTACATGCTAGTGAACAGCTTAAGAACCACTTCTCCTGAGACTGACC 1685
QY 244 TCTGTGACTGCGCGGAGACGCGCGTCTATTACTGTGCGCGGTAGATGGTATATCTTNG 303
Db 1684 TCTGTGACTGCGCGGAGACGCGCGTGTATTATTGTGCGAGATTAACCTGGGATCGCG 1625
QY 304 GACAACCTGGGGCCAGGGAACCTGTGATCAACCTGTCTCTCA 342
Db 1624 GACTACTGGGGCCAGGGAACCTGTGATCAACCTGTCTCTCA 1586
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RESULT 10

US-10-330-613-7
; Sequence 7, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX 022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26

PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 352
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-330-613-7

Query Match 76.7%; Score 262.2; DB 15; Length 352;
Best Local Similarity 87.9%; Pred. No. 3.3e-76;
Matches 298; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 4 GAGTCTGAGCCAGAGTGGTGAAGCCCTTGCACAGCCCTGTCCTGACCTGACGTGTCTCT 63
DB 16 GAGTCGGAGCCAGAGTGGTGAAGCCCTTGCACAGCCCTGTCCTGACCTGACGTGTCTCT 75
QY 64 GGTGGCTCCATCCCGACGTGTGTATTATTGAGTTGGTCCGCGACGCTCCAGGGAG 123
DB 76 GGTGGCTCCATCCCGACGTGTGTATTATTGAGTTGGTCCGCGACGCTCCAGGGAG 135
QY 124 GGCCTGAGTGGATCGGCAACATCTATCAAGTGGCAACCTTAACAACCCGTCCTC 183
DB 136 GGCCTGAGTGGATCGGCAACATCTATCAAGTGGCAACCTTAACAACCCGTCCTC 195
QY 184 AAGAGTGAATTACCATGTCTAGTAGACGCTTAAGAACCACTTCTCCTGAGACTGACC 243
DB 196 AAGAGTGAATTACCATGTCTAGTAGACGCTTAAGAACCACTTCTCCTGAGACTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGCGGTGAGATGGTATCTTTG 303
DB 256 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGAG--AGGGGAGATGGCTAC 312
QY 304 GACAACTGGGGCCAGGGAACCTGTGACCGTCTCCCTCA 342
DB 313 AAGTACTGGGGCCAGGGAACCTGTGACCGTCTCCCTCA 351

RESULT 11

US-10-330-530-7
Sequence 7, Application US/10330530
Publication No. US2003015251A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
FILE REFERENCE: AGENIX.031A
CURRENT APPLICATION NUMBER: US/10/330,530
PRIOR FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: US 60/346414
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 352
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-330-530-7

Query Match 76.7%; Score 262.2; DB 16; Length 352;
Best Local Similarity 87.9%; Pred. No. 3.3e-76;
Matches 298; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 4 GAGTCTGAGCCAGAGTGGTGAAGCCCTTGCACAGCCCTGTCCTGACCTGACGTGTCTCT 63
DB 16 GAGTCGGAGCCAGAGTGGTGAAGCCCTTGCACAGCCCTGTCCTGACCTGACGTGTCTCT 75
QY 64 GGTGGCTCCATCCCGACGTGTGTATTATTGAGTTGGTCCGCGACGCTCCAGGGAG 123
DB 76 GGTGGCTCCATCCCGACGTGTGTATTATTGAGTTGGTCCGCGACGCTCCAGGGAG 135
QY 124 GGCCTGAGTGGATCGGCAACATCTATCAAGTGGCAACCTTAACAACCCGTCCTC 183
DB 136 GGCCTGAGTGGATCGGCAACATCTATCAAGTGGCAACCTTAACAACCCGTCCTC 195
QY 184 AAGAGTGAATTACCATGTCTAGTAGACGCTTAAGAACCACTTCTCCTGAGACTGACC 243
DB 196 AAGAGTGAATTACCATGTCTAGTAGACGCTTAAGAACCACTTCTCCTGAGACTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGCGGTGAGATGGTATCTTTG 303
DB 256 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGAG--AGGGGAGATGGCTAC 312
QY 304 GACAACTGGGGCCAGGGAACCTGTGACCGTCTCCCTCA 342
DB 313 AAGTACTGGGGCCAGGGAACCTGTGACCGTCTCCCTCA 351

DB 136 GGCCTGAGTGGATCGGCAACATCTATCAAGTGGCAACCTTAACAACCCGTCCTC 195
QY 184 AAGAGTGAATTACCATGTCTAGTAGACGCTTAAGAACCACTTCTCCTGAGACTGACC 243
DB 196 AAGAGTGAATTACCATGTCTAGTAGACGCTTAAGAACCACTTCTCCTGAGACTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGCGGTGAGATGGTATCTTTG 303
DB 256 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGAG--AGGGGAGATGGCTAC 312
QY 304 GACAACTGGGGCCAGGGAACCTGTGACCGTCTCCCTCA 342
DB 313 AAGTACTGGGGCCAGGGAACCTGTGACCGTCTCCCTCA 351

RESULT 12

US-10-660-357-7
Sequence 7, Application US/10660357
Publication No. US20040115205A1
GENERAL INFORMATION:
APPLICANT: Bar-Eli, Menashe
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
FILE REFERENCE: AGENIX.030C1
CURRENT APPLICATION NUMBER: US/10/660,357
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 10/330,580
PRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 352
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-660-357-7

Query Match 76.7%; Score 262.2; DB 19; Length 352;
Best Local Similarity 87.9%; Pred. No. 3.3e-76;
Matches 298; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 4 GAGTCTGAGCCAGAGTGGTGAAGCCCTTGCACAGCCCTGTCCTGACCTGACGTGTCTCT 63
DB 16 GAGTCGGAGCCAGAGTGGTGAAGCCCTTGCACAGCCCTGTCCTGACCTGACGTGTCTCT 75
QY 64 GGTGGCTCCATCCCGACGTGTGTATTATTGAGTTGGTCCGCGACGCTCCAGGGAG 123
DB 76 GGTGGCTCCATCCCGACGTGTGTATTATTGAGTTGGTCCGCGACGCTCCAGGGAG 135
QY 124 GGCCTGAGTGGATCGGCAACATCTATCAAGTGGCAACCTTAACAACCCGTCCTC 183
DB 136 GGCCTGAGTGGATCGGCAACATCTATCAAGTGGCAACCTTAACAACCCGTCCTC 195
QY 184 AAGAGTGAATTACCATGTCTAGTAGACGCTTAAGAACCACTTCTCCTGAGACTGACC 243
DB 196 AAGAGTGAATTACCATGTCTAGTAGACGCTTAAGAACCACTTCTCCTGAGACTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGCGGTGAGATGGTATCTTTG 303
DB 256 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGAG--AGGGGAGATGGCTAC 312
QY 304 GACAACTGGGGCCAGGGAACCTGTGACCGTCTCCCTCA 342
DB 313 AAGTACTGGGGCCAGGGAACCTGTGACCGTCTCCCTCA 351

RESULT 13

US-10-684-109-54
Sequence 54, Application US/10684109
Publication No. US20040175379A1
GENERAL INFORMATION:
APPLICANT: Devries, Peter J.
APPLICANT: Green, Larry L.

```

; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989 US 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 355
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-684-109-54

Query Match      76.7%; Score 262.2; DB 19; Length 355;
Best Local Similarity 85.8%; Pred. No. 3.4e-76;
Matches 291; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 4 GAGCTGAGCCAGAGCTGTGGAAGCTTCAACAGACCCGTCCTCACCTGACCTGCTCT 63
Db 16 GAGTCGGGCCCAAGAGCTGTGGAAGCTTTCACAGACCTGTCCTCACCTGACCTGCTCT 75
QY 64 GGTGGCTCCATCCGACAGTGTGTATTATTATTTAGATTGGTCCGACAGCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCAGCAAGTGTGTATTATTATTTAGATTGGTCCGACAGCTCCAGGGAAG 135
QY 124 GGCCTGAGTGTGATCGGCAACATTTATCAAGTGGCAACCTTCAACAAACCCGTCCTC 183
Db 136 GGCCTGAGTGTGATTTGGTATCTATATACAGTAAAGACCTTCTATTATTAATCCGTCCTC 195
QY 184 AAGAGTGAATTTACCATGTAGTACAGACCGCTTAAGAACCTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTGAATTTACCATGTATGAGACCGCTTAAGAACCGTTCCTGAACTTATC 255
QY 244 TCTGTGACTGCGCGGACAGCGCCGTATATTACTGTGCGCGGTGAGATGGGTATATCTT 303
Db 256 TCTGTGACTGCGCGGACAGCGCCGTATATTACTGTGCGAGATTAATTGGGATGCGG 315
QY 304 GACAACTGGGGCCAGGGAACCTTGTGTACCGTCTCTCA 342
Db 316 GACTACTGGGGCCAGGGAACCTTGTGTACCGTCTCTCA 354

RESULT 14
US-10-684-109-110
; Sequence 110, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989 US 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-684-109-110

Query Match      76.7%; Score 262.2; DB 19; Length 1996;

```

```

Best Local Similarity 85.8%; Pred. No. 5.4e-76;
Matches 291; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 4 GAGCTGAGCCAGAGCTGTGGAAGCTTCAACAGACCCGTCCTCACCTGACCTGCTCT 63
Db 73 GAGTCGGGCCCAAGAGCTGTGGAAGCTTTCACAGACCTGTCCTCACCTGACCTGCTCT 132
QY 64 GGTGGCTCCATCCGACAGTGTGTATTATTATTTAGATTGGTCCGACAGCTCCAGGGAAG 123
Db 133 GGTGGCTCCATCCAGCAAGTGTGTATTATTATTTAGATTGGTCCGACAGCTCCAGGGAAG 192
QY 124 GGCCTGAGTGTGATCGGCAACATTTATCAAGTGGCAACCTTCAACAAACCCGTCCTC 183
Db 193 GGCCTGAGTGTGATTTGGTATCTATATACAGTAAAGACCTTCTATTATTAATCCGTCCTC 252
QY 184 AAGAGTGAATTTACCATGTAGTACAGACCGCTTAAGAACCTTCTCCCTGAGACTGACC 243
Db 253 AAGAGTGAATTTACCATGTATGAGACCGCTTAAGAACCGTTCCTGAACTTATC 312
QY 244 TCTGTGACTGCGCGGACAGCGCCGTATATTACTGTGCGCGGTGAGATGGGTATATCTT 303
Db 313 TCTGTGACTGCGCGGACAGCGCCGTATATTACTGTGCGAGATTAATTGGGATGCGG 372
QY 304 GACAACTGGGGCCAGGGAACCTTGTGTACCGTCTCTCA 342
Db 373 GACTACTGGGGCCAGGGAACCTTGTGTACCGTCTCTCA 411

RESULT 15
US-10-684-109-111/c
; Sequence 111, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989 US 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-684-109-111

Query Match      76.7%; Score 262.2; DB 19; Length 1996;
Best Local Similarity 85.8%; Pred. No. 5.4e-76;
Matches 291; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 4 GAGCTGAGCCAGAGCTGTGGAAGCTTCAACAGACCCGTCCTCACCTGACCTGCTCT 63
Db 1924 GAGTCGGGCCCAAGAGCTGTGGAAGCTTTCACAGACCTGTCCTCACCTGACCTGCTCT 1865
QY 64 GGTGGCTCCATCCGACAGTGTGTATTATTATTTAGATTGGTCCGACAGCTCCAGGGAAG 123
Db 1864 GGTGGCTCCATCCAGCAAGTGTGTATTACTGAGCTGAGATCCGCCAGACCCAGGGAAG 1805
QY 124 GGCCTGAGTGTGATCGGCAACATTTATCAAGTGGCAACCTTCAACAAACCCGTCCTC 183
Db 1804 GGCCTGAGTGTGATTTGGTATCTATATTAACAGTAAAGACCTCTATTATTAATCCGTCCTC 1745
QY 184 AAGAGTGAATTTACCATGTAGTACAGACCGCTTAAGAACCTTCTCCCTGAGACTGACC 243
Db 1744 AAGAGTGAATTTACCATGTATGAGACCGCTTAAGAACCGTTCCTGAACTTATC 1685

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Qy	244	TCTGTGACTGCGCGGACACGCGCGCTATTACTGTGCGCGGTCAAGATGGGTACTTTG	303
Db	1684	TCTGTGACTGCGCGGACACGCGCGCTATTACTGTGCGCGGTCAAGATGGGTACTTTG	1625
Qy	304	GACAACTGGGGCCGAGGGAACCTGTGTCACCGTCTCTCA	342
Db	1624	GACTACTGGGGCCGAGGGAACCTGTGTCACCGTCTCTCA	1586

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 Job time : 513.827 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 27, 2005, 04:09:06 ; Search time 1956.83 Seconds
(without alignments)
8468.649 Million cell updates/sec

Title: US-10-027-725A-1

Perfect score: 342

Sequence: 1 ctgcagactcggccaggaact.....ccctgctaccgctctctca 342

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hhg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	340.4	99.5	342	9	HSAA58382 Homo sapi
2	308.4	90.2	342	9	HSAA58384 Homo sapi
3	297.2	86.9	342	9	HSAA58383 Homo sapi
4	291	85.1	355	9	HSAA58383 Homo sapi
5	287.8	84.2	355	9	AY640579 Homo sapi
6	286.2	83.7	355	9	AY640580 Homo sapi
7	283	82.7	355	9	AY640509 Homo sapi
8	281.4	82.3	355	9	AY640564 Homo sapi
9	278.2	81.3	355	9	AY640507 Homo sapi
10	278.2	81.3	432	9	HSAA491911 Homo sapi
11	277.2	81.1	411	9	HSR22X1 Homo sapi
12	276.6	80.9	432	9	HSAA491912 Homo sapi
13	276.4	80.8	351	9	HSR244930 Homo sapi
14	276.4	80.8	360	6	AX061463 Sequence
15	275	80.4	414	9	AP062112 Homo sapi
16	273.8	80.1	414	9	HST14X13 Homo sapi
17	273.8	80.1	414	9	HST14X4 Homo sapi
18	272	79.5	357	9	HSR244949 Homo sapi
19	271.8	79.5	354	9	HSR245064 Homo sapi

20	271.8	79.5	360	9	HSU80129 Human immun
21	271.8	79.5	360	9	HSU80130 Human immun
22	271.6	79.4	358	9	AF021954 Homo sapi
23	270.6	79.1	341	9	AF607380 Homo sapi
24	270.6	79.1	403	12	AF452917 Synthetic
25	270.4	79.1	363	9	HSU80131 Human immun
26	269.2	78.7	354	9	HSR244955 Homo sapi
27	269.2	78.7	417	9	HST14X9 Homo sapi
28	268.8	78.6	366	9	HSR233698 Homo sapi
29	268.6	78.5	351	9	HSR245020 Homo sapi
30	268.4	78.5	357	9	HSR279523 Homo sapi
31	267.4	78.2	400	12	AF452909 Synthetic
32	267	78.1	354	9	HSR579125 Homo sapi
33	266.8	78.0	357	9	HSR279541 Homo sapi
34	266.8	78.0	357	9	HSU80168 Homo sapi
35	266.2	77.8	412	12	AF452912 Synthetic
36	265.8	77.7	366	9	HSR244928 Homo sapi
37	265.8	77.7	369	6	AX061433 Homo sapi
38	265.6	77.7	363	9	HSU80128 Homo sapi
39	265.4	77.6	339	9	AY607360 Homo sapi
40	265.4	77.6	351	9	HSR244958 Homo sapi
41	265	77.5	362	9	HSU80169 Homo sapi
42	264.6	77.4	351	9	AY607364 Homo sapi
43	264.4	77.3	355	9	AY640551 Homo sapi
44	264	77.2	328	9	AY607437 Homo sapi
45	264	77.2	362	9	AF126269 Homo sapi

ALIGNMENTS

RESULT 1	HSAA58382	342 bp	mRNA	linear	PRI 30-APR-2002
LOCUS	Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 94.				
DEFINITION	HSAA58382				
ACCESSION	AJ58382.1	GI:20387063			
VERSION	IGHV gene; immunoglobulin heavy chain; variable region.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	Flicker, S., Steinberger, P., Nordhaug, L., Sperr, W.R., Majlesi, Y., Valent, P., Kraft, D. and Valenta, R.				
AUTHORS	Conversion of grass allergen-specific human IGB into a protective IgG1 antibody				
TITLE	Unpublished				
JOURNAL	2 (bases 1 to 342)				
REFERENCE	Flicker, S.				
AUTHORS	Direct Submission				
TITLE	Submitted (24-APR-2002) Flicker S., Department of Pathophysiology, General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090 Vienna, AUSTRIA				
JOURNAL					
FEATURES	Location/Qualifiers				
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gene	/organism="Homo sapiens"				
CDS	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="94"				
	/rearranged				
	1..342				
	/gene="IGHV"				
	<1..>342				
	/gene="IGHV"				
	/codon_start=1				
	/product="immunoglobulin heavy chain"				
	/protein_id="CA030444.1"				
	/db_xref="GI:20387064"				
	/translation="LESFGPLVKKPAQTLISCAVSGSIRSGYVSWIRHPGKGLT				
	WIGYVHSGNTYVNPISLKSRIAMSVDISENKFSLRLNSVTADTAAYVCARLDGVTLD				
	IMGQGLIVTVSS"				

V_region 1..342
/gene="IGHV"
/product="immunoglobulin heavy chain variable region"

ORIGIN

Query Match 99.5%; Score 340.4; DB 9; Length 342;
Best Local Similarity 99.7%; Pred. No. 1.3e-84;
Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTCAGTCTGGCCAGAGACTGGTAAGCCTGCACAGACCTGTCCTCCAGCTGGCGCTTC 60
Db 1 CTCAGTCTGGCCAGAGACTGGTAAGCCTGCACAGACCTGTCCTCCAGCTGGCGCTTC 60

Qy 61 TCTGGCGGCTCCATCCGAGTGTGTACTACTGAGATTGGATCCGCCAACCCAGGG 120
Db 61 TCTGGCGGCTCCATCCGAGTGTGTACTACTGAGATTGGATCCGCCAACCCAGGG 120

Qy 121 AAGGGCTGGAGTGGATTGGGTACATCTATACAGTGGGAACCTTAACAACCCGCTCC 180
Db 121 AAGGGCTGGAGTGGATTGGGTACATCTATACAGTGGGAACCTTAACAACCCGCTCC 180

Qy 181 CTCAGAGTGCAGATTGCGATGCGTAGACAGCTCTGAACAAGTTCTCCCTGAGGCTG 240
Db 181 CTCAGAGTGCAGATTGCGATGCGTAGACAGCTCTGAACAAGTTCTCCCTGAGGCTG 240

Qy 241 AACTCTGTACTGCCCGCGGACACGCGCGTGTATTACTGTGCGAGGTTAGATGGCTAC 300
Db 241 AACTCTGTACTGCCCGCGGACACGCGCGTGTATTACTGTGCGAGGTTAGATGGCTAC 300

Qy 301 TTGGACATCTGGGGCCAGGGAACCTGTGCAACCGCTCTCTCA 342
Db 301 TTGGACATCTGGGGCCAGGGAACCTGTGCAACCGCTCTCTCA 342

RESULT 2
HSA458384 342 bp mRNA linear PRI 30-APR-2002
LOCUS HSA458384
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 100.
ACCESSION AJ458384
VERSION AJ458384.1 GI:20387067
KEYWORDS IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Flicker S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y., Valent, P., Kraft, D. and Valenta, R.,
Conversion of grass allergen-specific human IGE into a protective
IgG1 antibody
Unpublished
2 (bases 1 to 342)
Flicker, S.
Direct Submission
Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090
Vienna, AUSTRIA

FEATURES
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CDS

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Query Match 90.2%; Score 308.4; DB 9; Length 342;
Best Local Similarity 93.9%; Pred. No. 1.3e-75;
Matches 321; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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Db 1 CTCAGTCTGGCCAGAGACTGGTAAGCCTGCACAGACCTGTCCTCCAGCTGGCGCTTC 60

Qy 61 TCTGGCGGCTCCATCCGAGTGTGTACTACTGAGATTGGATCCGCCAACCCAGGG 120
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Qy 181 CTCAGAGTGCAGATTGCGATGCGTAGACAGCTCTGAACAAGTTCTCCCTGAGGCTG 240
Db 181 CTCAGAGTGCAGATTGCGATGCGTAGACAGCTCTGAACAAGTTCTCCCTGAGGCTG 240

Qy 241 AACTCTGTACTGCCCGCGGACACGCGCGTGTATTACTGTGCGAGGTTAGATGGCTAC 300
Db 241 AACTCTGTACTGCCCGCGGACACGCGCGTGTATTACTGTGCGAGGTTAGATGGCTAC 300

Qy 301 TTGGACATCTGGGGCCAGGGAACCTGTGCAACCGCTCTCTCA 342
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RESULT 3
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LOCUS HSA458383
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 60.
ACCESSION AJ458383
VERSION AJ458383.1 GI:20387065
KEYWORDS IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Flicker S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y., Valent, P., Kraft, D. and Valenta, R.,
Conversion of grass allergen-specific human IGE into a protective
IgG1 antibody
Unpublished
2 (bases 1 to 342)
Flicker, S.
Direct Submission
Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090
Vienna, AUSTRIA

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CDS

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Best Local Similarity 91.8%; Pred. No. 1.8e-72;
Matches 314; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCCAAGAGCTGTAAGCTTGACACAGACCTGTGCTCAGCTGCGCTGTC 60
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QY 181 CTCAGAGTCAATTCGATGTGGTAGACAAGTCTGAGAACAGTTCTCCCTGAGGCTG 240
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QY 241 AACTCTGTGACTGCGCGGACACCGCCGTATTAATCTGTGAGAGTTGATGGCTACACT 300
Db 241 AACTCTGTGACTGCGCGGACACCGCCGTATTAATCTGTGAGAGTTGATGGCTACACT 300
QY 301 TTGGACATCTGGGGCCAGGAAACCTGTGTCAACCGTCTCTCA 342
Db 301 TTGGACATCTGGGGCCAGGAAACCTGTGTCAACCGTCTCTCA 342

RESULT 4 355 bp mRNA linear PRI 03-JUL-2004
LOCUS AY640579
DEFINITION Homo sapiens clone RT immunoglobulin E variable region mRNA,
partial cds.
ACCESSION AY640579
VERSION AY640579.1 GI:49354899
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.
TITLE Biased use of VHS Igb+ B cells in the nasal mucosa of allergic
rhinitis patients
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 355)
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St
Thomas Street, London SE1 1UL, UK

FEATURES

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Best Local Similarity 91.2%; Pred. No. 9.7e-71;
Matches 309; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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QY 64 GCGCGCTCCATCCGAGTGTGTGTTACTACTGAGTTGATTCGCCCAACCCAGGAAAG 123
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QY 184 AAGAGTCAATTCGATGTGGTAGACAAGTCTGAGAACAGTTCTCCCTGAGGCTGAAC 243
Db 196 AAGAGTCAATTCGATGTGGTAGACAAGTCTGAGAACAGTTCTCCCTGAGGCTGAAC 255
QY 244 TCTGTGACTGCGCGGACACCGCGGTATTAATCTGTGAGAGTTAGATGCTTACACTTTG 303
Db 256 TCTGTACTGCGCGGACACCGCGGTATTAATCTGTGAGAGTTAGATGCTTACACTTTT 315
QY 304 GACATCTGGGGCCAGGAAACCTGTGTCAACCGTCTCTCA 342
Db 316 GACTACTGGGGCCAGGAAACCTGTGTCAACCGTCTCTCA 354

RESULT 5 355 bp mRNA linear PRI 03-JUL-2004
LOCUS AY640487
DEFINITION Homo sapiens clone AP immunoglobulin E variable region mRNA,
partial cds.
ACCESSION AY640487
VERSION AY640487.1 GI:49354726
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.
TITLE Biased use of VHS Igb+ B cells in the nasal mucosa of allergic
rhinitis patients
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 355)
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St
Thomas Street, London SE1 1UL, UK

FEATURES

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Query Match 84.2%; Score 287.8; DB 9; Length 355;
Best Local Similarity 90.6%; Pred. No. 7.7e-70;
Matches 307; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGAGACTGTGTAGAGCCCTGACAGACCCCTGTCCTGAGCTGCTGTCTT 63
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QY 64 GGGCGCTCCATCCGACAGTGTGTACTACTGAGATTGCGCAACCCAGGGAG 123
DB 76 GGTGGCTCCATCAGCAGTGTGTGTACTACTGAGATTGCGCAACCCAGGGAG 135
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DB 136 GGCCTGAGTGGATTGGGTATCATCTATCAGTGGGAACACTTCAACCCGTCCTC 195
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DB 256 TCTGTGACTCCCGGACACGCGCGTATTAATCTGTGCGAGGTTAGATGCTACACTTTT 315
QY 304 GACATCTGGGGCCAGGGAACCTGTGACCGTCTCTCA 342
DB 316 GACTACTGGGGCCAGGGAACCTGTGACCGTCTCTCA 354

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LOCUS AY640580
DEFINITION Homo sapiens clone RU immunoglobulin E variable region mRNA,
partial cds.

ACCESSION AY640580
VERSION AY640580.1 GI:49354901

KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Coker,H.A., Durham,S.R. and Gould,H.J.
1 (bases 1 to 355)
REFERENCE Coker,H.A., Durham,S.R. and Gould,H.J.
TITLE Biased use of VHS IGB+ B cells in the nasal mucosa of allergic
rhinitis patients
JOURNAL Unpublished
2 (bases 1 to 355)
REFERENCE Coker,H.A., Durham,S.R. and Gould,H.J.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St
Thomas Street, London SE1 1UL, UK

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Query Match 83.7%; Score 286.2; DB 9; Length 355;

Best Local Similarity 90.3%; Pred. No. 2.2e-69;
Matches 306; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGAGACTGTGTAGAGCCCTGACAGACCCCTGTCCTGAGCTGCTGTCTT 63
DB 16 GAGTCGGGCCAGAGACTGTGTAGAGCCCTGACAGACCCCTGTCCTGAGCTGCTGTCTT 75
QY 64 GGGCGCTCCATCCGACAGTGTGTACTACTGAGATTGCGCAACCCAGGGAG 123
DB 76 GGTGGCTCCATCAGCAGTGTGTGTACTACTGAGATTGCGCAACCCAGGGAG 135
QY 124 GGCCTGAGTGGATTGGGTATCATCTATCAGTGGGAACACTTCAACCCGTCCTC 183
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DB 256 TCTGTGACTCCCGGACACGCGCGTATTAATCTGTGCGAGGTTAGATGCTACACTTTT 315
QY 304 GACATCTGGGGCCAGGGAACCTGTGACCGTCTCTCA 342
DB 316 GACTACTGGGGCCAGGGAACCTGTGACCGTCTCTCA 354

RESULT 7 355 bp mRNA linear PRI 03-JUL-2004
LOCUS AY640509
DEFINITION Homo sapiens clone BM immunoglobulin E variable region mRNA,
partial cds.

ACCESSION AY640509
VERSION AY640509.1 GI:49354765

KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Coker,H.A., Durham,S.R. and Gould,H.J.
1 (bases 1 to 355)
REFERENCE Coker,H.A., Durham,S.R. and Gould,H.J.
TITLE Biased use of VHS IGB+ B cells in the nasal mucosa of allergic
rhinitis patients
JOURNAL Unpublished
2 (bases 1 to 355)
REFERENCE Coker,H.A., Durham,S.R. and Gould,H.J.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-2004) Randall Centre, King's College London, St
Thomas Street, London SE1 1UL, UK

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ORIGIN

Query Match 82.7%; Score 283; DB 9; Length 355;
Best Local Similarity 89.7%; Pred. No. 1.7e-68;
Matches 304; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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Db 76 GGTGGCTTCACACAGAGTGTGTACTACTGAGATTGGATCCGCAACACCCAGGAAAG 135

Qy 124 GCGCTGAGTGGATTGGGTATCATCTATCAGTGGGAACACTTCAACAAACCGTCCCTC 183

Db 136 GGCCTGAGATGGATTGGATCATCTATTAACAGTGGAGACCCACTAACCCGTCCTC 195

Qy 184 AAGAGTCGAATTGGCATGTCCGTAGACACGCTGTAGAACATTTCTCCCTGAGGCTGAC 243

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Qy 304 GACATCTGGGGCCAGGAAACCTGTGACCGCTCTCTCA 342

Db 316 GACTACTGGGGCCAGGAAACCTGTGACCGCTCTCTCA 354

RESULT 8
AY640564 355 bp mRNA linear PRI 03-JUL-2004
LOCUS Homo sapiens clone RE immunoglobulin E variable region mRNA,
partial cds.
AY640564 GI:49354872

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
Coker, H.A., Durham, S.R. and Gould, H.J.
Blased use of VHS IGE+ B cells in the nasal mucosa of allergic
rhinitis patients
Unpublished
2 (bases 1 to 355)
Direct Submission
Submitted (28-MAY-2004) Randall Centre, King's College London, St
Thomas Street, London SE1 1UL, UK

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Query Match 82.3%; Score 281.4; DB 9; Length 355;
Best Local Similarity 89.4%; Pred. No. 4.8e-68;
Matches 303; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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4 GAGTCTGGCCAGAGACTGTGAAGCTTCTCAGACCCCTGTCCCTCACTGACGTCTCT 63
16 GAGTGGGGCCAGAGACTGTGAAGCTTCTCAGACCCCTGTCCCTCACTGACGTCTCT 75
64 GCGCGCTTCATCCGAGTGTGTACTACTGAGATTGGATCCGCAACACCCAGGAAAG 123
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316 GACTACTGGGGCCAGGAAACCTGTGACCGCTCTCTCA 354

Db 76 GGTGGCTTCACACAGAGTGTGTACTACTGAGATTGGATCCGCAACACCCAGGAAAG 135

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Qy 184 AAGAGTCGAATTGGCATGTCCGTAGACACGCTGTAGAACATTTCTCCCTGAGGCTGAC 243

Db 196 AAGAGTGGGGTATACACATCAGTAGACACGCTTAAGAACAGTTCTCCCTGAGGCTGAC 255

Qy 244 TCTGTACTGCGCGGACACGCGCGTATTACTGTGCGAGATTAGATGCTTCACTTTG 303

Db 256 TCTGTACTGCGCGGACACGCGCGTATTACTGTGCGAGATTAGATGCTTCACTTTG 315

Qy 304 GACATCTGGGGCCAGGAAACCTGTGACCGCTCTCTCA 342

Db 316 GACTACTGGGGCCAGGAAACCTGTGACCGCTCTCTCA 354

RESULT 9
AY640507 355 bp mRNA linear PRI 03-JUL-2004
LOCUS Homo sapiens clone BK immunoglobulin E variable region mRNA,
partial cds.
AY640507 GI:49354762

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
Coker, H.A., Durham, S.R. and Gould, H.J.
Blased use of VHS IGE+ B cells in the nasal mucosa of allergic
rhinitis patients
Unpublished
2 (bases 1 to 355)
Direct Submission
Submitted (28-MAY-2004) Randall Centre, King's College London, St
Thomas Street, London SE1 1UL, UK

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WTFPDMQGLTVSVS"

CDS
Query Match 81.3%; Score 278.2; DB 9; Length 355;
Best Local Similarity 88.8%; Pred. No. 3.8e-67;
Matches 301; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

ORIGIN
4 GAGTCTGGCCAGAGACTGTGAAGCTTCTCAGACCCCTGTCCCTCACTGACGTCTCT 63
16 GAGTGGGGCCAGAGACTGTGAAGCTTCTCAGACCCCTGTCCCTCACTGACGTCTCT 75
64 GCGCGCTTCATCCGAGTGTGTACTACTGAGATTGGATCCGCAACACCCAGGAAAG 123
76 GGTGGCTTCACACAGAGTGTGTACTACTGAGATTGGATCCGCAACACCCAGGAAAG 135
124 GCGCTGAGTGGATTGGGTATCATCTATCAGTGGGAACACTTCAACAAACCGTCCCTC 183
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304 GACATCTGGGGCCAGGAAACCTGTGACCGCTCTCTCA 342
316 GACTACTGGGGCCAGGAAACCTGTGACCGCTCTCTCA 354

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Db 136 GGCCTGAGTGTGATTGATCATCTATTAACGGGGAGACACCTACTACACCCTCCCTC 195
Qy 184 AAGAGTCGAATTGCGATGCGGTAGACACGCTGTGAGAACAGATTCTCCCTGAGGCTGAC 243
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Qy 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGTGGAGTTAGATGCTTACACTTTG 303
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Qy 304 GACATCTGGGGCCAGGAAACCTGTGACCCGTCCTCTCA 342
Db 316 GACTACTGGGGCCAGGAAACCTGTGACCGTCTCTCTCA 354

RESULT 10
LOCUS HSA491911 432 bp mRNA linear PRI 20-NOV-2003
DEFINITION Homo sapiens mRNA for immunoglobulin heavy chain V-D-J-Ce region
            (clone HD17 C9) .
ACCESSION AJ491911
VERSION AJ491911.1 GI:24415808
KEYWORDS constant region; epsilon chain; IGH gene; immunoglobulin heavy
SOURCE chain, variable region.
ORGANISM Homo sapiens
            Homo sapiens (human)
REFERENCE 1
AUTHORS Coker,H.A., Durham,S.R. and Gould,H.J.
TITLE Local somatic hypermutation and class switch recombination in the
JOURNAL J. Immunol. 171 (10), 5602-5610 (2003)
MEDLINE 22970235
PUBMED 14607969
REFERENCE 2 (bases 1 to 432)
AUTHORS Coker,H.A.
TITLE Direct Submision
JOURNAL Submitted (26-JUN-2002) Coker H.A., Biomedical Sciences, Randall
CENTRE, King's College London, Guy's Campus, London, SE1 1UL,
UNITED KINGDOM
FEATURES
SOURCE Location/Qualifiers
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allergic rhinitis patient"
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1..297
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/note="VH segment"
298..315
/gene="IGHV4-30"
/note="HD5-24 rf 3"
316..355
/gene="IGHV4-30"
/note="region VH4b"
356..432
/gene="IGHB"
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/gene="IGHB"
/product="Immunoglobulin epsilon heavy chain constant
region"

ORIGIN
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Best Local Similarity 88.8%; Pred. No. 3.8e-67;
Matches 301; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 4 GAGCTGGCCAGAGACTGTGTAAGCCGTGCACAGACCCGTCTCCCTGAGCTGCGTCTCT 63
Db 16 GAGTCGGGCCAGAGACTGTGTAAGCCGTGCACAGACCCGTCTCCCTGAGCTGCGTCTCT 75
Qy 64 GCGCGCTCCATCCGCACTGTGTGTTACTACTGAGATTGGATCCGCCAACCCAGGGAAG 123
Db 76 GTTGCGCCCATCATGATAGTGTGTGTTACTACTGAGCTGTGATCCGCCAACCCAGGGAAG 135
Qy 124 GGCCTGAGTGGAGTTGGGTATCATCTATCAAGTGGGAGACCTTACAAACACCCGTCCTC 183
Db 136 GGCCTGAGTGGAGTTGGGTATCATCTATTAACAGGGGAGACCTTACAAACCCGTCCTC 195
Qy 184 AAGAGTCGAATTGCGATGCGGTAGACACGCTGTGAGAACAGTTCTCCCTGAGGCTGAC 243
Db 196 AGAGTGGAAATATCATCTCAATTGACACGCTGCAAAATCAGTTCTCCCTGAGGCTGACC 255
Qy 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGTTAGATGCTTACACTTTG 303
Db 256 TCTCTGACTGCGCGGACACGCGCGTGTATTCTGTGTGGCTGTAGATGGTACAGTTTG 315
Qy 304 GACATCTGGGGCCAGGAAACCTGTGACCGTCTCTCTCA 342
Db 316 GACTACTGGGGCCAGGAAACCTGTGACCGTCTCTCTCA 354

RESULT 11
HST22X1 411 bp mRNA linear PRI 09-SEP-2004
LOCUS H.sapiens mRNA for Ig heavy chain variable region (VH4D) (clone
DEFINITION T22.1).
ACCESSION 275385
VERSION 275385.1 GI:2062048
KEYWORDS immunoglobulin; immunoglobulin heavy chain; immunoglobulin
superfamily; variable region.
SOURCE Homo sapiens
ORGANISM Homo sapiens
            Homo sapiens (human)
REFERENCE 1
AUTHORS Tonnelie,C., D'Ercole,C., Depraetere,V., Metras,D., Boudli,L. and
FOUGEREAU,M.
TITLE Human thymic B cells largely overexpress the VH4 Ig gene family. A
possible role in the control of tolerance in situ?
JOURNAL Int. Immunol. 9 (3), 407-414 (1997)
MEDLINE 97244170
PUBMED 9088979
REFERENCE 2 (bases 1 to 411)
AUTHORS Tonnelie,C.
TITLE Direct Submision
JOURNAL Submitted (26-JUN-1996) Cecile Tonnelie, Centre d'Immunologie
Marseille Luminy, Marseille, 13288, France
FEATURES
SOURCE Location/Qualifiers
1..411
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/chromosome="14"
/clone="T2.1"
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/tissue_type="thymus"
/clone_id="T2"
/dev_stage="infant"
1.411
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1.57
sig_peptide
58.354
V_segment
/note="Ig VH4-segment"
355.377
D_segment
J_segment
378.411
ORIGIN
Query Match      81.1%; Score 277.2; DB 9; Length 411;
Best Local Similarity 88.8%; Pred. No. 7.3e-67;
Matches 300; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 4 GAGTCTGCCCCAGAGCTGTGAAGCCTGCACAGACCCCTGCTCCTGAGCTGCTCTCT 63
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Db 73 GAGTCGGGCCAGAGCTGTGAAGCCTTCACAGACCCCTGCTCCTGAGCTGCTCTCT 132
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Qy 64 GCGCGCTCCATCCGCACTGTGTCTTACTCTGAGTTGATCCGCCAACCCAGGAG 123
    |||
Db 133 GGTGGCTCCATCAGACAGTGTGTCTTACTCTGAGTGTGATCCGCCAACCCAGGAG 192
    |||
Qy 124 GGCCTGAGAGGATTTGGTATCATCTATCAGATGGGAAACCTTCAACACCCGCTCC 183
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Db 193 GGCCTGAGAGGATTTGGTATCATCTATCAGATGGGAAACCTTCAACACCCGCTCC 252
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Qy 184 AAGAGTCGAATTGCCATGTCCGTAGACACGCTGTGAGAACAGTTCTCCCTGAGGCTG 243
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Db 253 AAGAGTCGAATTACATATCATATGACACGCTGTGAGAACAGTTCTCCCTGAGGCTG 312
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Qy 244 TCTGTGACTGCGCGGACACGCGGTGTATTACTGTGGAGATTAGATGGCTACACTTTG 303
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Db 313 TCTGTGACTGCGCGGACACGCGGTGTATTACTGTGGAGATTAGATGGCTACACTTTG 372
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Qy 304 GACATCTGGGGCCAGGAGACCCGTGTACACCGTCTCCTC 341
    |||
Db 373 TCCAGCTGGGGCCAGGAGACCCGTGTACACCGTCTCCTC 410
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RESULT 12
HSA491912      432 bp      mRNA      linear      PRI 20-NOV-2003
LOCUS          HSA491912      432 bp      mRNA      linear      PRI 20-NOV-2003
DEFINITION     Homo sapiens mRNA for immunoglobulin heavy chain V-D-J-Ce region
                (clone HD17 C37).
ACCESSION      AJ491912
VERSION        AJ491912.1 GI:24415810
KEYWORDS       constant region; epsilon chain; IGH gene; immunoglobulin heavy
                chain; variable region.
SOURCE          Homo sapiens (human)
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1
AUTHORS        Coker H.A., Duram S.R. and Gould H.J.
TITLE          Local somatic hypermutation and class switch recombination in the
                nasal mucosa of allergic rhinitis patients
JOURNAL        J. Immunol. 171 (10), 5602-5610 (2003)
MEDLINE        22970235
PUBMED        14607969
REFERENCE      2 (bases 1 to 432)
AUTHORS        Coker H.A.
TITLE          Direct Submission
JOURNAL        Submitted (26-JUN-2002) Coker H.A., Biomedical Sciences, Randall
                Centre, King's College London, Guy's Campus, London, SE1 1UL,
                UNITED KINGDOM

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FEATURES
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location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/isolation_source="nasal biopsy from inferior turbinate of
allergic rhinitis patient"
/db_xref="taxon:9606"
/clone="HD17 C37"
/sex="female"
/cell_type="B lymphocyte"
/tissue_type="nasal mucosa"
/dev_stage="adult"
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gene
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<1..>355
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/protein_id="CAD38015.1"
/db_xref="GI:24415811"
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KGLWETGYIYRGSITYNPSLRIRIIMSIDTSANQPSLRITSLPADTAVYFCARLDG
YSLDYNQGCTLVYSS"
1..355
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/ gene="IGHV4-30"
/product="immunoglobulin heavy chain variable region"
1..297
V_segment
/ gene="IGH"
/ note="VH segment"
298..315
D_segment
/ gene="IGH"
/ note="D5-24 rf 3"
316..355
J_segment
/ gene="IGH"
/ note="region JH4b"
356..432
gene
/ gene="IGH"
356..432
C_region
/ gene="IGH"
/product="immunoglobulin epsilon heavy chain constant
region"
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Query Match      80.9%; Score 276.6; DB 9; Length 432;
Best Local Similarity 88.5%; Pred. No. 1.1e-66;
Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 4 GAGTCTGCCCCAGAGCTGTGAAGCCTGCACAGACCCCTGCTCCTGAGCTGCTCTCT 63
    |||
Db 16 GAGTCGGGCCAGAGCTGTGAAGCCTTCACAGAACCTGTCTCCCTGAGCTGCTCTCT 75
    |||
Qy 64 GCGCGCTCCATCCGCACTGTGTCTTACTCTGAGTTGATCCGCCAACCCAGGAG 123
    |||
Db 76 GGTGGCTCCATCAGACAGTGTGTCTTACTCTGAGTGTGATCCGCCAACCCAGGAG 135
    |||
Qy 124 GGCCTGAGAGGATTTGGTATCATCTATCAGATGGGAAACCTTCAACACCCGCTCC 183
    |||
Db 136 GGCCTGAGAGGATTTGGTATCATCTATCAGATGGGAAACCTTCAACACCCGCTCC 195
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Qy 184 AAGAGTCGAATTGCCATGTCCGTAGACACGCTGTGAGAACAGTTCTCCCTGAGGCTG 243
    |||
Db 196 AAGAGTCGAATTACATATCATATGACACGCTGTGAGAACAGTTCTCCCTGAGGCTG 255
    |||
Qy 244 TCTGTGACTGCGCGGACACGCGGTGTATTACTGTGGAGATTAGATGGCTACACTTTG 303
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Db 256 TCTGTGACTGCGCGGACACGCGGTGTATTACTGTGGAGATTAGATGGCTACACTTTG 315
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Qy 304 GACATCTGGGGCCAGGAGACCCGTGTACACCGTCTCCTCA 342
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Db 316 GACTACTGGGCGCAGGGAACCTGTCACCGTCTCTCA 354

RESULT 13
LOCUS HSA244930 351 bp mRNA linear PRI 01-JUN-2000
DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone I-A34.
ACCESSION AJ244930
VERSION AJ244930.1 GI:4995319
KEYWORDS IGM; IGM heavy chain; immunoglobulin mu heavy chain; variable region.

SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
TITLE Chiorazzi, N., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A., Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents
JOURNAL J. Immunol. 164 (11), 5596-5604 (2000)
MEDLINE 10820234
PUBMED 2 (bases 1 to 351)

REFERENCE
AUTHORS Direct Submission
TITLE Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova, ITALY

FEATURES
SOURCE Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="14"
/clone="I-A34"
/cell_type="B-lymphocyte"
/tissue_type="tonsil"
/rearranged
1..351
/gene="IGHV4-31"
/c1..>351
/gene="IGHV4-31"
/codon_start=1
/product="immunoglobulin mu heavy chain variable region"
/protein_id="CAB44065.1"
/db_xref="GI:4995320"
/translation="QLOBSEGRGLYKPSQTLSTCTVGGGSSSGGYTWSMRQPKG LEWIGYLYSGSTYINPSLKSRTVISVDTSKNPSLKLSTVADTAVYICARGKEDF YFDYWGQGLTVTSS"
<1..>351
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/product="immunoglobulin mu heavy chain variable region"

ORIGIN

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Best Local Similarity 90.1%; Pred. No. 1.2e-66;
Matches 308; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

Db 4 GAGTCTGGCCAGAGACTGTGAAGCTTCACAGACCCCTGCTCAGCTGGCTCTCT 63
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10 GAGTCGGGCCAGAGACTGTGAAGCTTCACAGACCCCTGCTCAGCTGGCTCTCT 69
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64 GGCAGCTCCATCCGAGAGTGTGTTACTGAGTGGATCCGCCAACCCCAAGGAG 123
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70 GGTGGCTTCATCAGCAGTGTGTGTTACTGAGCTGGATCCGCCAACCCCAAGGAG 129
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124 GGCCTGAGTGGATGGTATCATCATCAAGTGGGAAACACTCAACACCCGCTCCTC 183
|||
130 GGCCTGAGTGGATGGTATCATCATCAAGTGGGAAACACTCAACACCCGCTCCTC 189
|||
184 AAGAGTGAATTGCTATGCTGCTAGACACGCTGAGAACCAAGTTCTCCCTGAGGCTGAC 243

Db 190 AAGAGTGAATTGCTATGCTATGAGACAGCTGTAAGAACCAAGTTCTCCCTGAGGCTGAGC 249
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244 TCTGTGACTGCGCGGAGACAGCGCGGTATTACTGTGCGA---GGTTAGTGGTCACT 300
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250 TCTGTGACTGCGCGGAGACAGCGCGGTATTACTGTGCGAGAGCAAAAGGACTTCTAC 309
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301 TTGGACATCTGGGGCCAGGGAACCTGTCACCGTCTCTCA 342
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310 TTGACTACTGGGGCCAGGGAACCTGTCACCGTCTCTCA 351
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RESULT 14
LOCUS AX061463 360 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 32 from Patent WO0100678.
ACCESSION AX061463
VERSION AX061463.1 GI:12406598
KEYWORDS Human immunodeficiency virus 1 (HIV-1)
SOURCE Human immunodeficiency virus 1
ORGANISM Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.

REFERENCE
AUTHORS 1
TITLE Watkins, B.A. and Reitz, M.S.
JOURNAL Human monoclonal antibodies to hiv-1 envelope glycoprotein gp120
Patent: WO 0100678-A 32 04-JAN-2001;
THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)

FEATURES
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/organism="Human immunodeficiency virus 1"
/mol_type="unassigned DNA"
/db_xref="taxon:11676"
/note="VH"

ORIGIN

Query Match 80.8%; Score 276.4; DB 6; Length 360;
Best Local Similarity 90.1%; Pred. No. 1.2e-66;
Matches 308; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

Db 4 GAGTCTGGCCAGAGACTGTGAAGCTTCACAGACCCCTGCTCAGCTGGCTCTCT 63
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19 GAGTCGGGCCAGAGACTGTGAAGCTTCACAGACCCCTGCTCAGCTGGCTCTCT 78
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64 GGCAGCTCCATCCGAGAGTGTGTTACTGAGTGGATCCGCCAACCCCAAGGAG 123
|||
79 GGTGGCTTCATCAGCAGTGTGTGTTACTGAGCTGGATCCGCCAACCCCAAGGAG 138
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124 GGCCTGAGTGGATGGTATCATCATCAAGTGGGAAACACTCAACACCCGCTCCTC 183
|||
139 GGCCTGAGTGGATGGTATCATCATCAAGTGGGAAACACTCAACACCCGCTCCTC 198
|||
184 AAGAGTGAATTGCTATGCTGCTAGACACGCTGAGAACCAAGTTCTCCCTGAGGCTGAC 243
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199 AAGAGTGAATTGCTATGCTGCTAGACACGCTGAGAACCAAGTTCTCCCTGAGGCTGAC 258
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244 TCTGTGACTGCGCGGAGACAGCGCGGTATTACTGTGCGA---GGTTAGTGGTCACT 300
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259 TCTGTGACTGCGCGGAGACAGCGCGGTATTACTGTGCGAGAGGAGTGAAGTGG 318
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301 TTGGACATCTGGGGCCAGGGAACCTGTCACCGTCTCTCA 342
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319 TTGACACCTGCGGGCCAGGGAACCTGTCACCGTCTCTCA 360
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RESULT 15
LOCUS AF062112 414 bp mRNA linear PRI 08-MAY-2001
DEFINITION Homo sapiens clone 21u-26 immunoglobulin heavy chain variable region (IGH) mRNA, partial cds.
ACCESSION AF062112
VERSION AF062112.1 GI:3170686
KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 414)
Wang, X. and Stollar, B.D.
Immunoglobulin VH gene expression in human aging

JOURNAL

Clin. Immunol. 93 (2), 132-142 (1999)

MEDLINE

99459182

PubMed

10527689

REFERENCE

2 (bases 1 to 414)

AUTHORS

Wang, X. and Stollar, B.D.

TITLE

Submitted (22-APR-1998)

JOURNAL

Biochemistry Department, Tufts University

FEATURES

School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA

Location/Qualifiers

1..414

source

/organism="Homo sapiens"

mol_type="mRNA"

/db_xref="taxon:9606"

chromosome="14"

/map="14q32.33"

clone="21u-26"

/cell_type="peripheral B lymphocyte"

tissue_type="blood"

/note="From elderly repertoire 21u"

gene

1..>414

CDS

/gene="IGH"

sig_peptide

1..57

V_region

/gene="IGH"

ORIGIN

58..>414

Query Match

Best Local Similarity 80.4%; Score 275; DB 9; Length 414;

Matches

299; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Job time : 1958.83 secs

4 GAGTGTGAGCCAGAGCTGGTGAAGCTGACAGACCTGTCCTGAGCTGGCTGTCT 63
73 GAGTGTGAGCCAGAGCTGGTGAAGCTGACAGACCTGTCCTGAGCTGGCTGTCT 132
64 GAGTGTGAGCCAGAGCTGGTGAAGCTGACAGACCTGTCCTGAGCTGGCTGTCT 123
133 GAGTGTGAGCCAGAGCTGGTGAAGCTGACAGACCTGTCCTGAGCTGGCTGTCT 192
124 GAGTGTGAGCCAGAGCTGGTGAAGCTGACAGACCTGTCCTGAGCTGGCTGTCT 183
193 GAGTGTGAGCCAGAGCTGGTGAAGCTGACAGACCTGTCCTGAGCTGGCTGTCT 252
184 GAGTGTGAGCCAGAGCTGGTGAAGCTGACAGACCTGTCCTGAGCTGGCTGTCT 243
253 GAGTGTGAGCCAGAGCTGGTGAAGCTGACAGACCTGTCCTGAGCTGGCTGTCT 312
244 GAGTGTGAGCCAGAGCTGGTGAAGCTGACAGACCTGTCCTGAGCTGGCTGTCT 303
313 GAGTGTGAGCCAGAGCTGGTGAAGCTGACAGACCTGTCCTGAGCTGGCTGTCT 372
304 GAGTGTGAGCCAGAGCTGGTGAAGCTGACAGACCTGTCCTGAGCTGGCTGTCT 342
373 GAGTGTGAGCCAGAGCTGGTGAAGCTGACAGACCTGTCCTGAGCTGGCTGTCT 411

Search completed: July 27, 2005, 09:08:38

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ORIGIN
Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."

Query Match 75.0%; Score 256.6; DB 4; Length 677;
Best Local Similarity 88.1%; Pred. No. 4,3e-65;
Matches 304; Conservative 0; Mismatches 34; Indels 7; Gaps 2;

QY 4 GAGTGGCCAGGAGCTGTGAGAGCTTGACAGACCTGTCTCCAGCTGCTCTCT 63
DB 99 GAGTGGCCAGGAGCTGTGAGAGCTTGACAGACCTGTCTCCAGCTGCTCTCT 158
QY 64 GCGGCTCCATCCGAGAGTGTGTACTACTGAGATTGGATCCGCAACCCAGGAG 123
DB 159 GGTGCTCCATCAGAGAGTGTGTACTACTGAGACTGGATCCGCAACCCAGGAG 217
QY 124 GCGGCTCCATCCGAGAGTGTGTACTACTGAGATTGGATCCGCAACCCAGGAG 183
DB 218 GCGGCTCCATCAGAGAGTGTGTACTACTGAGACTGGATCCGCAACCCAGGAG 277
QY 184 AAGAGTCCATTCATCCATGTCTGTAGACAGCTGTGAGAACAAATTCTCCCTGAGCTGAG 243
DB 278 AAGAGTCCATTCATCCATGTCTGTAGACAGCTGTGAGAACAAATTCTCCCTGAGCTGAG 337
QY 244 TCTGTACTGCCCGGAGACAGCGCCGTGTATTACTGTGGA-----GTTAGATGCTTAC 297
DB 338 TCTGTACTGCCCGGAGACAGCGCCGTGTATTACTGTGAGAACAAATTCTCCCTGAGCTGAG 397
QY 298 ACTTGGACATCTGGGGCCAGGAGAACCTGTGTACCGTCTCTCTCA 342
DB 398 GGGTTCAGACCCCTGGGGCCAGGAGAACCTGTGTACCGTCTCTCTCA 442

RESULT 4
LOCUS CD689564 490 bp mRNA linear EST 25-JUN-2003
DEFINITION EST6087 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD689564
VERSION CD689564.1 GI:32209443
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 490)
Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.

TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gszsums.edu.cn.

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
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/release_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 74.0%; Score 253; DB 6; Length 490;
Best Local Similarity 85.9%; Pred. No. 4.7e-64;
Matches 293; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

QY 5 AGTGGCCAGGAGCTGTGAGAGCTTGACAGACCTGTCTCCAGCTGCTCTCTG 64
DB 111 AGTGGCCAGGAGCTGTGAGAGCTTGACAGACCTGTCTCCAGCTGCTCTCTG 170
QY 65 GCGGCTCCATCCGAGAGTGTGTACTACTGAGATTGGATCCGCAACCCAGGAG 124
DB 171 GTGACTCCATCAGAGAGTGTGTACTACTGAGATTGGATCCGCAACCCAGGAG 230
QY 125 GCGGAGTGTGAGTGTGTACTACTGAGATTGGATCCGCAACCCAGGAG 184
DB 231 GCGGAGTGTGAGTGTGTACTACTGAGATTGGATCCGCAACCCAGGAG 290
QY 185 AAGAGTCCATTCATCCATGTCTGTAGACAGCTGTGAGAACAAATTCTCCCTGAGCTGAG 244
DB 291 AAGAGTCCATTCATCCATGTCTGTAGACAGCTGTGAGAACAAATTCTCCCTGAGCTGAG 350
QY 245 CTGTGAGTCCCGGAGACAGCGCCGTGTATTACTGTGAGATTGAT---GGTACACTT 301
DB 351 CTGTGAGTCCCGGAGACAGCGCCGTGTATTACTGTGAGATTGAT---GGTACACTT 410
QY 302 TGGACATCTGGGGCCAGGAGAACCTGTGTACCGTCTCTCTCA 342
DB 411 TTGACTACTGGGGCCAGGAGAACCTGTGTACCGTCTCTCTCA 451

RESULT 5
LOCUS AU134293 643 bp mRNA linear EST 01-AUG-2002
DEFINITION AU134293 OVARC1 Homo sapiens cDNA clone OVARC1001672 5', mRNA sequence.
ACCESSION AU134293
VERSION AU134293.1 GI:10994832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 643)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Iwagaki, T.

TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Iwagaki
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES
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/clone="OVARC1001672"
/release_type="ovary, tumor tissue"
/clone_lib="OVARC1"
/note="Vector: pME18SFLJ"

ORIGIN

Query Match 73.3%; Score 250.8; DB 1; Length 643;
Best Local Similarity 84.6%; Pred. No. 2.2e-63;
Matches 301; Conservative 0; Mismatches 37; Indels 18; Gaps 1;

QY 5 AGTGGCCAGGAGCTGTGAGAGCTTGACAGACCTGTCTCCAGCTGCTCTCTG 64
DB 110 AGTGGCCAGGAGCTGTGAGAGCTTGACAGACCTGTCTCCAGCTGCTCTCTG 169

Db 54 GAGTCGGGCGCAGACTGTGTAAGCCTTCGAGACCTTCCTCCCTACCTGACTGTCTCT 113
 Qy 64 GCGGCTTCATCCGACGAGTGTGTTACTTACTGAGATTGGATCCGCAACCCAGGGAG 123
 Db 114 GGTGCTTCATCCGACGAGTGTGTTACTTACTGAGATTGGATCCGCAACCCAGGGAG 173
 Qy 124 GCGGCTTCATCCGACGAGTGTGTTACTTACTGAGATTGGATCCGCAACCCAGGGAG 183
 Db 174 GGTGCTTCATCCGACGAGTGTGTTACTTACTGAGATTGGATCCGCAACCCAGGGAG 233
 Qy 184 AAGAGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 243
 Db 234 AAGAGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 293
 Qy 244 TCTGTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 300
 Db 294 TCTGTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 353
 Qy 301 TTGGCATCTGGGGCGAGGAAACCTGTCACCGCTCTCTCA 342
 Db 354 TTGGCATCTGGGGCGAGGAAACCTGTCACCGCTCTCTCA 395

RESULT 8
 AM401348 582 bp mRNA linear EST 16-FEB-2000
 LOCUS
 DEFINITION UI-HF-BK0-aau-d-08-0-UT.r1 NIH_MGC_36 Homo sapiens cDNA clone
 IMAGE:3055142 5', mRNA sequence.
 ACCESSION AM401348
 VERSION AM401348.1 GI:6920130
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE NIH-MGC http://mgi.nci.nih.gov/.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.lnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward

FEATURES
 source
 Location/Qualifiers
 1..582

/organism="Homo sapiens"
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 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_id="NIH_MGC_36"
 /note="Vector: pT7T3-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
 Query Match 71.9%; Score 245.8; DB 2; Length 582;
 Best Local Similarity 86.1%; Pred. No. 6.7e-62;
 Matches 297; Conservative 0; Mismatches 42; Indels 6; Gaps 2;
 4 GAGTCGGGCGCAGACTGTGTAAGCCTTCGAGACCTTCCTCCCTACCTGACTGTCTCT 63

Db 34 GAGTCGGGCGCAGACTGTGTAAGCCTTCGAGACCTTCCTCCCTACCTGACTGTCTCT 93
 Qy 64 GCGGCTTCAT--CCGACGAGTGTGTTACTTACTGAGATTGGATCCGCAACCCAGGG 120
 Db 94 GGTGCTTCATCTTCAACAGGTGTGATTTACTTGTGACTGGATTCGCGACAGCCAGGG 153
 Qy 121 AAGGCTTCGAGTGGATTGGGTATCTATCTACAGTGGGAACACTTACAAACCCGCTC 180
 Db 154 AAGGCTTCGAGTGGATTGGGTATCTATCTACAGTGGGAACACTTACAAACCCGCTC 213
 Qy 181 CTCAAGAGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 240
 Db 214 CTCAAGAGTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 273
 Qy 241 AACTGTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 297
 Db 274 AGTCTGTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 333
 Qy 298 ACTTTGACATCTGGGGCGAGGAAACCTGTCACCGCTCTCTCA 342
 Db 334 GCTTTGATATCTGGGGCGAGGAAACATGTGTACCGCTCTCTCA 378

RESULT 9
 BM920469 1108 bp mRNA linear EST 12-MAR-2002
 LOCUS
 DEFINITION AGENCOURT 6709612 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5750444
 5', mRNA sequence.
 ACCESSION BM920469
 VERSION BM920469.1 GI:19370848
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE NIH-MGC http://mgi.nci.nih.gov/.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 plate: LHAM12781 row: g column: 21
 High quality sequence stop: 626.

FEATURES
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 Location/Qualifiers
 1..1108

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5750444"
 /lab_host="DH10B"
 /clone_id="NIH_MGC_122"
 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
 Site 1: NotI; Site 2: EcoRV (destroyed); RNA source:
 anonymous pool of 24 week female lung, 16 week female
 spleen, and 20-22 week male spleens. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.4 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 026. Note:
 this is a NIH_MGC Library."

ORIGIN
 Query Match 71.5%; Score 244.6; DB 5; Length 1108;
 Best Local Similarity 84.1%; Pred. No. 1.8e-61;
 4 GAGTCGGGCGCAGACTGTGTAAGCCTTCGAGACCTTCCTCCCTACCTGACTGTCTCT 63

ORIGIN

Query Match 70.2%; Score 240; DB 2; Length 363;

Best Local Similarity 90.7%; Pred. No. 3.2e-60; Matches 255; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

OY 4 GAGTGTGCCCCAGAGCTGTGAAGCCCTGACAGACCCCTGCTCAGCTGGCTGTCT 63
DB 34 GAGTGTGCCCCAGAGCTGTGAAGCCCTGACAGACCCCTGCTCAGCTGGCTGTCT 93
OY 64 GCGCGCTCCATCCGAGTGTGTGTACTACTGAGATTGGATCCGCCAACCAGAGGAG 123
DB 94 GGTGCTCCATCAGAGTGTGTGTACTACTGAGATTGGATCCGCCAACCAGAGGAG 153
OY 124 GGCCTGAGTGTGATTTGGTACTATCTATCAAGTGGGAAACCTTACAAACCCGCTCC 183
DB 154 GGCCTGAGTGTGATTTGGTACTATCTATCAAGTGGGAGCGCCTTACTACAAATCCGCTCC 213
OY 184 AAGAGTGAATTGCGATGCGGTAGACACGCTGAGAACCAAGTTCCCTGAGGCTGAG 243
DB 214 AAGAGTGAATTGCGATGCGGTAGACACGCTGAGAACCAAGTTCCCTGAGGCTGAG 273
OY 244 TCTGTGACTGCGCGGAGACACGCGCGGTGATTACTGTGCGAG 284
DB 274 TCTGTGACTGCGCGGAGACACGCGCGGTGATTACTGTGAG 314

RESULT 12 B0710364 813 bp mRNA linear EST 16-JUL-2002

LOCUS B0710364 AGENCOURT_8351485 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6282412

DEFINITION 5', mRNA sequence.

ACCESSION B0710364.1 GI:21849263

VERSION B0710364.1

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

TITLE NIH-MGC http://mgi.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-remail.nih.gov

Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

Plate: LUCM2476 row: m column: 05

High quality sequence stop: 529.

Location/Qualifiers

1. 813

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6282412"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_113"

/note="Organ: spleen; Vector: pOT7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

Best Local Similarity 90.7%; Pred. No. 5.8e-60; Matches 255; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

OY 4 GAGTGTGCCCCAGAGCTGTGAAGCCCTGACAGACCCCTGCTCAGCTGGCTGTCT 63
DB 82 GAGTGTGCCCCAGAGCTGTGAAGCCCTGACAGACCCCTGCTCAGCTGGCTGTCT 141
OY 64 GCGCGCTCCATCCGAGTGTGTGTACTACTGAGATTGGATCCGCCAACCAGAGGAG 123
DB 142 GGTGCTCCATCAGAGTGTGTGTACTACTGAGATTGGATCCGCCAACCAGAGGAG 201
OY 124 GGCCTGAGTGTGATTTGGTACTATCTATCAAGTGGGAAACCTTACAAACCCGCTCC 183
DB 202 GGCCTGAGTGTGATTTGGTACTATCTATCAAGTGGGAGACCTTACTACAAACCCGCTCC 261
OY 184 AAGAGTGAATTGCGATGCGGTAGACACGCTGAGAACCAAGTTCCCTGAGGCTGAG 243
DB 262 AAGAGTGAATTGCGATGCGGTAGACACGCTGAGAACCAAGTTCCCTGAGGCTGAG 321
OY 244 TCTGTGACTGCGCGGAGACACGCGCGGTGATTACTGTGCGAG 284
DB 322 TCTGTGACTGCGCGGAGACACGCGCGGTGATTACTGTGCGAG 362

RESULT 13 B0706579

LOCUS B0706579 903 bp mRNA linear EST 16-JUL-2002

DEFINITION AGENCOURT_8487944 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6300935

ACCESSION B0706579 5', mRNA sequence.

VERSION B0706579.1 GI:21845478

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

TITLE NIH-MGC http://mgi.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-remail.nih.gov

Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

Plate: LUCM2515 row: p column: 24

High quality sequence start: 4

High quality sequence stop: 584.

Location/Qualifiers

1. 903

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6300935"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_113"

/note="Organ: spleen; Vector: pOT7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

Query Match 69.6%; Score 238.2; DB 5; Length 903;

Best Local Similarity 82.9%; Pred. No. 1.3e-59; Matches 286; Conservative 0; Mismatches 53; Indels 6; Gaps 1;

QY 4 GAGTCTGCCCGAGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCAGCTGGCTGTCTCT 63
Db 98 GAGTCGGGCCCCAGGAGCTGGTGAAGCCTTCGAGAGACCTGTCCCTCAGCTGACCTGTCTCT 157
QY 64 GCGCGCTCCATCCCGAGTGGTGTACTATCACTGAGATTGGATTCGCCCAACACCCAGGAGAG 123
Db 158 GGTGGCTCATCAGCAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 217
QY 124 GCGCTGAGTGAATGGGTATCATCTATCACTGAGTGAAGACCTTCAACAACCCGCTCCTC 183
Db 218 GGGCTGAGTGAATGGGAATATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 277
QY 184 AAGAGTCGAATTCGATGTGGTATGACACGTGTGAAGAACAACTTCTCCCTGAGGCTGAAC 243
Db 278 AAGAGTCGATCACCATATTCGTAGACACGTTCAGAAACAGATTCTCCCTGAGGCTGAGG 337
QY 244 TCTGTGACTGCGCGGAGACAGCGCCGTGTATTAATTAATTAATTAATTAATTAATTAATTA 297
Db 338 TCTGTGACCGCGGAGACAGCGCTGTCTATTAATTAATTAATTAATTAATTAATTAATTAATTA 397
QY 298 ACTTTCGACATCTGGGCGGAGGAGAACCTGTGTCACCGTCTCTCTCA 342
Db 398 TGGTTCGACCCCTGGGGCGGAGGAGAACCTGTGTCACCGTCTCTCTCA 442

RESULT 14
BF974568 828 bp mRNA linear EST 22-JAN-2001
LOCUS 602243482P1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4334541 5',
DEFINITION mRNA sequence.
ACCESSION BF974568
VERSION BF974568.1 GI:12341783
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 828)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1204 row: c column: 22
High quality sequence stop: 800.
Location/Qualifiers
1..828
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4334541"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site: 1; XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 69.5%; Score 237.8; DB 4; Length 828;
Best Local Similarity 90.4%; Pred. No. 1.7e-59;
Matches 254; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 4 GAGTCTGCCCGAGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCAGCTGGCTGTCTCT 63
Db 92 GAGTCGGGCCCCAGGAGCTGGTGAAGCCTTCGAGAGACCTGTCCCTCAGCTGACCTGTCTCT 151
QY 64 GCGCGCTCCATCCCGAGTGGTGTACTATCACTGAGATTGGATTCGCCCAACACCCAGGAGAG 123
Db 152 GGTGGCTCATCAGCAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 211
QY 124 GCGCTGAGTGAATGGGTATCATCTATCACTGAGTGAAGACCTTCAACAACCCGCTCCTC 183
Db 212 GGTGGCTCATCAGCAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 271
QY 184 AAGAGTCGAATTCGATGTGGTATGACACGTGTGAAGAACAACTTCTCCCTGAGGCTGAAC 243
Db 272 AAGAGTCGATCACCATATTCGTAGACACGTTCAGAAACAGATTCTCCCTGAGGCTGAGG 331
QY 244 TCTGTGACTGCGCGGAGACAGCGCCGTGTATTAATTAATTAATTAATTAATTAATTAATTA 284
Db 332 TCTGTGATTCGCGGAGACAGCGCGGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTA 372

RESULT 15
BQ710488 904 bp mRNA linear EST 16-JUL-2002
LOCUS AGENCOURT 8352970 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278137
DEFINITION 5', mRNA sequence.
ACCESSION BQ710488
VERSION BQ710488.1 GI:21849387
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 904)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2465 row: k column: 02
High quality sequence stop: 728.
Location/Qualifiers
1..904
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6278137"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site: 1; XhoI; Site: 2;
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 69.2%; Score 236.8; DB 5; Length 904;
Best Local Similarity 82.5%; Pred. No. 3.5e-59;
Matches 287; Conservative 0; Mismatches 52; Indels 9; Gaps 1;

Oy 4 GAGTGTGGGCCCAGGAACTGGTGAAGCCCTGCAACAGCCCTGTCCTCAGCTGGGCTGCTC 63
 Db 86 GAGTGGGGCCCAAGACTGGTGAAGCCTTGGAGAACCTGTGCTCACTGCATCTGTCTT 145
 Oy 64 GCGCGCTCCATCCGACAGTGGTGTACTAATTGAGTTGGATCCGCCAACCCAGGGAAG 123
 Db 146 GGTGGCTCATCAGACGTAGTAGTTACTATGGGGCTGGATCCGCCAGGCCCAAGGGAAG 205
 Oy 124 GGCCTGGAGTGAATTGGGTACTATATCAACAGTGGAAACCTTACAACACCCGTCCCTC 183
 Db 206 GGGCTGGAGTGAATTGGAGTATCTATTTAATGAGGAGACCTTAACAACCCGTCCCTC 265
 Oy 184 AAGATCCGAATTGCCATGTCGGTGAACAAGCTCTGAAGACAAGTTCTCCCTGAGGCTGAAC 243
 Db 266 AAGATCCGAATCAACCATATCCGTAGACAGCTCCAAACCAAGTTCTCCCTGAAGCTGAGC 325
 Oy 244 TCTGTGACTCGCGCGGACACGCGCGGTATTAATGTGGCAGAGGTTAA-----TGGC 294
 Db 326 TCTGTGACCGCGGACACACGCGTGTATTAATGTGGCAGAGCAAGACGACGACTGGTA 385
 Oy 295 TACACTTTGGACATCTGCGGAGGAAACCCCTGTCACAGTCTCTCA 342
 Db 366 CATTACTTCACAGACTGGGAGCCAGGACCCCTGCTGTACCGCTCTCCTCA 433

Search completed: July 27, 2005, 12:32:06
Job time : 2112.58 secs

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XX  WO200253595-A1.
XX  11-JUL-2002.
XX  27-DEC-2001; 2001WO-SE002908.
XX  29-DEC-2000; 2000SE-00004892.
XX  (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX  Flicker S, Steinberger P, Kraft D, Valenta R;
XX  WPI; 2002-583604/62.
XX  P-PSDB; ABG30445.
XX  Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
XX  variable region of group 2 allergen specific-human IgE Fabs, useful for
XX  diagnosing or passive immunotherapy of type I allergy, for environmental
XX  allergen detection.
XX  Disclosure; Page 31-32; 45pp; English.
XX  This invention relates to the DNA and protein sequences of group 2
XX  allergen-specific human IgE Fabs and methods for their use. The proteins
XX  of the invention may have antiallergic activities and may be used as a
XX  vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
XX  antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
XX  2 allergen-specific fabs of the invention may be useful for environmental
XX  allergen detection and for standardisation of allergen extracts. The fabs
XX  - or a vaccine againsts a type I allergy is useful for passive
XX  immunotherapy of type I allergy, it is also useful for diagnosing a type
XX  I allergy. The allergen-specific fabs of the invention are useful for
XX  inter alia, diagnosis, therapy and prevention of type I allergy. They are
XX  also useful for identification of group 2 allergen-containing pollen and
XX  may be used for blocking the binding of grass pollen allergic patients
XX  IgE antibodies to Phi p 2. The present sequence represents the DNA
XX  encoding the human IgG fab, clone 94 heavy chain protein of the invention
XX  Sequence 342 BP; 69 A; 100 C; 98 G; 75 T; 0 U; 0 Other;
XX
XX  Query Match          99.5%; Score 340.4; DB 6; Length 342;
XX  Best Local Similarity 99.7%; Pred. No. 1.2e-87;
XX  Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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XX  DB  1 CTCGAGTCTGGCCCGAGACTGGTGAAGCCTGCACAGACCTTCCCTCAGCTGCCTGTC 60
XX
XX  QY  61 TCTGGCGGCTTCATCCGAGTGTGTGTTACTGAGTTGGATCCGCCAACACCCAGGG 120
XX  DB  61 TCTGGCGGCTTCATCCGAGTGTGTGTTACTGAGTTGGATCCGCCAACACCCAGGG 120
XX
XX  QY  121 AAGGGCCGTGGAGTGGTATGATCATCATGAGTGGGAACCTATAAACCCTGCC 180
XX  DB  121 AAGGGCCGTGGAGTGGTATGATCATCATGAGTGGGAACCTATAAACCCTGCC 180
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XX  QY  181 CTCAAGAGTCGATTCGATTCGGTAGACAGCTGTGAGAACAAAGTTCTCCCTGAGGCTG 240
XX  DB  181 CTCAAGAGTCGATTCGATTCGGTAGACAGCTGTGAGAACAAAGTTCTCCCTGAGGCTG 240
XX
XX  QY  241 AACTCTGTGACTGCCCGCGGACACCGCCGTGTATTACTGTGCGAGGTAGATGCTACACT 300
XX  DB  241 AACTCTGTGACTGCCCGCGGACACCGCCGTGTATTACTGTGCGAGGTAGATGCTACACT 300
XX
XX  QY  301 TTGACATCTGGGGCCAGGGAACCTGTGTACCCGCTCCTCA 342
XX  DB  301 TTGACATCTGGGGCCAGGGAACCTGTGTACCCGCTCCTCA 342
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XX  RESULT 2
XX  ABR89639
XX  ID ABR89639 standard; DNA; 342 BP.

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XX  ABR89639;
XX  21-OCT-2002 (first entry)
XX  DNA encoding human IgE Fab clone 100 heavy chain.
XX  Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;
XX  timothy grass pollen allergen; passive immunotherapy.
XX  Homo sapiens.
XX
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XX  CDS 1..342
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XX  FT 7..78
XX  FT /*tag= b
XX  FT /note= "FR1 region"
XX  FT 79..99
XX  FT /*tag= c
XX  FT /note= "CDR1 region"
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XX  FT 190..285
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XX  FT 286..309
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XX  FT 310..342
XX  FT /*tag= i
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XX  WO200253595-A1.
XX  11-JUL-2002.
XX  27-DEC-2001; 2001WO-SE002908.
XX  29-DEC-2000; 2000SE-00004892.
XX  (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX  Flicker S, Steinberger P, Kraft D, Valenta R;
XX  WPI; 2002-583604/62.
XX  P-PSDB; ABG30447.
XX
XX  Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
XX  variable region of group 2 allergen specific-human IgE Fabs, useful for
XX  diagnosing or passive immunotherapy of type I allergy, for environmental
XX  allergen detection.
XX  Disclosure; Page 33; 45pp; English.
XX
XX  This invention relates to the DNA and protein sequences of group 2
XX  allergen-specific human IgE Fabs and methods for their use. The proteins
XX  of the invention may have antiallergic activities and may be used as a
XX  vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
XX  antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
XX  2 allergen-specific fabs of the invention may be useful for environmental
XX  allergen detection and for standardisation of allergen extracts. The fabs
XX  - or a vaccine againsts a type I allergy is useful for passive
XX  immunotherapy of type I allergy, it is also useful for diagnosing a type
XX  I allergy. The allergen-specific fabs of the invention are useful for

```

CC inter alla, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for identification of group 2 allergen-containing pollen and
CC can be used for blocking the binding of grass pollen allergenic patients
CC IGE antibodies to Phi P 2. The present sequence represents the DNA
CC encoding the human Ige fab, clone 100 heavy chain protein of the
CC invention
SQ Sequence 342 BP; 69 A; 103 C; 94 G; 76 T; 0 U; 0 Other;
Query Match 90.2%; Score 308.4; DB 6; Length 342;
Best Local Similarity 93.9%; Pred. No. 1.9e-78;
Matches 321; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 CTCGAGTCTGGCCGAGAGCTGGTGAAGCTGACAGACCCCTGCTCAGCTGGCTGTC 60
DB 1 CTCGAGTCTGGCCGAGAGCTGGTGAAGCTGACAGACCCCTGCTCAGCTGGCTGTC 60
QY 61 TCTGGCGGCTTCATCCGAGTGTGTACTACTGAGTTGGATCCGCCAACCCAGGG 120
DB 61 TCTGGTGGCTTCATCCGAGTGTGTATTACTGAGTTGGATCCGCCAACCCAGGG 120
QY 121 AAGGCGCTGAGTGATGGTGGTATCATCTATCAAGTGGAAACCTTACAAACCCGTC 180
DB 121 AAGGCGCTGAGTGATGGTGGTATCATCTATCAAGTGGAAACCTTACAAACCCGTC 180
QY 181 CTCGAAGTGAATTGCGATGCGTGAACAGCTGTGAACAACAGTTCTCCCTGAGGCTG 240
DB 181 CTCGAAGTGAATTGCGATGCGTGAACAGCTGTGAACAACAGTTCTCCCTGAGGCTG 240
QY 241 AACTCTGTGACTGCGCGGAGACACGCGCTGTATTACTGTGCGAGTTAGATGGCTAC 300
DB 241 AGCTCTGTGACTGCGCGGAGACACGCGCTGTATTACTGTGCGAGTTAGATGGCTAC 300
QY 301 TTGACATCTGGGCGCAGGGAACCTTGTCAACCGTCTCTCA 342
DB 301 TTGACATCTGGGCGCAGGGAACCTTGTCAACCGTCTCTCA 342
RESULT 3
ABK89638
ID ABR89638 standard; DNA; 342 BP.
AC ABR89638;
XX 21-OCT-2002 (first entry)
DT
XX DNA encoding human Ige Fab clone 60 heavy chain.
DE
XX Human; fab; ds; gene; anti-allergic; vaccine; grass pollen; Phi p 2;
KW timothy grass pollen allergen; passive immunotherapy.
KW
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1.342
FT CDS /tag= a
FT /product= "Fab clone 60 heavy chain"
FT misc_feature /tag= b
FT 7.78
FT /note= "FR1 region"
FT 79.99
FT /note= "CDR1 region"
FT 100.123
FT misc_feature /tag= c
FT /note= "CDR2 region"
FT 134.141
FT misc_feature /tag= d
FT /note= "FR2 region"
FT 142.189
FT misc_feature /tag= e
FT /note= "FR3 region"
FT /tag= f
FT /note= "CDR2 region"
FT 190.285
FT misc_feature

FT /tag= g
FT /note= "FR3 region"
FT 286.309
FT misc_feature /tag= h
FT /note= "CDR3 region"
FT 310.342
FT misc_feature /tag= i
FT /note= "FR4 region"
XX
XX W0200253595-A1.
XX
XX 11-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-SE002908.
XX
XX 29-DEC-2000; 2000SE-00004892.
XX
XX (PHAA) PHARMACIA DIAGNOSTICS AB.
XX
XX Flicker S, Steinberger P, Kraft D, Valenta R;
XX
XX WPI; 2002-583604/62.
XX
XX P-PSDB; ABG30446.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
XX variable region of group 2 allergen specific-human Ige Fabs, useful for
XX diagnosing or passive immunotherapy of type I allergy, for environmental
XX allergen detection.
XX
XX Disclosure; Page 32; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
XX allergen-specific human Ige Fabs and methods for their use. The proteins
XX of the invention may have anti-allergic activities and may be used as a
XX vaccine or an inhibitor of binding of grass pollen allergenic patient's Ige
XX antibodies to Phi P 2 (a major timothy grass pollen allergen). The group
XX 2 allergen-specific fabs of the invention may be useful for environmental
XX allergen detection and for standardisation of allergen extracts. The fabs
XX - or a vaccine against a type I allergy is useful for passive
XX immunotherapy of type I allergy, it is also useful for diagnosing a type
XX I allergy. The allergen-specific fabs of the invention are useful for
XX inter alla, diagnosis, therapy and prevention of type I allergy. They are
XX also useful for identification of group 2 allergen-containing pollen and
XX may be used for blocking the binding of grass pollen allergic patients
XX Ige antibodies to Phi p 2. The present sequence represents the DNA
XX encoding the human Ige fab, clone 60 heavy chain protein of the invention
XX
SQ Sequence 342 BP; 70 A; 105 C; 90 G; 77 T; 0 U; 0 Other;
Query Match 86.9%; Score 297.2; DB 6; Length 342;
Best Local Similarity 91.8%; Pred. No. 3e-75;
Matches 314; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 1 CTCGAGTCTGGCCGAGAGCTGGTGAAGCTGACAGACCCCTGCTCAGCTGGCTGTC 60
DB 1 CTCGAGTCTGGCCGAGAGCTGGTGAAGCTGACAGACCCCTGCTCAGCTGGCTGTC 60
QY 61 TCTGGCGGCTTCATCCGAGTGTGTACTACTGAGTTGGATCCGCCAACCCAGGG 120
DB 61 TCTGGTGGCTTCATCCGAGTGTGTATTACTGAGTTGGATCCGCCAACCCAGGG 120
QY 121 AAGGCGCTGAGTGATGGTGGTATCATCTATCAAGTGGAAACCTTACAAACCCGTC 180
DB 121 AAGGCGCTGAGTGATGGTGGTATCATCTATCAAGTGGAAACCTTACAAACCCGTC 180
QY 181 CTCGAAGTGAATTGCGATGCGTGAACAGCTGTGAACAACAGTTCTCCCTGAGGCTG 240
DB 181 CTCGAAGTGAATTGCGATGCGTGAACAGCTGTGAACAACAGTTCTCCCTGAGGCTG 240
QY 241 AACTCTGTGACTGCGCGGAGACACGCGCTGTATTACTGTGCGAGTTAGATGGCTAC 300
DB 241 AACTCTGTGACTGCGCGGAGACACGCGCTGTATTACTGTGCGAGTTAGATGGCTAC 300

QY 301 TTGGACATCTGGGGCCAGGGAACCCCTGTCACCGTCTCTCA 342
DB 301 TTGGACACTGGGGCCAGGGAACCCCTGTCACCGTCTCTCA 342

RESULT 4

AAAF29076
ID AAF29076 standard; DNA, 360 BP.

AC AAF29076;

DT 03-APR-2001 (first entry)

DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 32.

KM Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;

KW envelope glycoprotein; gp120; diagnosis; ds.

OS Homo sapiens.

PN MO20010678-A1.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000WO-US017327.

PR 30-JUN-1999; 99US-0141701P.

PA (USSS) US DEPT HEALTH & HUMAN SERVICES.

PI Watkins BA, Reitz MS;

DR WPI; 2001-112438/12.

DR P-PSDB; AAB62775.

XX Novel human monoclonal antibody immunoreactive with human

PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1

PT in biological sample and providing passive immunotherapy to HIV-1

PT infected mammal.

PS Claim 4; Page 45; 81pp; English.

XX The present invention provides the protein and coding sequences for the

CC variable regions of human monoclonal antibodies which are immunoreactive

CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.

CC These can be used in diagnosis and therapy of HIV-1 infection

XX Sequence 360 BP; 73 A; 104 C; 107 G; 76 T; 0 U; 0 Other;

Query Match 80.8%; Score 276.4; DB 4; Length 360;

Best Local Similarity 90.1%; Pred. No. 2.9e-69;

Matches 308; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

QY 4 GAGTCTGGGCCAGAGCTGTGTAAGCTTCACAGACCCCTGCTCAGTGGCTCTCT 63

DB 19 GAGTCGGGCCAGAGCTGTGTAAGCTTCACAGACCCCTGCTCAGTGGCTCTCT 78

QY 64 GGCCTGCTCCATCCGCACTGTGTACTACTGAGTTGGATCCGCAACCCAGGGAAG 123

DB 79 GGTGGCTCCATCAGACAGTGTGTACTACTGAGCTGGATCCGCAACCCAGGGAAG 138

QY 124 GGCCTGAGATGGATTGGGTACATCTATCAGAGTGGGAACACCTTACAAACCCGTCCTC 183

DB 139 GGCCTGAGATGGATTGGGTACATCTATCAGAGTGGGAACACCTTACAAACCCGTCCTC 198

QY 184 AAGAGTGAATTTGCAATGCTGTGTAAGCAAGTCTGAGAAACAAGTTCTCCCTAGGCTGAC 243

DB 199 AAGAGTGAATTTGCAATGCTGTGTAAGCAAGTCTGAGAAACAAGTTCTCCCTAGGCTGAC 258

QY 244 TCTGTGACTGCGCGGACACCGCGGTGATTACTGTGCGA---GGTTGATGGCTACT 300

DB 259 TCTGTGACTGCGCGGACACCGCGGTGATTACTGTGCGAAGGGGTGATTGTGACTGCG 318

QY 301 TTGGACATCTGGGGCCAGGGAACCCCTGTCACCGTCTCTCA 342
DB 319 TTGCACCCCTGGGGCCAGGGAACCCCTGTCACCGTCTCTCA 360

RESULT 5

ADC99786
ID ADC99786 standard; DNA, 352 BP.

AC ADC99786;

DT 01-JAN-2004 (first entry)

DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 15.

KM anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;

KW cytosolic; melanoma; oesophageal; pancreatic; colorectal tumour;

KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;

OS Homo sapiens.

PN MO2003057838-A2.

PD 17-JUL-2003.

PF 26-DEC-2002; 2002WO-US041581.

PR 28-DEC-2001; 2001US-0346299P.

PA (ABGE-) ABGENIX INC.

PI Gudas J;

DR WPI; 2003-587113/55.

DR P-PSDB; ADC99784.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease

PT or condition associated with expression of MUC18 in a patient, e.g.

PT tumors, cancers, and other malignancies.

PS Claim 8; SEQ ID NO 15; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising

CC a heavy or light chain amino acid or a heavy or light chain variable

CC domain where the antibody binds to MUC18. The monoclonal antibody of the

CC invention demonstrates cytosolic activity and may be useful for treating

CC a disease or condition associated with the expression of MUC18 on the

CC cell surface such as tumours, specifically melanoma, oesophageal,

CC pancreatic and colorectal tumours, carcinomas, particularly cervical

CC carcinomas and cervical intraepithelial neoplasia and cancers including

CC colorectal, breast or lung cancer, as well as other malignancies. The

CC current sequence is that of the anti-human MUC18 monoclonal antibody

XX heavy chain variable domain DNA of the invention.

XX Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;

Query Match 80.4%; Score 275; DB 10; Length 352;

Best Local Similarity 90.3%; Pred. No. 7.2e-69;

Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGGGCCAGAGCTGTGTAAGCTTCACAGACCCCTGCTCAGTGGCTCTCT 63

DB 16 GAGTCGGGCCAGAGCTGTGTAAGCTTCACAGACCCCTGCTCAGTGGCTCTCT 75

QY 64 GGCCTGCTCCATCCGCACTGTGTACTACTGAGTTGGATCCGCAACCCAGGGAAG 123

DB 76 GGTGGCTCCATCAGACAGTGTGTACTACTGAGCTGGATCCGCAACCCAGGGAAG 135

QY 124 GGCCTGAGATGGATTGGGTACATCTATCAGAGTGGGAACACCTTACAAACCCGTCCTC 183

DB 136 GGCCTGAGATGGATTGGGTACATCTATCAGAGTGGGAACACCTTACAAACCCGTCCTC 195

OY	4	GAGCTGGCCCAAGACTGGTGAAGCTGTGACACAGCCCTGTCCCTCAGCTGCTCTCT	63
Db	16	GAGTGGGCCCCAGAACTGGTGAAGCTTTCACAGACCCCTGTCCCTCAGCTGCTCTCT	75
OY	64	GGCGGCTTCATCCGCGAGTGGTGGTACTACTGAGTGGATCCGCCAACCCAGGGAAG	123
Db	76	GGTGGCTTCATCAGCAGTGGTGGTACTACTGAGCTTGGATCCGCCAACCCAGGGAAG	135
OY	124	GGCTTGAAGTGGATGGGTATCATCTATACAGTGGGAACCTTACACAAACCCGTCCCTC	183
Db	136	GGCTTGAAGTGGATGGGTATCATCTATACAGTGGGAAGCACTTACAAACCCGTCCCTC	195
OY	184	AAGAGTCAATTGCCATGCTGGTAGACACGTTGTAGAAACAAGTTCCTGTAGAGCTGAAC	243
Db	196	AAGAGTCAAGTTCATCATATCACTAGACACAGTGTAAAGAACAGTTCTCTCTGAAGCTGAGC	255
OY	244	TCTGTGACTGTCGCGCGACACGCGCGTGTATTACTGTGCGAGGTTAGATGGCTTACACTTTG	303
Db	256	TCTGTGACTGTCGCGCGGACACGCGCGTGTATTACTGTGCGAG--AGAGGAGATGCTTT	312
OY	304	GACATCTGGGGCCAGGGAACCTTGATCACCCGTCTCTCA	342
Db	313	GACTACTGGGGCCAGGGAACCTTGATCACCCGTCTCTCA	351

RESULT 7
ADFO9828
ID ADFO9828 standard; DNA; 352 BP.
XX
XX ADF09828;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human anti-MUC18 monoclonal antibody heavy chain coding sequence #4.
XX
XX cell proliferation inhibition; MUC18 tumour antigen;
XX anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
KW carcinoma; cancer; malignancy; heavy chain; human; ds; gene.
XX
OS Homo sapiens.
XX
PN WO2003057837-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041580.
XX
PR 28-DEC-2001; 2001US-0346414P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-598367/56.
XX
PT P-Psdb; ADF09826.
XX
PT Inhibiting cell proliferation associated with expression of MUC18 tumor
XX antigen, involves incubating and inhibiting cell by administering anti-
XX MUC18 monoclonal antibody.
XX
PS Disclosure; SEQ ID NO 15; 83bp; English.
XX
CC The invention comprises a method for inhibiting cell proliferation
XX associated with expression of MUC18 tumour antigen. The method involves
XX administering anti-MUC18 monoclonal antibody. The method of the invention
XX is useful for inhibiting cell (e.g. melanoma or tumour cell)
XX proliferation associated with the expression of MUC18 tumour antigen, the
XX method is preferably useful for inhibiting tumour metastasis. The method
XX is useful for inhibiting cell proliferation in patients with tumours,
XX carcinoma, cancer and other malignancies. The present DNA sequence
XX encodes a heavy chain from an MUC18 tumour antigen-specific monoclonal
XX antibody.

SQ Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;

Query Match 80.4%; Score 275; DB 10; Length 352;
 Best Local Similarity 90.3%; Pred. No. 7.2e-69;
 Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCAAGACTGTGTAGACCTGACACAGACCTGTCTCCCTGAGCTGGCTGTCTT 63
 DB 16 GAGTCGGGCCCAAGACTGTGTAGACCTGTCTCCCTGAGCTGGCTGTCTT 75
 QY 64 GGGCGCTCCACCCGAGTGTGTACTACTGAGTGTGATCCGCCCAACCCGAGGAG 123
 DB 76 GGTGGCTTCACACAGAGTGTGTACTACTGAGTGTGATCCGCCCAACCCGAGGAG 135
 QY 124 GGCCTGAGTGTGATGTGTATCATCTATCAAGTGGGAACACTTCAACACCCGCTCC 183
 DB 136 GGCCTGAGTGTGATGTGTATCATCTATCAAGTGGGAACACTTCAACACCCGCTCC 195
 QY 184 AAGAGTGAATTTGCCATGTCTGTAGACAGCTGTGAGAACAAAGTTCTCCCTGAGCTGAA 243
 DB 196 AAGAGTGAATTTGCCATGTCTGTAGACAGCTGTGAGAACAAAGTTCTCCCTGAGCTGAGC 255
 QY 244 TCTGTGACTGCGCGGACAGCGCGGTGATTACTGTGCGAGTTAGATGGCTACACTTTG 303
 DB 256 TCTGTGACTGCGCGGACAGCGCGGTGATTACTGTGCGAG--AGAGGAGATGGCTTT 312
 QY 304 GACATCTGGGGCCAGGGAACCTGTGTACCGTCTCTCA 342
 DB 313 GACTACTGGGGCCAGGGAACCTGTGTACCGTCTCTCA 351

RESULT 8
 ID ADS84403 standard; DNA; 354 BP.
 AC ADS84403;
 DT 18-NOV-2004 (first entry)
 DE Human anti-EPO-R antibody heavy chain variable region DNA SEQ ID NO:42.
 XX human: erythropoietin receptor; EPO receptor;
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;
 KW antianaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;
 KW wound healing; neural cell damage protection;
 KW neural tissue damage protection; brain injury; spinal cord injury;
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;
 KW ds.
 XX Homo sapiens.
 OS WO2004035603-A2.
 PN 29-APR-2004.
 PD 14-OCT-2003; 2003WO-US032243.
 PF 14-OCT-2003; 2002US-0026711.
 PR 10-OCT-2003; 2003US-00684109.
 XX (ABBO) ABBOTT LAB.
 PA Devries PJ, Green LL, Ostrow DH, Rellly EB, Wiele J;
 PI WPI; 2004-348433/32.
 DR P-PSDB; ADS84404.
 XX New antibodies that bind to or activate an endogenous human
 PT erythropoietin receptor, useful for diagnosing, preventing or treating
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.
 PT anemia.
 XX Claim 47; SEQ ID NO 42; 192pp; English.

XX The present invention describes an antibody or its fragment that binds to
 CC or activates an endogenous activity of a human erythropoietin (EPO)
 CC receptor in a mammal, but does not interact with a peptide having a
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)
 CC methods of modulating or activating an endogenous activity of a human EPO
 CC receptor in a mammal, comprising administering to the mammal a
 CC therapeutic amount of the above antibody or its fragment to modulate or
 CC activate the receptor; (2) a method of treating a mammal suffering from
 CC aplasia, comprising administering to the mammal a therapeutic amount of
 CC the above antibody or its fragment to modulate or activate the receptor;
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)
 CC an isolated and purified polynucleotide sequence; and (5) an isolated and
 CC purified amino acid sequence, and their fragments. The EPO receptor
 CC binding antibody has antianaemic, neuroprotective and vulnerary
 CC activities, and can be used in gene therapy. The compositions and methods
 CC from the present invention can be used for modulating an endogenous
 CC activity of a human EPO receptor or for treating mammals suffering from
 CC aplasia or anaemia. They may also be used for identifying mammals having
 CC a dysfunctional EPO receptor. The composition may also be used in
 CC promoting wound healing or in protecting against neural cell and/or
 CC tissue damage resulting from brain/spinal cord injury, stroke and the
 CC like. The present sequence encodes a human anti-EPO-R antibody heavy
 CC chain variable region, which is given in the exemplification of the
 CC present invention.

SQ Sequence 354 BP; 76 A; 105 C; 97 G; 76 T; 0 U; 0 Other;

Query Match 78.5%; Score 268.6; DB 13; Length 354;
 Best Local Similarity 87.0%; Pred. No. 5e-67;
 Matches 295; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCCAAGACTGTGTAGACCTGACACAGACCTGTCTCCCTGAGCTGGCTGTCTT 63
 DB 16 GAGTCGGGCCCAAGACTGTGTAGACCTGTCTCCCTGAGCTGGCTGTCTT 75
 QY 64 GGCCTGCTCCATCCGACAGTGTGTGTACTACTGAGTGTGATCCGCCCAACCCGAGGAG 123
 DB 76 GGTGCTTCATCAGCAATGTGTGTACTACTGAGTGTGATCCGCCCAACCCGAGGAG 135
 QY 124 GGCCTGAGTGTGATGTGTATCATCTATCAAGTGGGAACACTTCAACACCCGCTCC 183
 DB 136 GGCCTGAGTGTGATGTGTATCATCTATCAAGTGGGAACACTTCAACACCCGCTCC 195
 QY 184 AAGAGTGAATTTGCCATGTCTGTAGACAGCTGTGAGAACAAAGTTCTCCCTGAGCTGAA 243
 DB 196 AAGAGTGAATTTGCCATGTCTGTAGACAGCTGTGAGAACAAAGTTCTCCCTGAGCTGATC 255
 QY 244 TCTGTGACTGCGCGGACAGCGCGGTGATTACTGTGCGAGTTAGATGGCTACACTTTG 303
 DB 256 TCTGTGACTGCGCGGACAGCGCGGTGATTACTGTGCGAGTTAGATGGGATGCGG 315
 QY 304 GACATCTGGGGCCAGGGAACCTGTGTACCGTCTCTCA 342
 DB 316 GACTACTGGGGCCAGGGAACCTGTGTACCGTCTCTCA 354

RESULT 9
 ID ADR68545 standard; DNA; 354 BP.
 AC ADR68545;
 DT 02-DEC-2004 (first entry)
 DE Anti-EPO-R-antibody heavy chain variable region DNA seqid 42.
 XX antianaemic; respiratory; vulnerary; gene therapy; vaccine;
 KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
 KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;
 KW wound healing; neural cell damage; tissue damage; brain injury;

KM spinal cord injury; stroke; anti-EPO-R-antibody; heavy chain;
 KM variable region, de.
 XX Homo sapiens.
 OS
 XX US2004175379-A1.
 PN
 XX
 PD 09-SEP-2004.
 XX
 PF 10-OCT-2003; 2003US-00684109.
 XX
 PR 14-OCT-2002; 2002US-0418031P.
 XX
 PA (DEVIR/) DEVIRIES P. J.
 PA (OSTR/) OSTROW D. H.
 PA (REIL/) REILLY E. B.
 PA (GREEN/) GREEN L. L.
 PA (WIEL/) WIELER J.
 XX
 PI Devires PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;
 XX
 DR WPI; 2004-661369/64.
 DR P-PSDB; ADR68546.
 XX
 PT New antibody or its antibody fragment that activates an endogenous
 PT activity or is capable of binding to a human erythropoietin receptor in a
 PT mammal, useful for treating a mammal suffering aplasia or anemia.
 XX
 PS Claim 47; SEQ ID NO 42; 156bp; English.
 XX
 XX The invention describes an antibody or its fragment that activates an
 CC endogenous activity or capable of binding to a human erythropoietin an
 CC receptor in a mammal, or that comprises at least one heavy or light chain
 CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
 CC given in the specification. Also described are: a method of activating or
 CC modulating an endogenous activity of a human erythropoietin receptor in a
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an
 CC isolated and purified polynucleotide sequence selected from 28 sequences
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
 CC the specification, and their fragments, complements, and degenerate codon
 CC equivalents; and an isolated and purified amino acid sequence selected
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
 CC their fragments. The antibody or its antibody fragment that activates or
 CC modulates the activity of the receptor is useful in a method of treating
 CC a mammal suffering aplasia or anemia. The antibodies are also useful for
 CC treating disorders characterised by decreased or subnormal levels of
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue
 CC hypoxia and/or diseases characterised by inadequate blood circulation or
 CC reduced blood flow. They are also useful for promoting wound healing or
 CC for protecting against neural cell and/or tissue damage, resulting from
 CC brain/spinal cord injury, stroke and the like. The antibodies are also
 CC useful for identifying or diagnosing mammals having dysfunctional
 CC erythropoietin receptor. This sequence encodes an anti-EPO-R-antibody
 CC heavy chain variable region.
 XX
 XX Sequence 354 BP; 76 A; 105 C; 97 G; 76 T; 0 U; 0 Other;
 SQ
 Query Match 78.5%; Score 268.6; DB 13; Length 354;
 Best Local Similarity 87.0%; Pred. No. 5e-67;
 Matches 295; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
 QY 4 GAGTCTGAGCCAGAGCTGTGAAGCCTGACAGCCCTGCTCAGCTGGCTGTCTCT 63
 DB 16 GAGTCTGAGCCAGAGCTGTGAAGCCTGACAGCCCTGCTCAGCTGGCTGTCTCT 75
 QY 64 GGGGCTTCATCCGAGTGTGTGTTACTACTGAGTTGATGCCCAACACCCAGGGAAG 123
 DB 76 GGTGCTTCATCCAGAGTGTGTGTTACTACTGAGTTGATGCCCAACACCCAGGGAAG 135

QY 124 GGCCTGAGTGTGATGGGTATCATCTATCACAGTGGGAACCTACACAAACCCGTCCTC 183
 DB 136 GGCCTGAGTGTGATGGGTATCATCTATCACAGTGGGAACCTACACAAACCCGTCCTC 195
 QY 184 MAGAGTCGAATTGCGATGTCGTAGACACGTCGTAGAAACAAGTTCCTCGAGGCTGAAC 243
 DB 196 MAGAGTCGATTAACCTGATCATGAGACAGCTCTAAAGAACAGTTCCTCGAAGCTGATC 255
 QY 244 TCTGTGACTGCGCGGACACAGCGCGGTATTAATTAATTAATTAATTAATTAATTAATTA 303
 DB 256 TCTGTGACTGCGCGGACACAGCGCGGTATTAATTAATTAATTAATTAATTAATTAATTA 315
 QY 304 GACATCTGGGGCCAGGGAACCTGTCACCGTCTCTCA 342
 DB 316 GACTACTGGGGCCAGGGAACCTGTCACCGTCTCTCA 354
 RESULT 10
 ADS84454/C
 ID ADS84454 standard; DNA; 1996 BP.
 XX
 AC ADS84454;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human anti-EPO-R antibody Ab412 heavy chain complementary DNA SEQ ID:93.
 XX
 XX human; erythropoietin receptor; EPO receptor;
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;
 KW antianemic; neuroprotective; vulnerrary; gene therapy; aplasia; anaemia;
 KW wound healing; neural cell damage protection;
 KW neural tissue damage protection; brain injury; spinal cord injury;
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;
 ds.
 OS Homo sapiens.
 XX
 XX W02004035603-A2.
 PN
 XX
 XX 29-APR-2004.
 PD
 XX
 PF 14-OCT-2003; 2003WO-US032243.
 XX
 PR 14-OCT-2002; 2002US-00269711.
 PR 10-OCT-2003; 2003US-00684109.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Devires PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;
 XX
 DR WPI; 2004-348433/32.
 DR P-PSDB; ADS84455.
 XX
 PT New antibodies that bind to or activate an endogenous human
 PT erythropoietin receptor, useful for diagnosing, preventing or treating
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.
 PT anemia.
 PS
 XX Disclosure; SEQ ID NO 93; 192bp; English.
 XX
 XX The present invention describes an antibody or its fragment that binds to
 CC or activates an endogenous activity of a human erythropoietin (EPO)
 CC receptor in a mammal, but does not interact with a peptide having a
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)
 CC methods of modulating or activating an endogenous activity of a human EPO
 CC receptor in a mammal, comprising administering to the mammal a
 CC therapeutic amount of the above antibody or its fragment to modulate or
 CC activate the receptor; (2) a method of treating a mammal suffering from
 CC aplasia, comprising administering to the mammal a therapeutic amount of
 CC the above antibody or its fragment to modulate or activate the receptor;
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)
 CC an isolated and purified polynucleotide sequence, and their fragments,

CC complements and degenerate codon equivalents; and (5) an isolated and
CC purified amino acid sequence, and their fragments. The EPO receptor
CC binding antibody has antineutropenic, neuroprotective and vulnary
CC activities, and can be used in gene therapy. The compositions and methods
CC from the present invention can be used for modulating an endogenous
CC activity of a human EPO receptor or for treating mammals suffering from
CC aplasia or anaemia. They may also be used for identifying mammals having
CC a dysfunctional EPO receptor. The composition may also be used in
CC promoting wound healing or in protecting against neural cell and/or
CC tissue damage resulting from brain/spinal cord injury, stroke and the
CC like. The present sequence represents a human anti-EPO-R antibody heavy
CC chain complementary DNA sequence, which is given in the exemplification
CC of the present invention.

XX
XX Sequence 1996 BP; 351 A; 537 C; 686 G; 422 T; 0 U; 0 Other;

Query Match 78.5%; Score 268.6; DB 13; Length 1996;
Best Local Similarity 87.0%; Pred. No. 8.1e-67;
Matches 295; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 4 GAGCTCTGGCCAGAGCTGTGTAACCTGACAGACCCCTGCTCAGCTGCTGCTCT 63
Db 1924 GAGTCGGGGCCAGAGCTGTGTAACCTGACAGACCCCTGCTCAGCTGCTGCTCT 1865

QY 64 GGGGGCTTCATCCGAGTGTGTTACTGAGTTGATCCGCCAACACCCAGGAAAG 123
Db 1864 GGTGGCTTCATCCAGAGTGTGTTACTGAGTTGATCCGCCAACACCCAGGAAAG 1805

QY 124 GGGCTGAGAGGAGTGGGTACATCTATCAGCTGGGAACCTTCAACACCCCTCCCTC 183
Db 1804 GGGCTGAGAGGAGTGGGTACATCTATCAGCTGGGAACCTTCAACACCCCTCCCTC 1745

QY 184 AAGAGTGAATTGGCATGTGGTAGACACGTCGTGAAACAAGTCTCCCTGAGGCTGAC 243
Db 1744 AAGAGTGAATTGGCATGTGGTAGACACGTCGTGAAACAAGTCTCCCTGAGGCTGAC 1685

QY 244 TCTGTGACTGCGGGGACAGCGCGGTGATTATCTGTGGAGGTTAGTGGCTACACTTTG 303
Db 1684 TCTGTGACTGCGGGGACAGCGCGGTGATTATCTGTGGAGGTTAGTGGGATGCGG 1625

QY 304 GACATCTGGGGCCAGGGAAACCTGTGACCGCTCTCCTCA 342
Db 1624 GACATCTGGGGCCAGGGAAACCTGTGACCGCTCTCCTCA 1586

RESULT 11
ADS84453
ID ADS84453 standard; DNA; 1996 BP.
AC ADS84453;
XX
XX 18-NOV-2004 (first entry)
DT
XX
DE Human anti-EPO-R antibody Ab412 heavy chain DNA SEQ ID NO:92.
XX
XX human; erythropoietin receptor; EPO receptor;
KM erythropoietin receptor binding antibody; EPO receptor binding antibody;
KM antianaemic; neuroprotective; vulnary; gene therapy; aplasia; anaemia;
KM wound healing; neural cell damage protection;
KM neural tissue damage protection; brain injury; spinal cord injury;
KM stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody; gene;
KM ds.
XX
XX Homo sapiens.
OS
XX
PN WO2004035603-A2.
XX
PD 29-APR-2004.
XX
PF 14-OCT-2003; 2003WO-US032243.
XX
PR 14-OCT-2002; 2002US-00269711.
PR 10-OCT-2003; 2003US-00684109.

XX
PA (ABBO) ABBOTT LAB.
XX
PI Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;
XX
XX WPI; 2004-348433/32.
DR P-PDSB; ADS84455.
XX
PT New antibodies that bind to or activate an endogenous human
PT erythropoietin receptor, useful for diagnosing, preventing or treating
PT disorders associated with dysfunctional erythropoietin receptor, e.g.
PT anaemia.
XX
XX Disclosure; SEQ ID NO 92; 192bp; English.

XX
PS The present invention describes an antibody or its fragment that binds to
CC or activates an endogenous activity of a human erythropoietin (EPO)
CC receptor in a mammal, but does not interact with a peptide having a
CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)
CC methods of modulating or activating an endogenous activity of a human EPO
CC receptor in a mammal, comprising administering to the mammal a
CC therapeutic amount of the above antibody or its fragment to modulate or
CC activate the receptor; (2) a method of treating a mammal suffering from
CC aplasia, comprising administering to the mammal a therapeutic amount of
CC the above antibody or its fragment to modulate or activate the receptor;
CC (3) a pharmaceutical composition comprising a therapeutic amount of the
CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)
CC an isolated and purified polynucleotide sequence, and their fragments,
CC complements and degenerate codon equivalents; and (5) an isolated and
CC purified amino acid sequence, and their fragments. The EPO receptor
CC binding antibody has antineutropenic, neuroprotective and vulnary
CC activities, and can be used in gene therapy. The compositions and methods
CC from the present invention can be used for modulating an endogenous
CC activity of a human EPO receptor or for treating mammals suffering from
CC aplasia or anaemia. They may also be used for identifying mammals having
CC a dysfunctional EPO receptor. The composition may also be used in
CC promoting wound healing or in protecting against neural cell and/or
CC tissue damage resulting from brain/spinal cord injury, stroke and the
CC like. The present sequence encodes a human anti-EPO-R antibody heavy
CC chain, which is given in the exemplification of the present invention.

XX
SQ Sequence 1996 BP; 422 A; 686 C; 537 G; 351 T; 0 U; 0 Other;

Query Match 78.5%; Score 268.6; DB 13; Length 1996;
Best Local Similarity 87.0%; Pred. No. 8.1e-67;
Matches 295; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 4 GAGCTCTGGCCAGAGCTGTGTAACCTGACAGACCCCTGCTCAGCTGCTGCTCT 63
Db 73 GAGTCGGGGCCAGAGCTGTGTAACCTGACAGACCCCTGCTCAGCTGCTGCTCT 132

QY 64 GGGGGCTTCATCCGAGTGTGTTACTGAGTTGATCCGCCAACACCCAGGAAAG 123
Db 133 GGTGGCTTCATCCAGAGTGTGTTACTGAGTTGATCCGCCAACACCCAGGAAAG 192

QY 124 GGGCTGAGAGGAGTGGGTACATCTATCAGCTGGGAACCTTCAACACCCCTCCCTC 183
Db 193 GGGCTGAGAGGAGTGGGTACATCTATCAGCTGGGAACCTTCAACACCCCTCCCTC 252

QY 184 AAGAGTGAATTGGCATGTGGTAGACACGTCGTGAAACAAGTCTCCCTGAGGCTGAC 243
Db 253 AAGAGTGAATTGGCATGTGGTAGACACGTCGTGAAACAAGTCTCCCTGAGGCTGAC 312

QY 244 TCTGTGACTGCGGGGACAGCGCGGTGATTATCTGTGGAGGTTAGTGGCTACACTTTG 303
Db 313 TCTGTGACTGCGGGGACAGCGCGGTGATTATCTGTGGAGGTTAGTGGGATGCGG 372

QY 304 GACATCTGGGGCCAGGGAAACCTGTGACCGCTCTCCTCA 342
Db 373 GACATCTGGGGCCAGGGAAACCTGTGACCGCTCTCCTCA 411

RESULT 12

ID	ADRe68595
ID	ADRe68595 standard; DNA; 1996 BP.
XX	
AC	ADRe68595;
XX	
DT	02-DEC-2004 (first entry)
XX	
DE	Human antibody Ab412 heavy chain polynucleotide seqid 92.
XX	
KW	antianaemic; respiratory; vulnery; gene therapy; vaccine;
KW	erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
KW	hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;
KW	wound healing; neural cell damage; tissue damage; brain injury;
KW	spinal cord injury; stroke; human; anti-EPO-R-antibody; heavy chain;
KW	Ab412; ds.
XX	
OS	Homo sapiens.
XX	
PN	US2004175379-A1.
PN	
PD	09-SEP-2004.
PF	10-OCT-2003; 2003US-00684109.
PR	14-OCT-2002; 2002US-0418031P.
PA	(DEVYR/) DEVRIES P J.
PA	(OSTRW/) OSTROW D H.
PA	(REIL/) REILLY E B.
PA	(GREE/) GREEN L L.
PA	(WIEL/) WIELER J.
PI	Deviies PJ, Ostrow DH, Reilly EB, Green LT, Wieler J;
DR	WPI: 2004-661369/64.
DR	P-PESDB; ADRe68597, ADRe68575, ADRe68576, ADRe68577.
PT	New antibody or its antibody fragment that activates an endogenous
PT	activity or is capable of binding to a human erythropoietin receptor in a
PT	mammal, useful for treating a mammal suffering aplasia or anemia.
PS	Disclosure; SEQ ID NO 92; 156bp; English.
CC	The invention describes an antibody or its fragment that activates an
CC	endogenous activity or capable of binding to a human erythropoietin
CC	receptor in a mammal, or that comprises at least one heavy or light chain
CC	variable region having a sequence comprising 116 or 107 amino acids (SEQ
CC	ID NO: 3 or 5) given in the specification or its fragment, but does not
CC	interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
CC	given in the specification. Also described are: a method of activating or
CC	modulating an endogenous activity of a human erythropoietin receptor in a
CC	mammal; a pharmaceutical composition comprising a therapeutic amount of
CC	an antibody or antibody fragment above and a pharmaceutical excipient; an
CC	isolated and purified polynucleotide sequence selected from 28 sequences
CC	comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
CC	the specification, and their fragments, complements, and degenerate codon
CC	equivalents; and an isolated and purified amino acid sequence selected
CC	from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
CC	SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
CC	their fragments. The antibody or its antibody fragment that activates or
CC	modulates the activity of the receptor is useful in a method of treating
CC	a mammal suffering aplasia or anaemia. The antibodies are also useful for
CC	treating disorders characterised by decreased or abnormal levels of
CC	oxygen in the blood or tissue such as hypoxaemia or chronic tissue
CC	hypoxia and/or diseases characterised by inadequate blood circulation or
CC	reduced blood flow. They are also useful for promoting wound healing or
CC	for protecting against neural cell and/or tissue damage, resulting from
CC	brain/spinal cord injury, stroke and the like. The antibodies are also
CC	useful for identifying or diagnosing mammals having dysfunctional
CC	erythropoietin receptor. This sequence represents a human Ab412 antibody
CC	heavy chain polynucleotide.
SQ	Sequence 1996 BP; 422 A; 686 C; 537 G; 351 T; 0 U; 0 Other;

Query Match	Similarity	78.5%	Score 268.6	DB 13	Length 1996
Best Local	Similarity	87.0%	Pred. No. 8.1e-67		
Matches 295	Conservative	0	Mismatches 44	Indels 0	Gaps 0

Query	DB	Score	Length	Identity	Mismatches	Indels	Gaps
4 GAGTCTGGCCAGGACTGTGAAGCCCTGCACAGACCCCTGTCCCTGACCTGGCTGTCTCT		63					
73 GAGTCTGGCCAGGACTGTGAAGCCCTGCACAGACCCCTGTCCCTGACCTGGCTGTCTCT		132					
64 GGCAGGCTTCATCCGCACTGTGTGTACTTACTTGTGAAGTTGGATCCGCCCAACCCAGGGAG		123					
133 GGTCCCTTCATACACAGCTGTGTGTACTTACTTGTGAAGTTGGATCCGCCCAACCCAGGGAG		192					
124 GGCCTGGAGT		183					
193 GGCCTGGAGT		252					
184 AAGAGTGAATGTGCATGT		243					
253 AAGAGTGAATGTGCATGT		312					
244 TCTGTGACTGCGCGGACACCGCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT		303					
313 TCTGTGACTGCGCGGACACCGCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT		372					
304 GACATCTGGGCGCAGGGAACCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT		342					
373 GACTACTGTGGCGCAGGGAACCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT		411					

Result ID	Score	Length	Identity	Mismatches	Indels	Gaps
13	268.6	1996	87.0%	44	0	0
ADR68596/c						
ADR68596						
02-DEC-2004						
Human antibody Ab412 heavy chain polynucleotide seqid 93.						
antianaemic; respiratory; vulnery; gene therapy; vaccine;						
erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;						
hypoxemia; chronic tissue hypoxia; blood circulation; blood flow;						
wound healing; neural cell damage; tissue damage; brain injury;						
spinal cord injury; stroke; human; anti-EPO-R-antibody; heavy chain;						
AB412; ds.						
Homo sapiens.						
US2004175379-A1.						
09-SEP-2004.						
10-OCT-2003; 2003US-00684109.						
14-OCT-2002; 2002US-0418031P.						
(DEVIR/) DEVIRIES P J.						
(OSTR/) OSTROW D H.						
(REIL/) REILLY E B.						
(GREE/) GREEN L L.						
(WIEL/) WIELER J.						
Deviries PJ, Ostrow DH, Reilly EB, Green LL, WIELER J;						
WPI; 2004-661369/64.						
New antibody or its antibody fragment that activates an endogenous						
activity or is capable of binding to a human erythropoietin receptor in a						
mammal, useful for treating a mammal suffering aplasia or anemia.						
Disclousre; SEQ ID NO 93; 156pp; English.						

CC The invention describes an antibody or its fragment that activates an
CC endogenous activity or capable of binding to a human erythropoietin
CC receptor in a mammal, or that comprises at least one heavy or light chain
CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
CC ID NO: 3 or 5) given in the specification or its fragment, but does not
CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
CC given in the specification. Also described are: a method of activating or
CC modulating an endogenous activity of a human erythropoietin receptor in a
CC mammal; a pharmaceutical composition comprising a therapeutic amount of
CC an antibody or antibody fragment above and a pharmaceutical excipient; an
CC isolated and purified polynucleotide sequence selected from 28 sequences
CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
CC the specification, and their fragments, complements, and degenerate codon
CC equivalents; and an isolated and purified amino acid sequence selected
CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
CC their fragments. The antibody or its antibody fragment that activates or
CC modulates the activity of the receptor is useful in a method of treating
CC a mammal suffering aplasia or anaemia. The antibodies are also useful for
CC treating disorders characterised by decreased or subnormal levels of
CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue
CC hypoxia and/or diseases characterised by inadequate blood circulation or
CC reduced blood flow. They are also useful for promoting wound healing or
CC for protecting against neural cell and/or tissue damage, resulting from
CC brain/spinal cord injury, stroke and the like. The antibodies are also
CC useful for identifying or diagnosing mammals having dysfunctional
CC erythropoietin receptor. This sequence represents a human Ab412 antibody
CC heavy chain polynucleotide.

XX Sequence 1996 BP; 351 A; 537 C; 686 G; 422 T; 0 U; 0 Other;

Query Match 78.5%; Score 268.6; DB 13; Length 1996;

Best Local Similarity 87.0%; Pred. No. 8.1e-67; Matches 295; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCCAAGAGCTGTGGAAGCCCTGCACAGACCCCTGTCCTGAGTGGCTGCTCT 63
DB 1924 GAGTCGGGCCCAAGAGCTGTGGAAGCCCTGCACAGACCCCTGTCCTGAGTGGCTGCTCT 1865
QY 64 GGGGGCTCCATCCGACAGTGTGTGTTACTGATGAGTTGATCCGCCAACCAGGAG 123
DB 1864 GGTGGCTCCATCCGACAGTGTGTGTTACTGATGAGTTGATCCGCCAACCAGGAG 1805
QY 124 GGCCTGAGTGGATGGGTATCATCTATCAAGTGGGAACACTTAAACAACCCGCTCCTC 183
DB 1804 GGCCTGAGTGGATGGGTATCATCTATCAAGTGGGAACACTTAAACAACCCGCTCCTC 1745
QY 184 AAGAGTGAATTGGCATGTGGTGTAGACACGCTGAGAACAAAGTTCTCCGAGGCTGAC 243
DB 1744 AAGAGTGAATTGGCATGTGGTGTAGACACGCTGAGAACAAAGTTCTCCGAGGCTGAC 1685
QY 244 TCTGTGACTGCGCGGACAGCGCCGTATATTACTGTGCGAGGTTAGAGTGAACCTTTG 303
DB 1684 TCTGTGACTGCGCGGACAGCGCCGTATATTACTGTGCGAGGTTAGAGTGAACCTTTG 1625
QY 304 GACATCTGGGGCCAGGGAACCTTGTCACCGTCTCTCA 342
DB 1624 GACATCTGGGGCCAGGGAACCTTGTCACCGTCTCTCA 1586

RESULT 14
ADK52387
ID ADK52387 standard; DNA, 560 BP.

XX ADK52387;

XX 20-MAY-2004 (first entry)

DE Human anti-MCP-1 variable region heavy chain DNA sequence #24.
XX monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KM Antipneumatic; Nephrotoxic; Antiartherosclerotic; Antipsoriatic;
KM Vasotropic; Immunosuppressive; Neuroprotective; Neoplastic;

KW inflammatory condition; cancer; arthritis; multiple sclerosis; de;
KM anti-MCP-1; heavy chain; light chain.

XX Homo sapiens.

OS W02004016769-A2.

PN 26-FEB-2004.

PF 19-AUG-2003; 2003WO-US026232.

PR 19-AUG-2002; 2002US-0404802P.

PA (ABGE-) ABGENIX INC.

PI Gudas JM, Haak-Frendescho M, Foord O, Liang ML, Ahluwalia K,

DR WPI; 2004-203794/19.

PS P-PDB; ADK52388.

PT New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.

XX Disclosure; SEQ ID NO 93; 154pp; English.

CC The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region heavy chain DNA sequence.

XX Sequence 560 BP; 106 A; 191 C; 151 G; 112 T; 0 U; 0 Other;

Query Match 78.3%; Score 267.8; DB 12; Length 560;

Best Local Similarity 88.0%; Pred. No. 9.6e-67; Matches 307; Conservative 0; Mismatches 32; Indels 10; Gaps 1;

QY 4 GAGTCTGGCCCAAGAGCTGTGGAAGCCCTGCACAGACCCCTGTCCTGAGTGGCTGCTCT 63
DB 16 GAGTCTGGCCCAAGAGCTGTGGAAGCCCTGCACAGACCCCTGTCCTGAGTGGCTGCTCT 75
QY 64 GGGGGCTCCATCCGACAGTGTGTGTTACTGATGAGTTGATCCGCCAACCAGGAG 123
DB 76 GGTGGCTCCATCCGACAGTGTGTGTTACTGATGAGTTGATCCGCCAACCAGGAG 135
QY 124 GGCCTGAGTGGATGGGTATCATCTATCAAGTGGGAACACTTAAACAACCCGCTCCTC 183
DB 136 GGCCTGAGTGGATGGGTATCATCTATCAAGTGGGAACACTTAAACAACCCGCTCCTC 195
QY 184 AAGAGTGAATTGGCATGTGGTGTAGACACGCTGAGAACAAAGTTCTCCGAGGCTGAC 243
DB 196 AAGAGTGAATTGGCATGTGGTGTAGACACGCTGAGAACAAAGTTCTCCGAGGCTGAC 255
QY 244 TCTGTGACTGCGCGGACAGCGCCGTATATTACTGTGCGAGGTTAGAGTGAACCTTTG 293
DB 256 TCTGTGACTGCGCGGACAGCGCCGTATATTACTGTGCGAGGTTAGAGTGAACCTTTG 315
QY 294 CTAACCTTTGAGATCTGGGCGCAGGGAACCTTGTCACCGTCTCTCA 342
DB 316 CTAACCTTTGAGATCTGGGCGCAGGGAACCTTGTCACCGTCTCTCA 364

RESULT 15
AAFP29046
ID AAFP29046 standard; DNA, 369 BP.

XX AAFP29046;

XX AC AAFP29046;

XX DT 03-APR-2001 (first entry)

XX DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 2.

XX KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;

XX KM envelope glycoprotein; gp120; diagnosis; ds.

XX OS Homo sapiens.

XX PN WO20010678-A1.

XX PD 04-JAN-2001.

XX PF 23-JUN-2000; 2000MO-US017327.

XX PR 30-JUN-1999; 99US-0141701P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Watkins BA, Reitz MS;

XX DR WPI; 2001-112438/12.

XX PT P-PSDB; AAB62745.

XX PT Novel human monoclonal antibody immunoreactive with human

XX PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1

XX PT in biological sample and providing passive immunotherapy to HIV-1

XX PT infected mammal.

XX PS Claim 4; Page 34-35; 81pp; English.

XX CC The present invention provides the protein and coding sequences for the

XX CC variable regions of human monoclonal antibodies which are immunoreactive

XX CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.

XX CC These can be used in diagnosis and therapy of HIV-1 infection

XX CC

XX SQ Sequence 369 BP; 75 A; 104 C; 107 G; 83 T; 0 U; 0 Other;

QY Query Match 77.7%; Score 265.8; DB 4; Length 369;

Db Best Local Similarity 87.5%; Pred. No. 3.2e-66;

Matches 307; Conservative 0; Mismatches 32; Indels 12; Gaps 1;

QY 4 GAGTCGAGCCGAGAGCTGTGTAAGCTGACAGACCCCTGCTCAGCTGGCTGCTCT 63

Db 19 GAGTCGAGCCGAGAGCTGTGTAAGCTGACAGACCCCTGCTCAGCTGGCTGCTCT 78

QY 64 GGCAGCTCCATCCGAGTGTGTTACTACTGAGTTGATCCGCAACACCCAGGAG 123

Db 79 GGTGGCTCCATCAGAGTGTGTTACTACTGAGTGTGATCCGCAACACCCAGGAG 138

QY 124 GGCCTGAGTGTGATTTGGTACATTTATCAGAGTGGAAACACCTTAACAACCCGCTC 183

Db 139 GGCCTGAGTGTGATTTGGTACATTTATCAGAGTGGAAACACCTTAACAACCCGCTC 198

QY 184 AAGAGTGAATTGCGATGCGTAGACACGCTGAGAACAGTCTCCCTGAGGCTGAAC 243

Db 199 AAGAGTGAATTGCGATGCGTAGACACGCTGAGAACAGTCTCCCTGAGGCTGAAC 258

QY 244 TCTGTGACTGCGGAGACACGCGGTATTTACTGTGCGAGG-----TTAGAT 291

Db 259 TCTGTGACTGCGGAGACACGCGGTATTTACTGTGCGAGGCGGCGGTATTTGTGTGT 318

QY 292 GGCCTACACTTTGAGCATTTGGGCGAGGAAACCTGTGACACCGTCTCTCA 342

Db 319 GATTGCTCTTGTGACTGAGGCGAGGAAACCTGTGACACCGTCTCTCA 369

Search completed: July 27, 2005, 05:59:43
Job time : 325.618 secs

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Score	Match	Length	DB	ID	Description
1	342	100.0	342	14	US-10-027-725A-1
2	310	90.6	342	14	US-10-027-725A-1
3	298.8	87.4	342	14	US-10-027-725A-2
4	275	80.4	352	15	US-10-330-613-15
5	275	80.4	352	16	US-10-330-530-15
6	275	80.4	352	19	US-10-660-357-15
7	268.6	78.5	354	19	US-10-684-109-42
8	268.6	78.5	354	19	US-10-684-109-42
9	268.6	78.5	354	19	US-10-684-109-42
10	268.6	78.5	354	19	US-10-684-109-42
11	268.6	78.5	354	19	US-10-684-109-42
12	268.6	78.5	354	19	US-10-684-109-42
13	268.6	78.5	354	19	US-10-684-109-42
14	268.6	78.5	354	19	US-10-684-109-42
15	268.6	78.5	354	19	US-10-684-109-42
16	268.6	78.5	354	19	US-10-684-109-42
17	268.6	78.5	354	19	US-10-684-109-42
18	268.6	78.5	354	19	US-10-684-109-42
19	268.6	78.5	354	19	US-10-684-109-42
20	268.6	78.5	354	19	US-10-684-109-42
21	268.6	78.5	354	19	US-10-684-109-42
22	268.6	78.5	354	19	US-10-684-109-42
23	268.6	78.5	354	19	US-10-684-109-42
24	268.6	78.5	354	19	US-10-684-109-42
25	268.6	78.5	354	19	US-10-684-109-42
26	268.6	78.5	354	19	US-10-684-109-42
27	268.6	78.5	354	19	US-10-684-109-42
28	268.6	78.5	354	19	US-10-684-109-42
29	268.6	78.5	354	19	US-10-684-109-42
30	268.6	78.5	354	19	US-10-684-109-42
31	268.6	78.5	354	19	US-10-684-109-42
32	268.6	78.5	354	19	US-10-684-109-42
33	268.6	78.5	354	19	US-10-684-109-42
34	268.6	78.5	354	19	US-10-684-109-42
35	268.6	78.5	354	19	US-10-684-109-42
36	268.6	78.5	354	19	US-10-684-109-42
37	268.6	78.5	354	19	US-10-684-109-42
38	268.6	78.5	354	19	US-10-684-109-42
39	268.6	78.5	354	19	US-10-684-109-42
40	268.6	78.5	354	19	US-10-684-109-42
41	268.6	78.5	354	19	US-10-684-109-42
42	268.6	78.5	354	19	US-10-684-109-42
43	268.6	78.5	354	19	US-10-684-109-42
44	268.6	78.5	354	19	US-10-684-109-42
45	268.6	78.5	354	19	US-10-684-109-42
46	268.6	78.5	354	19	US-10-684-109-42
47	268.6	78.5	354	19	US-10-684-109-42
48	268.6	78.5	354	19	US-10-684-109-42
49	268.6	78.5	354	19	US-10-684-109-42
50	268.6	78.5	354	19	US-10-684-109-42
51	268.6	78.5	354	19	US-10-684-109-42
52	268.6	78.5	354	19	US-10-684-109-42
53	268.6	78.5	354	19	US-10-684-109-42
54	268.6	78.5	354	19	US-10-684-109-42
55	268.6	78.5	354	19	US-10

C	8	268.6	78.5	1996	19	US-10-684-109-92	Sequence 92, Appl
	9	268.6	78.5	1996	19	US-10-684-109-93	Sequence 93, Appl
	10	267.8	78.3	560	21	US-10-644-277-93	Sequence 93, Appl
	11	265.4	77.6	352	15	US-10-330-613-7	Sequence 7, Appl
	12	265.4	77.6	352	16	US-10-330-530-7	Sequence 7, Appl
	13	265.4	77.6	352	19	US-10-660-357-7	Sequence 7, Appl
	14	265.2	77.5	358	15	US-10-330-613-27	Sequence 27, Appl
	15	265.2	77.5	358	16	US-10-330-530-27	Sequence 27, Appl
	16	265.2	77.5	358	19	US-10-660-357-27	Sequence 27, Appl
	17	265.2	77.5	1338	21	US-10-644-277-61	Sequence 61, Appl
	18	264.8	77.4	420	21	US-10-893-576-18	Sequence 18, Appl
	19	264.6	77.4	663	10	US-09-972-656-79	Sequence 79, Appl
	20	264.6	77.4	370	17	US-10-309-762-189	Sequence 79, Appl
	21	263.8	77.1	355	19	US-10-684-109-54	Sequence 54, Appl
	22	263.8	77.1	1996	19	US-10-684-109-110	Sequence 110, Appl
	C	23	263.8	77.1	1996	19	US-10-684-109-111
24		262.2	76.7	361	17	US-10-309-762-191	Sequence 110, Appl
25		261.4	76.4	429	17	US-10-309-762-110	Sequence 191, Appl
26		261	76.3	366	22	US-10-984-960A-19	Sequence 19, Appl
27		260.8	76.3	516	20	US-10-612-497-33	Sequence 33, Appl
28		260.8	76.3	516	20	US-10-776-649-33	Sequence 33, Appl
29		259.6	75.9	370	17	US-10-309-762-186	Sequence 186, Appl
30		259.4	75.8	367	17	US-10-309-762-195	Sequence 195, Appl
31		256.4	75.0	352	15	US-10-330-613-35	Sequence 35, Appl
32		256.4	75.0	352	16	US-10-330-530-35	Sequence 35, Appl
33		256.4	75.0	352	19	US-10-660-357-35	Sequence 35, Appl
34		256.4	75.0	370	17	US-10-309-762-200	Sequence 200, Appl
35		255.2	74.6	370	17	US-10-309-762-187	Sequence 187, Appl
36		254.8	74.5	370	17	US-10-309-762-201	Sequence 201, Appl
37		254.8	74.5	370	17	US-10-309-762-212	Sequence 212, Appl
C		38	254.6	74.4	366	22	US-10-984-960A-55
	39	253.8	74.2	370	17	US-10-309-762-185	Sequence 185, Appl
	40	253.6	74.2	376	17	US-10-309-762-184	Sequence 184, Appl
	41	253.6	74.2	376	17	US-10-309-762-197	Sequence 197, Appl
	42	253.6	74.2	376	17	US-10-309-762-197	Sequence 199, Appl
	43	252.8	73.9	432	21	US-10-893-576-12	Sequence 12, Appl
	44	252.6	73.9	1392	21	US-10-810-901-9	Sequence 9, Appl
	45	250.6	73.3	382	17	US-10-309-762-194	Sequence 194, Appl

ALIGNMENTS

RESULT 1
MS-10-02

Sequence 1, Application US/10027725A
Publication No. US20030082659A1
GENERAL INFORMATION:
APPLICANT: Flicker, Sabine
TITLE OF INVENTION: Group 2 Allergen Specific IGR-fabs and Use Thereof
FILE REFERENCE: 25401-4
CURRENT APPLICATION NUMBER: US/10/027,725A
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/259,436
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 342
TYPE: DNA
ORGANISM: Homo sapiens
US-10-027-725A-1

	Query Match	100.0%	Score 342;	DB 14;	Length 342;
	Best Local Similarity	100.0%	Prid. No. 3	8e-101;	
	Matches 342;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Oy	1	CTCAGACTGGGCCAGAGACTGGTGAACCTGCA	CAGACCTGTCCCTCAGCTGGCGCTGC	60	
Db	1	CTCAGACTGGGCCAGAGACTGGTGAACCTGCA	CAGACCTGTCCCTCAGCTGGCGCTGC	60	
Oy	61	TTGGCGGAGCTCATCCGAGTGATGGTTACTA	CTGGAGTTGGATCCGCAACCCAGGG	120	

Db 61 TCTGCGGCTCCATCCGAGTGTGTTACTGAGATTGGATCCGCCAACACCCAGGG 120
Qy 121 AAGGCGCTGAGTGGATTGGGTACATCATACAGTGGGACACCTCAACAACCCGCTCC 180
Db 121 AAGGCGCTGAGTGGATTGGGTACATCATACAGTGGGACACCTCAACAACCCGCTCC 180
Qy 181 CTCGAAGTGCATTTGGCATGTCCGTAGACACGTCGTGAGAACAAAGTTCTCCCTGAGGCTG 240
Db 181 CTCGAAGTGCATTTGGCATGTCCGTAGACACGTCGTGAGAACAAAGTTCTCCCTGAGGCTG 240
Qy 241 AACTCTGTACTGCCCGGAGACACGCGCTGTATTACTGTGCGAGTTAGATGCTTACACT 300
Db 241 AACTCTGTACTGCCCGGAGACACGCGCTGTATTACTGTGCGAGTTAGATGCTTACACT 300
Qy 301 TTGGACATCTGGGGCCAGGGAAACCTGTGTCACCGTCTCCCTCA 342
Db 301 TTGGACATCTGGGGCCAGGGAAACCTGTGTCACCGTCTCCCTCA 342

RESULT 2

US-10-027-725A-3
; Sequence 3, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-3

Query Match 90.6%; Score 310; DB 14; Length 342;

Best Local Similarity 94.2%; Pred. No. 1e-90; Mismatches 20; Indels 0; Gaps 0;

Matches 322; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Qy 1 CTCGAGTCTGGCCCGAGACTGTGTAAGCTGACAGACCTGTCCCTCAGCTGCGCTGTC 60
Db 1 CTCGAGTCTGGCCCGAGACTGTGTAAGCTGACAGACCTGTCCCTCAGCTGCGCTGTC 60
Qy 61 TCTGCGGCTTCATCCGAGTGTGTTACTTACTGAGATTGGATCCGCAACCCAGGG 120
Db 61 TCTGCGGCTTCATCCGAGTGTGTTACTTACTGAGATTGGATCCGCAACCCAGGG 120
Qy 121 AAGGCGCTGAGTGGATTGGGTACATCATACAGTGGGAAACACCTCAACAACCCGCTCC 180
Db 121 AAGGCGCTGAGTGGATTGGGTACATCATACAGTGGGAAACACCTCAACAACCCGCTCC 180
Qy 181 CTCGAAGTGCATTTGGCATGTCCGTAGACACGTCGTGAGAACAAAGTTCTCCCTGAGGCTG 240
Db 181 CTCGAAGTGCATTTGGCATGTCCGTAGACACGTCGTGAGAACAAAGTTCTCCCTGAGGCTG 240
Qy 241 AACTCTGTACTGCCCGGAGACACGCGCTGTATTACTGTGCGAGTTAGATGCTTACACT 300
Db 241 AACTCTGTACTGCCCGGAGACACGCGCTGTATTACTGTGCGAGTTAGATGCTTACACT 300
Qy 301 TTGGACATCTGGGGCCAGGGAAACCTGTGTCACCGTCTCCCTCA 342
Db 301 TTGGACATCTGGGGCCAGGGAAACCTGTGTCACCGTCTCCCTCA 342

RESULT 3

US-10-027-725A-2
; Sequence 2, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:

; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-2

Query Match 87.4%; Score 298.8; DB 14; Length 342;

Best Local Similarity 92.1%; Pred. No. 4.6e-87; Mismatches 27; Indels 0; Gaps 0;

Matches 315; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
Qy 1 CTCGAGTCTGGCCCGAGACTGTGTAAGCTGACAGACCTGTCCCTCAGCTGCGCTGTC 60
Db 1 CTCGAGTCTGGCCCGAGACTGTGTAAGCTGACAGACCTGTCCCTCAGCTGCGCTGTC 60
Qy 61 TCTGCGGCTTCATCCGAGTGTGTTACTTACTGAGATTGGATCCGCAACCCAGGG 120
Db 61 TCTGCGGCTTCATCCGAGTGTGTTACTTACTGAGATTGGATCCGCAACCCAGGG 120
Qy 121 AAGGCGCTGAGTGGATTGGGTACATCATACAGTGGGAAACACCTCAACAACCCGCTCC 180
Db 121 AAGGCGCTGAGTGGATTGGGTACATCATACAGTGGGAAACACCTCAACAACCCGCTCC 180
Qy 181 CTCGAAGTGCATTTGGCATGTCCGTAGACACGTCGTGAGAACAAAGTTCTCCCTGAGGCTG 240
Db 181 CTCGAAGTGCATTTGGCATGTCCGTAGACACGTCGTGAGAACAAAGTTCTCCCTGAGGCTG 240
Qy 241 AACTCTGTACTGCCCGGAGACACGCGCTGTATTACTGTGCGAGTTAGATGCTTACACT 300
Db 241 AACTCTGTACTGCCCGGAGACACGCGCTGTATTACTGTGCGAGTTAGATGCTTACACT 300
Qy 301 TTGGACATCTGGGGCCAGGGAAACCTGTGTCACCGTCTCCCTCA 342
Db 301 TTGGACATCTGGGGCCAGGGAAACCTGTGTCACCGTCTCCCTCA 342

RESULT 4

US-10-330-613-15
; Sequence 15, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ARGENIX 022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-15

Query Match 80.4%; Score 275; DB 15; Length 352;

Best Local Similarity 90.3%; Pred. No. 2.6e-79; Mismatches 30; Indels 3; Gaps 1;

Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

Qy 4 GAGTCTGAGCCAGGACTGTGTAAGCTGACAGACCTGTCCCTCAGCTGCGCTGCTCT 63
Db 16 GAGTCTGAGCCAGGACTGTGTAAGCTTTCACAGACCTGTCCCTCAGCTGCGCTGCTCT 75
Qy 64 GCGGCTTCATCCGAGTGTGTTACTGAGATTGGATCCGCCAACCCAGGGAG 123

Db 76 GGTGGCTCCATCAGCAGTGGTGTACTACTGAGCTTGGATCCCGCCAGACCCGAGAG 135
Qy 124 GGCCTGAGTGGATTTGGGTATCTATTCACAGTGGGAAACCTTCAACAACCCGTCCCTC 183
Db 136 GGCCTGAGTGGATTTGGGTATCTATTCACAGTGGGAAACCTTCAACAACCCGTCCCTC 195
Qy 184 AAGAGTGAATTCAGTGTGATGAGACCGTGTAGAACGATTCCTCCGAGGCTGAGC 243
Db 196 AAGAGTGAATTCAGTGTGATGAGACCGTGTAGAACGATTCCTCCGAGGCTGAGC 255
Qy 244 TCTGTGACTGCGCGGACACGCGCGTATTAATGAGAGTTAGAGTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCGTATTAATGAGAGTTAGAGTACACTTTG 312
Qy 304 GACATCTGGGGCCAGGAAACCTTGATCAACCGTCTCTCA 342
Db 313 GACTACTGGGGCCAGGAAACCTTGATCAACCGTCTCTCA 351

RESULT 5
US-10-330-530-15
; Sequence 15, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:

; APPLICANT: Gudea, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330.530
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-530-15

Query Match 80.4%; Score 275; DB 16; Length 352;
Best Local Similarity 90.3%; Pred. No. 2.6e-79;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

Qy 4 GAGTCTGGCCAGAGCTGATGAGACCTGACAGACCTGTCTCTGAGTGGCTCTCT 63
Db 16 GAGTCTGGCCAGAGCTGATGAGACCTGACAGACCTGTCTCTGAGTGGCTCTCT 75
Qy 64 GCGGCTCCATCCGAGTGTGTTACTGAGTGGATCCGCAACCCGAGAG 123
Db 76 GGTGGCTCCATCAGCAGTGGTGTACTACTGAGCTTGGATCCCGCCAGACCCGAGAG 135
Qy 124 GGCCTGAGTGGATTTGGGTATCTATTCACAGTGGGAAACCTTCAACAACCCGTCCCTC 183
Db 136 GGCCTGAGTGGATTTGGGTATCTATTCACAGTGGGAAACCTTCAACAACCCGTCCCTC 195
Qy 184 AAGAGTGAATTCAGTGTGATGAGACCGTGTAGAACGATTCCTCCGAGGCTGAGC 243
Db 196 AAGAGTGAATTCAGTGTGATGAGACCGTGTAGAACGATTCCTCCGAGGCTGAGC 255
Qy 244 TCTGTGACTGCGCGGACACGCGCGTATTAATGAGAGTTAGAGTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCGTATTAATGAGAGTTAGAGTACACTTTG 312
Qy 304 GACATCTGGGGCCAGGAAACCTTGATCAACCGTCTCTCA 342
Db 313 GACTACTGGGGCCAGGAAACCTTGATCAACCGTCTCTCA 351

RESULT 6
US-10-660-357-15
; Sequence 15, Application US/10660357
; Publication No. US20040115205A1

; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660.357
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/350,580
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-15

Query Match 80.4%; Score 275; DB 19; Length 352;
Best Local Similarity 90.3%; Pred. No. 2.6e-79;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

Qy 4 GAGTCTGGCCAGAGCTGATGAGACCTGACAGACCTGTCTCTGAGTGGCTCTCT 63
Db 16 GAGTCTGGCCAGAGCTGATGAGACCTGACAGACCTGTCTCTGAGTGGCTCTCT 75
Qy 64 GCGGCTCCATCCGAGTGTGTTACTGAGTGGATCCGCAACCCGAGAG 123
Db 76 GGTGGCTCCATCAGCAGTGGTGTACTACTGAGCTTGGATCCCGCCAGACCCGAGAG 135
Qy 124 GGCCTGAGTGGATTTGGGTATCTATTCACAGTGGGAAACCTTCAACAACCCGTCCCTC 183
Db 136 GGCCTGAGTGGATTTGGGTATCTATTCACAGTGGGAAACCTTCAACAACCCGTCCCTC 195
Qy 184 AAGAGTGAATTCAGTGTGATGAGACCGTGTAGAACGATTCCTCCGAGGCTGAGC 243
Db 196 AAGAGTGAATTCAGTGTGATGAGACCGTGTAGAACGATTCCTCCGAGGCTGAGC 255
Qy 244 TCTGTGACTGCGCGGACACGCGCGTATTAATGAGAGTTAGAGTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCGTATTAATGAGAGTTAGAGTACACTTTG 312
Qy 304 GACATCTGGGGCCAGGAAACCTTGATCAACCGTCTCTCA 342
Db 313 GACTACTGGGGCCAGGAAACCTTGATCAACCGTCTCTCA 351

RESULT 7

US-10-684-109-42
; Sequence 42, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Deviles, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Oetrow, David H.
; APPLICANT: Reilly, Edward B.
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989 US.02
; CURRENT APPLICATION NUMBER: US/10/684.109
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-684-109-42

Query Match 78.5%; Score 268.6; DB 19; Length 354;

[illegible]

```

RESULT 8
US-10-684-109-92
: Sequence 92, Application US/10684109
: Publication No. US20040175379A1
: GENERAL INFORMATION:
: APPLICANT: Devries, Peter J.
: APPLICANT: Green, Larry L.
: APPLICANT: Ostrow, David H.
: APPLICANT: Reilly, Edward B.
: APPLICANT: Wieleter, James
: TITLE OF INVENTION: Erythropoietin Receptor Binding
: TITLE OF INVENTION: Antibodies
: FILE REFERENCE: 6389, US .02
: CURRENT APPLICATION NUMBER: US/10/684, 109
: CURRENT FILING DATE: 2003-10-10
: PRIOR APPLICATION NUMBER: 10/269, 711
: PRIOR FILING DATE: 2002-10-14
: NUMBER OF SEQ ID NOS: 115
: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 92
: LENGTH: 1996
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-684-109-92

```

Query Match	78.5%	Score 268.6;	DB 19;	Length 1996;
Best Local Similarity	87.0%;	Pred. No. 4.7e-77;		
Matches 295; Conservative	0;	Mismatches 44;	Indels 0;	Gaps 0

OY	4	GAGTGTGGCCAGAGACTGGTGAAGGCTGACAGACCCGTGCTCTAGCTGAGCTGCTGCT	63
Db	73	GAGTGGGGCCAGAGACTGTGAAGCTTTCACAGACCCTGTCTCTA	132
OY	64	GGCGGCTTCATCCGACGTGGTGTTACTACTGAGTTGGATCCGCCAACCCAGGGAAG	123
Db	133	GGTGCTTCATCAGCAGTGGTGCTTACTACTGAGTTGGATCCGCCAGACCCAGGAAG	192
OY	124	GGCTTGGAGTGGATTGGGTACATCTATCACTAGTGGGAACCTTACACACACCCTGCTC	183
Db	193	GGCTTGGAGTGGATTGGGTACATCTATAAGAGTGAACCTCTACTACACACCCTGCTC	252
OY	184	AAGAGTGAATTGGCATGTGGGTAAACAGTGGAAACAATTCTCCCTGAGGCGAAG	243
Db	253	AAGATGCACCTTACCTCTACGTAGACAGCTTAAAGACCAAGTTCTCCTGGAACCTGAATC	312

Oy	244	TCGTGTAACGCGCGGACACAGCGCCGCTGATTACTGTGGAGAGTTAGAGCTACATTTC	303
Db	313	TCGTGTAACGCGCGGACACAGCGCCGCTGATTATTGTGGAGAGATTAACATCGGGATCGCG	372
Oy	304	GACATGTGGGGCAGAGAAACCTGTGACACGCTTCACCA	342
Db	373	GACTTACTGGGGCCAGGAAACCTGTGTACACGCTTCCTCA	411

```

RESULT 9
US-10-684-109-93/c
; Sequence 93. Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeWittes, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Rellily, Edward B.
; APPLICANT: Waieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6189 US. 02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Fasteq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-684-109-93

```

78.5%; Score 268.6; DB 19; Length 1996;

	Matches	295;	Conservative	0;	Mismatches	44;	Indels	0;	Gaps	0;
OY	4	GAGTCGTGGCCAGGAC	CTGGTGAAGCCCTG	CACACACCTGTG	CCCTCAGCTGGCTGTCT	CTCT	63			
Db	1924	GAGTCGGGGCCAGAC	CTGGTGAAGCCCTT	CACACCTGTG	CCCTCAGCTGGCTGTCT	CTCT	1865			
OY	64	GGCGGCTCCATCCG	CAGTGGTGTACT	CTAGAGATTGGAT	CCGCGCAACCCAGGGAA	G	123			
Db	1864	GGTGCTCTCATCAG	CAAGTGGTGTCT	ACTACTGGAGTTGGAT	CCGCGCAACCCAGGGAA	G	1805			
OY	124	GGCCTGAGTGGATT	GGGTACATCTAT	CACAGTGGGAA	CCCTCAACCCGCTC	CTC	183			
Db	1804	GGCCTGAGTGGATT	GGGTACATCTAT	AAGAAGTGA	CACTCTCACTCAAC	CCGCTCCTC	1745			
OY	184	AAGAGTCGAATTG	CCATGTGCGTGA	CAACGCTTGAGAA	CAAGTCTTCCCTGAG	CTGA	243			
Db	1744	AAGAGTCGAATTG	CCATGTGCGTGA	CAACGCTTGAGAA	CAAGTCTTCCCTGAG	CTGA	1685			
OY	244	TCTGTGACTGGCG	GGGACACGGCCGT	GTATTA	CTGTGCGAGGT	TAGATGGTACATT	TTG	303		
Db	1684	TCTGTGACTGGCG	GGGACACGGCCGT	GTATTA	CTGTGCGAGGT	TAGATGGTACATT	TTG	1625		
OY	304	GACATCTGGGGCC	AGGAAACCTGAT	CACCGTCCCTCA		342				
Db	1624	GACATCTGGGGCC	AGGAAACCTGAT	CACCGTCCCTCA		1586				

RESULT 10
US-10-644-277-93

Sequence 93, Application US/1064427/1
Publication No. US20050058639A1
GENERAL INFORMATION:
APPLICANT: Gudas, Uean M.
APPLICANT: Haak-Frandscho, Mary
APPLICANT: Foord, Orin
APPLICANT: Liang, Meina L.
APPLICANT: Ahluwalia, Kiran

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; APPLICANT: Bhakta, Sunil
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
; TITLE OF INVENTION: CHEMO-ATTRACTANT PROTEIN-1 (MCP-1) AND USES THEREOF
; FILE REFERENCE: ABGENIX.091A
; CURRENT APPLICATION NUMBER: US/10/644,277
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 60/404,802
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homosapien
US-10-644-277-93

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```

Query Match      78.3%; Score 267.8; DB 21; Length 560;
Best Local Similarity 88.0%; Pred. No. 6.5e-77;
Matches 307; Conservative 0; Mismatches 32; Indels 10; Gaps 1;

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QY 4 GAGTCTGCCCCAGAGACTGTGTAAGCTTGCACAGACCTGTCTCCTGAGCTGCGCTGTCT 63
DB 16 GAGTCGGGCCCCAGAGACTGTGTAAGCTTGCACAGACCTGTCTCCTGAGCTGCTCT 75
QY 64 GCGGCTCCATCCGAGTGTGTGTTACTACTGAGTTGATCCGCAACCCAGGGAG 123
DB 76 GGTGGCTCCATCCGAGTGTGTGTTACTACTGAGTTGATCCGCAACCCAGGGAG 135
QY 124 GCGCTGAGTGTGTTGGTATCATCTATCAGTGGGAGACCTTCAACACCCGCTCCTC 183
DB 136 GCGCTGAGTGTGTTGGTATCATCTATCAGTGGGAGACCTTCAACACCCGCTCCTC 195
QY 184 AAGAGTGAATTGGCATGTGGTGAACACCTGTGAAGAAAGTTCTCCCTGAGCTGAC 243
DB 196 AAGAGTGAATTGAATCATATCATATGAGACAGCTTAAAGAAAGTTCTCCCTGAGCTGAC 255
QY 244 TCTGTGACTGCGCGGAGACAGCGCGGTATTAAGTGTGAGGAGTTAGATG----- 293
DB 256 TCTGTGACTGCGCGGAGACAGCGCGGTATTAAGTGTGAGGAGTTAGATGCGCTGCC 315
QY 294 CTACATCTTGGACATCTTGGGCGCAGGAAACCTGTGTCACCGTCTCTCA 342
DB 316 CCATCTGTTGACACCCCTGCGGCGCAGGAAACCTGTGTCACCGTCTCTCA 364

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RESULT 11
US-10-330-613-7
; Sequence 7, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-7

```

```

Query Match      77.6%; Score 265.4; DB 15; Length 352;
Best Local Similarity 88.5%; Pred. No. 3.6e-76;
Matches 300; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

```

```

QY 4 GAGTCTGCCCCAGAGACTGTGTAAGCTTGCACAGACCTGTCTCCTGAGCTGCGCTGTCT 63
DB 16 GAGTCGGGCCCCAGAGACTGTGTAAGCTTGCACAGACCTGTCTCCTGAGCTGCTCT 75

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QY 64 GCGGCTCCATCCGAGTGTGTGTTACTACTGAGTTGATCCGCAACCCAGGGAG 123
DB 76 GGTGGCTCCATCCGAGTGTGTGTTACTACTGAGTTGATCCGCAACCCAGGGAG 135
QY 124 GCGCTGAGTGTGTTGGTATCATCTATCAGTGGGAGACCTTCAACACCCGCTCCTC 183
DB 136 GCGCTGAGTGTGTTGGTATCATCTATCAGTGGGAGACCTTCAACACCCGCTCCTC 195
QY 184 AAGAGTGAATTGGCATGTGGTGAACACCTGTGAAGAAAGTTCTCCCTGAGCTGAC 243
DB 196 AAGAGTGAATTGAATCATATCATATGAGACAGCTTAAAGAAAGTTCTCCCTGAGCTGAC 255
QY 244 TCTGTGACTGCGCGGAGACAGCGCGGTATTAAGTGTGAGGAGTTAGATGAGTCTTAC 303
DB 256 TCTGTGACTGCGCGGAGACAGCGCGGTATTAAGTGTGAGGAGTTAGATGAGTCTTAC 312
QY 304 GACATCTGGGGCCAGGAGACCTGTGTCACCGTCTCTCA 342
DB 313 AAGTACTGGGGCCAGGAGACCTGTGTCACCGTCTCTCA 351

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```

RESULT 12
US-10-530-7
; Sequence 7, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-530-530-7

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Query Match      77.6%; Score 265.4; DB 16; Length 352;
Best Local Similarity 88.5%; Pred. No. 3.6e-76;
Matches 300; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

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QY 4 GAGTCTGCCCCAGAGACTGTGTAAGCTTGCACAGACCTGTCTCCTGAGCTGCGCTGTCT 63
DB 16 GAGTCGGGCCCCAGAGACTGTGTAAGCTTGCACAGACCTGTCTCCTGAGCTGCTCT 75
QY 64 GCGGCTCCATCCGAGTGTGTGTTACTACTGAGTTGATCCGCAACCCAGGGAG 123
DB 76 GGTGGCTCCATCCGAGTGTGTGTTACTACTGAGTTGATCCGCAACCCAGGGAG 135
QY 124 GCGCTGAGTGTGTTGGTATCATCTATCAGTGGGAGACCTTCAACACCCGCTCCTC 183
DB 136 GCGCTGAGTGTGTTGGTATCATCTATCAGTGGGAGACCTTCAACACCCGCTCCTC 195
QY 184 AAGAGTGAATTGGCATGTGGTGAACACCTGTGAAGAAAGTTCTCCCTGAGCTGAC 243
DB 196 AAGAGTGAATTGAATCATATCATATGAGACAGCTTAAAGAAAGTTCTCCCTGAGCTGAC 255
QY 244 TCTGTGACTGCGCGGAGACAGCGCGGTATTAAGTGTGAGGAGTTAGATGAGTCTTAC 303
DB 256 TCTGTGACTGCGCGGAGACAGCGCGGTATTAAGTGTGAGGAGTTAGATGAGTCTTAC 312
QY 304 GACATCTGGGGCCAGGAGACCTGTGTCACCGTCTCTCA 342
DB 313 AAGTACTGGGGCCAGGAGACCTGTGTCACCGTCTCTCA 351

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RESULT 13
US-10-660-357-7
; Sequence 7, Application US/10660357

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; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-7
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Query Match 77.6%; Score 265.4; DB 19; Length 352;
Best Local Similarity 88.5%; Pred. No. 3.6e-76;
Matches 300; Conservative 0; Mismatches 36; Indels 3; Gaps 1;
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```
QY 4 GAGTCTGGCCCGCAGAGCTGTGAAGCTTGCACAGACCCCTGCTCAGCTGGCTGTCT 63
DB 16 GAGTCGGGCCCGCAGAGCTGTGAAGCTTGCACAGACCCCTGCTCAGCTGTCTCT 75
QY 64 GCGCGCTCCATCCGACAGTGTGTACTACTGAGTTGATCCGCAACCCCAAGGAG 123
DB 76 GGTGGCTCCATCAACAGTGTGTACTACTGAGTTGATCCGCAACCCCAAGGAG 135
QY 124 GCGCTGAGTGAATTGGGTACATCTATCAAGTGGAAACCTTCAACAAACCCGCTC 183
DB 136 GCGCTGAGTGAATTGGGTACATCTATCAAGTGGAAACCTTCAACAAACCCGCTC 195
QY 184 AAGAGTGAATTGGCATGTGGTGAACAGCTGTGAACAGCTTCTCCCTAGGCTGAC 243
DB 196 AAGAGTGAATTGGCATGTGGTGAACAGCTGTGAACAGCTTCTCCCTAGGCTGAC 255
QY 244 TCTGTGACTGCGCGGACACGCGGTGATTACTGTGCGAGTTAGATGCTACACTTTG 303
DB 256 TCTGTGACTGCGCGGACACGCGGTGATTACTGTGCGAG---AGGGGAGATGGCTAC 312
QY 304 GACATCTGGGGCCAGAGAACTTGTGACCGTCTCTCTCA 342
DB 313 AAGTACTGGGGCCAGAGAACTTGTGACCGTCTCTCTCA 351
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RESULT 14
US-10-330-613-27
; Sequence 27, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-27
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Query Match 77.5%; Score 265.2; DB 15; Length 358;
Best Local Similarity 88.0%; Pred. No. 4.1e-76;
Matches 301; Conservative 0; Mismatches 38; Indels 3; Gaps 1;
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```
QY 4 GAGTCTGGCCCGCAGAGCTGTGAAGCTTGCACAGACCCCTGCTCAGCTGGCTGTCT 63
```

```
DB 16 GAGTCGGGCCCGCAGAGCTGTGAAGCTTGCACAGACCCCTGCTCAGCTGTCTCT 75
QY 64 GCGCGCTCCATCCGACAGTGTGTACTACTGAGTTGATCCGCAACCCCAAGGAG 123
DB 76 GGTGGCTCCATCAACAGTGTGTACTACTGAGTTGATCCGCAACCCCAAGGAG 135
QY 124 GCGCTGAGTGAATTGGGTACATCTATCAAGTGGAAACCTTCAACAAACCCGCTC 183
DB 136 GCGCTGAGTGAATTGGGTACATCTATCAAGTGGAAACCTTCAACAAACCCGCTC 195
QY 184 AAGAGTGAATTGGCATGTGGTGAACAGCTGTGAACAGCTTCTCCCTAGGCTGAC 243
DB 196 AAGAGTGAATTGGCATGTGGTGAACAGCTGTGAACAGCTTCTCCCTAGGCTGAC 255
QY 244 TCTGTGACTGCGCGGACACGCGGTGATTACTGTGCGAG---GTTAGATGGCTACCT 300
DB 256 TCTGTGACTGCGCGGACACGCGGTGATTACTGTGCGAGATGGGAAACAGCTGCT 315
QY 301 TTGACATCTGGGGCCAGAGAACTTGTGACCGTCTCTCTCA 342
DB 316 TTGACTACTGGGGCCAGAGAACTTGTGACCGTCTCTCTCA 357
```

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RESULT 15
US-10-530-27
; Sequence 27, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-530-27
```

```
Query Match 77.5%; Score 265.2; DB 16; Length 358;
Best Local Similarity 88.0%; Pred. No. 4.1e-76;
Matches 301; Conservative 0; Mismatches 38; Indels 3; Gaps 1;
```

```
QY 4 GAGTCTGGCCCGCAGAGCTGTGAAGCTTGCACAGACCCCTGCTCAGCTGGCTGTCT 63
DB 16 GAGTCGGGCCCGCAGAGCTGTGAAGCTTGCACAGACCCCTGCTCAGCTGTCTCT 75
QY 64 GCGCGCTCCATCCGACAGTGTGTACTACTGAGTTGATCCGCAACCCCAAGGAG 123
DB 76 GGTGGCTCCATCAACAGTGTGTACTACTGAGTTGATCCGCAACCCCAAGGAG 135
QY 124 GCGCTGAGTGAATTGGGTACATCTATCAAGTGGAAACCTTCAACAAACCCGCTC 183
DB 136 GCGCTGAGTGAATTGGGTACATCTATCAAGTGGAAACCTTCAACAAACCCGCTC 195
QY 184 AAGAGTGAATTGGCATGTGGTGAACAGCTGTGAACAGCTTCTCCCTAGGCTGAC 243
DB 196 AAGAGTGAATTGGCATGTGGTGAACAGCTGTGAACAGCTTCTCCCTAGGCTGAC 255
QY 244 TCTGTGACTGCGCGGACACGCGGTGATTACTGTGCGAG---GTTAGATGGCTACCT 300
DB 256 TCTGTGACTGCGCGGACACGCGGTGATTACTGTGCGAGATGGGAAACAGCTGCT 315
QY 301 TTGACATCTGGGGCCAGAGAACTTGTGACCGTCTCTCTCA 342
DB 316 TTGACTACTGGGGCCAGAGAACTTGTGACCGTCTCTCTCA 357
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